

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 03:12:21 ; Search time 2619 Seconds

(without alignments)  
10545.809 Million cell updates/sec

Title: US-09-989-731-407

Perfect score: 570

Sequence: 1 ggcgagcagcgggtataaaga.....aaaaaaaaaaaaaaaaaaaaa 570

Scoring table: IDENTITY\_NUC

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

GenBank1:\*  
1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sbs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	570	100.0	570	6	AR252648 Sequence
2	570	100.0	570	6	AX403520 Sequence
3	570	100.0	570	9	AY359064 Homo sapi
4	569	99.8	569	6	AX201348 Sequence
5	569	92.8	543	6	BD222719 Human sig
6	529	92.8	543	6	BD226775 A novel m
7	519	91.1	519	6	BD082142 Reagents
8	518.6	91.0	562	6	BD082141 Reagents
9	513	90.0	530	9	BC072673 Homo sapi
10	503	88.2	503	9	BC029176 Homo sapi
11	471	82.6	471	9	AF086152 Homo sapi
12	461	80.9	461	9	AF436839 Homo sapi
13	457.8	80.3	461	6	CQ76781 Sequence
14	457.8	80.3	461	6	AY040564 Homo sapi
15	345.4	60.6	347	9	AF313458 Homo sapi
16	293.4	51.1	291	6	CQ714558 Sequence
17	241.4	42.4	244	6	BD082138 Reagents
18	241.4	42.4	130129	2	AC108083 Homo sapi
19	241.4	42.4	130129	2	AC108083 Homo sapi

20	241.4	42.4	166777	2	AC106813 Homo sapi
21	241.4	42.4	168347	2	AC025336 Homo sapi
22	241.4	42.4	190024	4	AC122714 Homo sapi
23	230.4	40.4	127488	2	AC022095 Homo sapi
24	225	39.5	225	6	BD082137 Reagents
25	144	25.3	190	6	BD082137 Reagents
26	135.2	23.7	525	10	AF313456 Mus muscu
27	118	20.7	630	10	AF313457 Mus muscu
28	115.8	20.3	377	10	AF36840 Mus muscu
29	114	20.0	114	6	BD082140 Reagents
30	110.6	19.4	331	10	AF36841 Ratius no
31	93.6	16.4	245659	2	AC098957 Ratius no
32	93.6	16.4	283593	2	AC131433 Ratius no
33	91	16.0	254981	10	AL606479 Mouse DNA
34	75.6	13.3	130129	2	AC108083 Homo sapi
35	74.6	13.1	664	10	BC061046 Homo sapi
36	69.4	12.2	1613	6	E23142 Homo sapi
37	69	12.1	623	5	BC067658 Homo sapi
38	69	12.1	1898	6	146765 Sequence 1
39	68.8	12.1	1507	9	BC002839 Homo sapi
40	68.8	12.1	1519	9	BC064621 Homo sapi
41	68.8	12.1	1798	9	BC042845 Homo sapi
42	68.6	12.0	1791	9	BC036709 Homo sapi
43	68	11.9	862	6	AX575614 Sequence
44	67.4	11.8	566	6	BD260638 49 human
45	67.4	11.8	1451	9	BC002816 Homo sapi
46	67.4	11.8	2070	9	BC074500 Homo sapi
47	67.4	11.8	3819	5	BC076831 Xenopus t
48	67	11.8	733	6	CQ769552 Sequence
49	67	11.8	733	6	CQ769554 Sequence
50	67	11.8	820	9	BC000785 Homo sapi
51	67	11.8	880	9	AF207829 Homo sapi
52	66.6	11.7	9884	6	AX347361 Sequence
53	66.6	11.7	9884	6	AX349082 Sequence
54	66.6	11.7	9884	6	AX657761 Sequence
55	66.6	11.7	9884	6	AX659035 Sequence
56	66.4	11.6	678	9	BC003602 Homo sapi
57	66.4	11.6	3985	5	RNGPROCR
58	66.2	11.6	1398	10	BC084466 Homo sapi
59	66.2	11.6	1774	10	BC028989 Homo sapi
60	66.2	11.6	2799	10	BC054462 Homo sapi
61	66.2	11.6	4143	5	GSDYNACT
62	66	11.5	974	9	BC056410 Homo sapi
63	65.6	11.5	550	6	CO821498 Sequence
64	65.6	11.5	550	9	BC024232 Homo sapi
65	65.6	11.5	562	9	BC053376 Homo sapi
66	65.6	11.5	923	10	BC049576 Homo sapi
67	65.6	11.5	2805	9	BC025665 Homo sapi
68	65.6	11.5	2965	10	BC057094 Homo sapi
69	65.4	11.5	527	9	BC032235 Homo sapi
70	65.4	11.5	646	6	BD266891 Homo sapi
71	65.4	11.5	1723	6	AX816464 Sequence
72	65.4	11.5	1723	9	BC012944 Homo sapi
73	65.4	11.5	2532	5	BC055227 Danio rer
74	65.4	11.5	3462	9	BC032668 Homo sapi
75	65.2	11.4	141	6	AR425949 Sequence
76	65.2	11.4	141	6	AX986643 Sequence
77	65.2	11.4	141	6	BD121502 EST and e
78	65.2	11.4	681	5	BC055187 Homo sapi
79	65.2	11.4	1693	9	BC064214 Xenopus t
80	65.2	11.4	2146	9	BC039148 Homo sapi
81	65	11.4	140	6	AR425952 Sequence
82	65	11.4	140	6	AX986646 Sequence
83	65	11.4	140	6	BD121505 EST and e
84	65	11.4	148	6	AR425950 Sequence
85	65	11.4	148	6	AX986644 Sequence
86	65	11.4	148	6	AX986647 Sequence
87	65	11.4	148	6	BD121503 EST and e
88	65	11.4	148	6	BD121506 EST and e
89	65	11.4	153	6	AR425954 Sequence
90	65	11.4	153	6	AX986648 Sequence
91	65	11.4	153	6	BD121507 EST and e
92	65	11.4	153	6	BD121507 EST and e

93	65	11.4	861	9	AK026600	AK026600 Homo sapi	166	63	11.1	394	6	C0525359
94	65	11.4	1986	9	BC002948	BC002948 Homo sapi	167	63	11.1	407	5	BC073638
95	65	11.4	2090	9	BC037555	BC037555 Homo sapi	168	63	11.1	407	5	C0522526
96	65	11.4	17553	2	AP001096	AP001096 Homo sapi	169	63	11.1	562	10	BC049668
97	64.8	11.4	326	6	C0527450	C0527450 Sequence	170	63	11.1	893	5	BC077861
98	64.8	11.4	983	6	BC005007	BC005007 Homo sapi	171	63	11.1	1129	9	BC013587
99	64.8	11.4	1023	5	BC011708	BC011708 Homo sapi	172	63	11.1	1490	9	BC001236
100	64.8	11.4	1026	5	BC084480	BC084480 Homo sapi	173	63	11.1	1539	9	BC002372
101	64.8	11.4	1050	6	BD18576	BD18576 71 human	174	63	11.1	2239	3	AK16078
102	64.8	11.4	1390	6	BD260732	BD260732 50 human	175	63	11.1	2239	3	AK025573
103	64.8	11.4	3287	10	BC028272	BC028272 Mus muscu	176	63	11.1	2335	6	AX834748
104	64.8	11.4	3329	10	BC054371	BC054371 Mus muscu	177	63	11.1	2335	6	AX834748
105	64.6	11.3	159	6	AR425951	AR425951 Sequence	178	63	11.1	2385	5	BC072951
106	64.6	11.3	159	6	AX986645	AX986645 Sequence	179	63	11.1	2385	5	BC072951
107	64.6	11.3	159	6	BD121504	BD121504 EST and e	180	63	11.1	113541	2	AC023769
108	64.6	11.3	503	6	AX548518	AX548518 Sequence	181	62.8	11.0	315	6	AR423832
109	64.6	11.3	1718	10	AF411056	AF411056 Rattus no	182	62.8	11.0	315	6	AX984526
110	64.6	11.3	1868	10	BC032280	BC032280 Mus muscu	183	62.8	11.0	814	5	BC059599
111	64.4	11.3	1277	5	BC074288	BC074288 Xenopus l	184	62.8	11.0	1198	9	BC000051
112	64.4	11.3	2037	4	AF200416	AF200416 Equus cab	185	62.8	11.0	1586	10	BC000051
113	64.4	11.3	2037	9	BC001963	BC001963 Homo sapi	186	62.8	11.0	1730	9	BC048345
114	64.4	11.3	2037	9	BC001963	BC001963 Homo sapi	187	62.8	11.0	1730	9	BC048345
115	64.4	11.3	2526	5	BC001963	BC001963 Homo sapi	188	62.8	11.0	1843	9	BC038796
116	64.2	11.3	162345	2	AC147606	AC147606 Mus muscu	189	62.8	11.0	1894	10	BC039124
117	64.2	11.3	144	6	AX986649	AX986649 Sequence	190	62.8	11.0	2042	6	AX086394
118	64.2	11.3	144	6	BD121508	BD121508 EST and e	191	62.8	11.0	2139	2	AC146916
119	64.2	11.3	495	6	C0423520	C0423520 Sequence	192	62.8	11.0	2042	6	AX086394
120	64.2	11.3	1592	9	BC015787	BC015787 Homo sapi	193	62.8	11.0	2139	2	AC146916
121	64.2	11.3	2116	9	BC063648	BC063648 Homo sapi	194	62.6	11.0	337	6	C0526416
122	64.2	11.3	19398	2	AF028823	AF028823 Mus muscu	195	62.6	11.0	511	5	BC078541
123	64	11.2	1451	9	AF028823	AF028823 Homo sapi	196	62.6	11.0	587	6	BD275408
124	64	11.2	1554	9	BC010430	BC010430 Homo sapi	197	62.6	11.0	610	6	C0427732
125	64	11.2	1559	10	BC061634	BC061634 Mus muscu	198	62.6	11.0	1442	9	HSM807864
126	64	11.2	1590	10	BC072486	BC072486 Homo sapi	199	62.6	11.0	1760	10	BC027078
127	64	11.2	1599	9	BC071708	BC071708 Homo sapi	200	62.6	11.0	2302	9	BC002356
128	64	11.2	1888	9	BC033677	BC033677 Homo sapi	201	62.6	11.0	2311	6	AX779817
129	64	11.2	2158	9	AB043547	AB043547 Homo sapi	202	62.6	11.0	2311	6	AX779817
130	64	11.2	2158	9	BC033677	BC033677 Homo sapi	203	62.6	11.0	2311	6	AX779817
131	64	11.2	2158	9	BC033677	BC033677 Homo sapi	204	62.6	11.0	2311	6	AX779817
132	64	11.2	2158	9	BC033677	BC033677 Homo sapi	205	62.6	11.0	2311	6	AX779817
133	64	11.2	2158	9	BC033677	BC033677 Homo sapi	206	62.6	11.0	2311	6	AX779817
134	63.8	11.2	734	9	BC006465	BC006465 Homo sapi	207	62.6	11.0	2311	6	AX779817
135	63.8	11.2	1621	6	BD107842	BD107842 36 human	208	62.6	11.0	2311	6	AX779817
136	63.8	11.2	2936	5	BC007842	BC007842 Xenopus l	209	62.6	11.0	2311	6	AX779817
137	63.8	11.2	2951	9	HSM801417	HSM801417 Homo sapi	210	62.6	11.0	2311	6	AX779817
138	63.6	11.2	214442	10	AC126115	AC126115 Rattus no	211	62.6	11.0	2311	6	AX779817
139	63.6	11.2	449	6	C0423617	C0423617 Sequence	212	62.6	11.0	2311	6	AX779817
140	63.6	11.2	481	9	BC070219	BC070219 Homo sapi	213	62.6	11.0	2311	6	AX779817
141	63.6	11.2	1087	5	AY069454	AY069454 Drosophila	214	62.6	11.0	2311	6	AX779817
142	63.6	11.2	1090	3	AR083266	AR083266 Sequence	215	62.6	11.0	2311	6	AX779817
143	63.6	11.2	1307	6	BD092208	BD092208 Secreted	216	62.6	11.0	2311	6	AX779817
144	63.6	11.2	2465	5	BC0070798	BC0070798 Xenopus l	217	62.6	11.0	2311	6	AX779817
145	63.6	11.2	4750	5	BC066499	BC066499 Dantio rer	218	62.6	11.0	2311	6	AX779817
146	63.4	11.1	451	6	BD219559	BD219559 Human gen	219	62.6	11.0	2311	6	AX779817
147	63.4	11.1	1280	9	CQ467469	CQ467469 Sequence	220	62.6	11.0	2311	6	AX779817
148	63.4	11.1	1280	9	CQ467469	CQ467469 Sequence	221	62.6	11.0	2311	6	AX779817
149	63.4	11.1	1350	9	BC047312	BC047312 Homo sapi	222	62.6	11.0	2311	6	AX779817
150	63.4	11.1	1550	9	BC033613	BC033613 Mus muscu	223	62.6	11.0	2311	6	AX779817
151	63.4	11.1	1564	9	BC033613	BC033613 Mus muscu	224	62.6	11.0	2311	6	AX779817
152	63.4	11.1	2576	9	BC051833	BC051833 Homo sapi	225	62.6	11.0	2311	6	AX779817
153	63.4	11.1	3336	5	BC054630	BC054630 Dantio rer	226	62.6	11.0	2311	6	AX779817
154	63.4	11.1	6582	6	AX481755	AX481755 Sequence	227	62.6	11.0	2311	6	AX779817
155	63.2	11.1	446	9	BC065233	BC065233 Homo sapi	228	62.6	11.0	2311	6	AX779817
156	63.2	11.1	474	6	CQ523622	CQ523622 Sequence	229	62.6	11.0	2311	6	AX779817
157	63.2	11.1	598	6	CQ523622	CQ523622 Sequence	230	62.6	11.0	2311	6	AX779817
158	63.2	11.1	882	9	AK025483	AK025483 Sequence	231	62.6	11.0	2311	6	AX779817
159	63.2	11.1	1252	5	BC054251	BC054251 Homo sapi	232	62.6	11.0	2311	6	AX779817
160	63.2	11.1	1990	5	AK098817	AK098817 Homo sapi	233	62.6	11.0	2311	6	AX779817
161	63.2	11.1	2230	5	BC067188	BC067188 Dantio rer	234	62.6	11.0	2311	6	AX779817
162	63.2	11.1	6262	9	HSM807046	HSM807046 Homo sapi	235	62.6	11.0	2311	6	AX779817
163	63.2	11.1	161823	2	AC136947	AC136947 Homo sapi	236	62.6	11.0	2311	6	AX779817
164	63.2	11.1	218821	2	AC116238	AC116238 Rattus no	237	62.6	11.0	2311	6	AX779817
165	63.2	11.1	248529	2	AC097592	AC097592 Rattus no	238	62.6	11.0	2311	6	AX779817
							239	62.6	11.0	2311	6	AX779817
							240	62.6	11.0	2311	6	AX779817
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							251	62.6	11.0	2311	6	AX779817
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							253	62.6	11.0	2311	6	AX779817
							254	62.6	11.0	2311	6	AX779817
							255	62.6	11.0	2311	6	AX779817
							256	62.6	11.0	2311	6	AX779817
							257	62.6	11.0	2311	6	AX779817
							258	62.6	11.0	2311	6	AX779817
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							263	62.6	11.0	2311	6	AX779817
							264	62.6	11.0	2311	6	AX779817
							265	62.6	11.0	2311	6	AX779817

C 239	62.2	10.9	448	6	CQ411846	CQ411846 Sequence	312	61.8	10.8	1484	9	AY358586	AY358586 Homo sapi
C 240	62.2	10.9	550	6	COS24549	COS24549 Sequence	313	61.8	10.8	1739	9	AB060873	AB060873 Macaca fa
241	62.2	10.9	623	10	BC059150	BC059150 Rattus no	314	61.8	10.8	1740	9	BC072395	BC072395 Homo sapi
242	62.2	10.9	947	5	AP266204	AP266204 Glllichth	315	61.8	10.8	2076	10	BC010309	BC010309 Mus muscu
243	62.2	10.9	1100	5	BC082894	BC082894 Xenopus t	316	61.8	10.8	2082	6	AR059958	AR059958 Sequence
244	62.2	10.9	1422	5	BC080890	BC080890 Xenopus t	317	61.8	10.8	2093	6	AB089677	AB089677 Prunus pe
245	62.2	10.9	1537	9	BSM803079	AL713709 Homo sapi	318	61.8	10.8	2158	10	BC031195	BC031195 Mus muscu
246	62.2	10.9	1584	5	BC042270	BC042270 Xenopus t	319	61.8	10.8	2195	9	BC009484	BC009484 Homo sapi
247	62.2	10.9	1679	9	BC018747	BC018747 Homo sapi	320	61.8	10.8	2291	9	BSM803423	BSM803423 Homo sapi
248	62.2	10.9	1680	10	BC049920	BC049920 Mus muscu	321	61.8	10.8	2249	9	BC073963	BC073963 Homo sapi
249	62.2	10.9	1848	9	BC053543	BC053543 Homo sapi	322	61.8	10.8	2376	9	BC016664	BC016664 Homo sapi
250	62.2	10.9	1950	9	BC033818	BC033818 Homo sapi	323	61.8	10.8	3225	5	BC063722	BC063722 Xenopus t
251	62.2	10.9	1986	5	BC074553	BC074553 Xenopus t	324	61.8	10.8	3665	10	BC046598	BC046598 Mus muscu
252	62.2	10.9	1996	6	BC011143	BC011143 Homo sapi	325	61.8	10.8	3737	9	BC024592	BC024592 Homo sapi
253	62.2	10.9	2329	6	AR374711	AR374711 Sequence	326	61.8	10.8	3985	9	BC063876	BC063876 Homo sapi
254	62.2	10.9	2403	9	BC063892	BC063892 Homo sapi	C 327	61.8	10.8	184332	2	AC141745	AC141745 Apis mell
255	62.2	10.9	2448	9	BC053867	BC053867 Homo sapi	328	61.6	10.8	442	6	CQ524766	CQ524766 Sequence
256	62.2	10.9	2846	6	AR170129	AR170129 Sequence	329	61.6	10.8	458	6	CQ516306	CQ516306 Sequence
C 257	62.2	10.9	2836	6	AR170130	AR170130 Sequence	330	61.6	10.8	541	6	CQ522930	CQ522930 Sequence
258	62.2	10.9	2836	6	AR438727	AR438727 Sequence	331	61.6	10.8	887	9	AB125184	AB125184 Macaca fa
C 259	62.2	10.9	2836	6	AR438728	AR438728 Sequence	332	61.6	10.8	1237	9	BC058927	BC058927 Homo sapi
C 260	62.2	10.9	2836	6	BD069549	BD069549 Novel cat	333	61.6	10.8	1301	10	BC016453	BC016453 Mus muscu
C 261	62.2	10.9	2836	6	BD069550	BD069550 Novel car	334	61.6	10.8	1331	10	BC048735	BC048735 Mus muscu
C 262	62.2	10.9	3018	12	AY452085	AY452085 Cloning v	335	61.6	10.8	1490	9	BC050458	BC050458 Homo sapi
263	62.2	10.9	3141	9	BSM805106	AL833829 Homo sapi	336	61.6	10.8	1591	10	AF087943	AF087943 Homo sapi
264	62.2	10.9	3309	10	BC051423	BC051423 Mus muscu	337	61.6	10.8	1607	10	BC048697	BC048697 Mus muscu
265	62.2	10.9	3309	10	BSM803596	BSM803596 Homo sapi	338	61.6	10.8	1630	5	BC055215	BC055215 Dario rer
266	62.2	10.9	3836	9	BC063854	BC063854 Homo sapi	339	61.6	10.8	1594	9	BSM806665	BSM806665 Homo sapi
267	62.2	10.9	6085	10	BC053387	BC053387 Mus muscu	340	61.6	10.8	1760	9	BC025749	BC025749 Homo sapi
C 268	62.2	10.9	6255	6	AX346318	AX346318 Sequence	341	61.6	10.8	1779	10	BC062406	BC062406 Xenopus no
269	62.2	10.9	203822	2	AC087146	AC087146 Mus muscu	342	61.6	10.8	1849	5	BC080995	BC080995 Homo sapi
270	62.2	10.9	256673	2	AC087146	AC087146 Mus muscu	343	61.6	10.8	1925	5	BC066381	BC066381 Dario rer
271	62	10.9	166	6	CQ708897	CQ708897 Sequence	344	61.6	10.8	2117	9	BC024300	BC024300 Homo sapi
272	62	10.9	190	6	AR425287	AR425287 Sequence	345	61.6	10.8	2127	9	BC049687	BC049687 Sequence
273	62	10.9	190	6	AX985981	AX985981 Sequence	346	61.6	10.8	2368	9	BSM802593	BSM802593 Homo sapi
274	62	10.9	190	6	BD120840	BD120840 EST and e	347	61.6	10.8	2376	3	AK112359	AK112359 Clona int
275	62	10.9	216	6	COS25990	COS25990 Sequence	C 348	61.6	10.8	2795	8	CBKPMERN	CBKPMERN
276	62	10.9	246	6	AR422120	AR422120 Sequence	349	61.6	10.8	2843	6	CQ488472	CQ488472 Sequence
277	62	10.9	246	6	AX982814	AX982814 Sequence	350	61.6	10.8	2843	6	CQ488693	CQ488693 Sequence
278	62	10.9	246	6	BD117673	BD117673 EST and e	351	61.6	10.8	2843	6	CQ491011	CQ491011 Sequence
C 279	62	10.9	360	6	CQ529133	CQ529133 Sequence	352	61.6	10.8	2843	6	CQ491990	CQ491990 Sequence
280	62	10.9	534	9	BC011021	BC011021 Homo sapi	353	61.6	10.8	2843	6	CQ492097	CQ492097 Sequence
281	62	10.9	722	9	BC042671	BC042671 Homo sapi	354	61.6	10.8	2843	6	CQ492259	CQ492259 Sequence
282	62	10.9	854	5	BC080013	BC080013 Xenopus t	355	61.6	10.8	2843	6	CQ494303	CQ494303 Sequence
283	62	10.9	964	9	BC009341	BC009341 Homo sapi	356	61.6	10.8	2843	6	CQ494530	CQ494530 Sequence
284	62	10.9	985	6	BD134733	BD134733 31 Human	357	61.6	10.8	2843	6	CQ496867	CQ496867 Sequence
285	62	10.9	1603	9	BC015756	BC015756 Homo sapi	358	61.6	10.8	2843	6	CQ497898	CQ497898 Sequence
286	62	10.9	1627	9	BC002519	BC002519 Homo sapi	359	61.6	10.8	2843	6	CQ498011	CQ498011 Sequence
287	62	10.9	1816	5	BC055610	BC055610 Dario rer	360	61.6	10.8	3050	5	AB125660	AB125660 Gallus ga
288	62	10.9	1935	9	BSM802519	AL161995 Homo sapi	361	61.6	10.8	3092	9	BC050377	BC050377 Homo sapi
289	62	10.9	2138	10	BC035945	BC035945 Mus muscu	362	61.6	10.8	3607	5	BC075569	BC075569 Xenopus t
290	62	10.9	2175	5	AB056480	AB056480 Rana cate	363	61.6	10.8	3683	9	BSM808647	BSM808647 Homo sapi
291	62	10.9	2847	10	BC006874	BC006874 Mus muscu	364	61.6	10.8	4168	6	AX393305	AX393305 Sequence
292	62	10.9	3154	10	BC027028	BC027028 Mus muscu	365	61.6	10.8	5277	9	BSM807015	BSM807015 Homo sapi
293	62	10.9	3459	6	AX348086	AX348086 Sequence	366	61.6	10.8	126290	2	AC099483	AC099483 Sequence
294	62	10.9	3459	6	AX348086	AX348086 Sequence	367	61.6	10.8	239	6	CQ524654	CQ524654 Sequence
295	62	10.9	152252	2	AC147683	AC147683 Pan trogl	368	61.4	10.8	257	6	AX334682	AX334682 Sequence
296	62	10.9	333321	3	AC116986	AC116986 Dictyoste	369	61.4	10.8	257	6	AX410615	AX410615 Sequence
297	61.8	10.8	447	10	BC055352	BC055352 Mus muscu	370	61.4	10.8	383	5	BC076322	BC076322 Dario rer
298	61.8	10.8	527	9	AK026542	AK026542 Homo sapi	371	61.4	10.8	457	10	BC064074	BC064074 Mus muscu
299	61.8	10.8	539	6	CQ655454	CQ655454 Sequence	372	61.4	10.8	505	6	CQ524936	CQ524936 Sequence
300	61.8	10.8	599	6	CQ626750	CQ626750 Sequence	373	61.4	10.8	571	8	AY554050	AY554050 Oryza sat
301	61.8	10.8	739	6	CQ769575	CQ769575 Sequence	374	61.4	10.8	762	3	LINE512840	LINE512840 Lethoceru
302	61.8	10.8	739	6	CQ769591	CQ769591 Sequence	375	61.4	10.8	775	9	BC056238	BC056238 Homo sapi
303	61.8	10.8	739	6	CQ769608	CQ769608 Sequence	C 376	61.4	10.8	794	6	BD018939	BD018939 Novel gen
C 304	61.8	10.8	754	6	BD018741	BD018741 Novel gen	377	61.4	10.8	794	6	BD098877	BD098877 Novel gen
C 305	61.8	10.8	754	6	BD098679	BD098679 Novel gen	378	61.4	10.8	1181	10	BC0049768	BC0049768 Mus muscu
C 306	61.8	10.8	835	10	AP260436	AP260436 Rattus no	379	61.4	10.8	1234	10	BC007381	BC007381 Homo sapi
307	61.8	10.8	1261	9	BC073957	BC073957 Homo sapi	380	61.4	10.8	1245	5	BC058310	BC058310 Dario rer
308	61.8	10.8	1476	6	BD227281	BD227281 Secretd	381	61.4	10.8	1316	5	BSM801735	BSM801735 Homo sapi
309	61.8	10.8	1484	6	AR252570	AR252570 Sequence	382	61.4	10.8	1554	5	AF065135	AF065135 Xenopus t
310	61.8	10.8	1484	6	AX376152	AX376152 Sequence	383	61.4	10.8	1554	6	BD132843	BD132843 W545 com
311	61.8	10.8	1484	6	AX403405	AX403405 Sequence	384	61.4	10.8	1554	6	CQ776558	CQ776558 Sequence

385	61.4	10.8	1554	9	AP285836	AP285836 Homo sapi	C 458	61	10.7	352	6	CQ529009	CQ529009 Sequence
386	61.4	10.8	1567	5	AB050540	AB050540 Xenopus t	C 459	61	10.7	438	6	CQ410292	CQ410292 Sequence
387	61.4	10.8	1590	5	BC041172	BC041172 Homo sapi	460	61	10.7	772	6	BD191024	BD191024 Secreted
388	61.4	10.8	1606	9	BC052258	BC052258 Homo sapi	461	61	10.7	1023	6	IC114145	IC114145 Sequence
389	61.4	10.8	1606	9	BC065488	BC065488 Homo sapi	462	61	10.7	1032	5	BC004937	BC004937 Homo sapi
390	61.4	10.8	1606	9	BC084560	BC084560 Homo sapi	463	61	10.7	1315	5	BC084499	BC084499 Xenopus t
391	61.4	10.8	1656	6	BD140460	BD140460 Secreted	464	61	10.7	1318	9	AY358200	AY358200 Homo sapi
392	61.4	10.8	1777	9	HSMB02904	AL512705 Homo sapi	465	61	10.7	1394	6	A07588	A07588 Synthetic H
393	61.4	10.8	1788	9	BC044944	BC044944 Homo sapi	466	61	10.7	1469	10	BC066218	BC066218 Mus muscu
394	61.4	10.8	1790	10	BC024638	BC024638 Mus muscu	467	61	10.7	1504	10	BC066801	BC066801 Mus muscu
395	61.4	10.8	1976	9	BC031663	BC031663 Homo sapi	468	61	10.7	1651	6	AR374741	AR374741 Sequence
396	61.4	10.8	1993	9	BC063485	BC063485 Homo sapi	469	61	10.7	1661	9	BC025753	BC025753 Homo sapi
397	61.4	10.8	1997	9	BC027903	BC027903 Homo sapi	470	61	10.7	1683	5	BC054553	BC054553 Homo sapi
398	61.4	10.8	2015	10	BC051455	BC051455 Mus muscu	471	61	10.7	1746	5	BC057744	BC057744 Xenopus t
399	61.4	10.8	2335	5	BC077539	BC077539 Xenopus t	472	61	10.7	1853	9	BC015202	BC015202 Homo sapi
400	61.4	10.8	2460	10	BC036985	BC036985 Mus muscu	473	61	10.7	1885	9	HSMB08768	HSMB08768 Homo sapi
401	61.4	10.8	2486	9	BC018702	BC018702 Homo sapi	474	61	10.7	1910	9	HSMB07435	HSMB07435 Homo sapi
402	61.4	10.8	2533	9	BC048282	BC048282 Homo sapi	475	61	10.7	1958	9	BC035369	BC035369 Homo sapi
403	61.4	10.8	2635	9	BC053869	BC053869 Homo sapi	476	61	10.7	1960	9	BC007355	BC007355 Homo sapi
404	61.4	10.8	2647	9	HSMB05697	BC053739 Homo sapi	477	61	10.7	2070	10	BC040774	BC040774 Mus muscu
405	61.4	10.8	2683	10	BC052924	BC052924 Mus muscu	478	61	10.7	2160	5	BC064874	BC064874 Xenopus t
406	61.4	10.8	2826	6	AX061719	AX061719 Sequence	479	61	10.7	2192	5	BC063223	BC063223 Xenopus t
407	61.4	10.8	2850	6	AX061719	AX061719 Sequence	480	61	10.7	2240	5	BC056309	BC056309 Danio rer
408	61.4	10.8	2968	6	AX061719	AX061719 Sequence	481	61	10.7	2328	9	BC028034	BC028034 Homo sapi
409	61.4	10.8	3049	10	BC046626	BC046626 Mus muscu	482	61	10.7	2380	9	BC003548	BC003548 Homo sapi
410	61.4	10.8	3282	10	BC080851	BC080851 Mus muscu	483	61	10.7	2427	9	AK000310	AK000310 Homo sapi
411	61.4	10.8	3303	10	BC080851	BC080851 Mus muscu	484	61	10.7	2431	10	BC026582	BC026582 Homo sapi
412	61.4	10.8	3546	10	BC058225	BC058225 Mus muscu	485	61	10.7	2460	10	BC028943	BC028943 Mus muscu
413	61.4	10.8	4479	10	BC051015	BC051015 Mus muscu	486	61	10.7	2484	9	AB066558	AB066558 Macaca fa
C 414	61.4	10.8	4399	10	AC116984_5	Continuation (6 of	487	61	10.7	2517	6	BD275916	BD275916 Uncoupln
C 415	61.4	10.8	55877	2	AC087300	AC087300 Homo sapi	488	61	10.7	2536	10	BC013637	BC013637 Homo sapi
C 416	61.4	10.8	153365	2	AC125271	AC125271 Mus muscu	489	61	10.7	2626	6	BC062618	BC062618 Homo sapi
C 417	61.2	10.7	789	6	BD241945	BD241945 Compounds	490	61	10.7	2923	10	BC062109	BC062109 Mus muscu
C 418	61.2	10.7	789	6	AR237128	AR237128 Sequence	491	61	10.7	3334	6	AX925268	AX925268 Sequence
C 419	61.2	10.7	789	6	AR237128	AR237128 Sequence	492	61	10.7	3334	6	AX925268	AX925268 Sequence
C 420	61.2	10.7	789	6	AR237128	AR237128 Sequence	493	61	10.7	3334	6	AX925268	AX925268 Sequence
C 421	61.2	10.7	789	6	AR237128	AR237128 Sequence	494	61	10.7	3334	6	AX925268	AX925268 Sequence
C 422	61.2	10.7	789	6	AR237128	AR237128 Sequence	495	61	10.7	3334	6	AX925268	AX925268 Sequence
C 423	61.2	10.7	789	6	AR237128	AR237128 Sequence	496	61	10.7	3334	6	AX925268	AX925268 Sequence
C 424	61.2	10.7	789	6	AR237128	AR237128 Sequence	497	61	10.7	3334	6	AX925268	AX925268 Sequence
C 425	61.2	10.7	789	6	AR237128	AR237128 Sequence	498	61	10.7	3334	6	AX925268	AX925268 Sequence
C 426	61.2	10.7	789	6	AR237128	AR237128 Sequence	499	61	10.7	3334	6	AX925268	AX925268 Sequence
C 427	61.2	10.7	789	6	AR237128	AR237128 Sequence	500	61	10.7	3334	6	AX925268	AX925268 Sequence
C 428	61.2	10.7	789	6	AR237128	AR237128 Sequence	501	61	10.7	3334	6	AX925268	AX925268 Sequence
C 429	61.2	10.7	789	6	AR237128	AR237128 Sequence	502	61	10.7	3334	6	AX925268	AX925268 Sequence
C 430	61.2	10.7	789	6	AR237128	AR237128 Sequence	503	61	10.7	3334	6	AX925268	AX925268 Sequence
C 431	61.2	10.7	789	6	AR237128	AR237128 Sequence	504	61	10.7	3334	6	AX925268	AX925268 Sequence
C 432	61.2	10.7	789	6	AR237128	AR237128 Sequence	505	61	10.7	3334	6	AX925268	AX925268 Sequence
C 433	61.2	10.7	789	6	AR237128	AR237128 Sequence	506	61	10.7	3334	6	AX925268	AX925268 Sequence
C 434	61.2	10.7	789	6	AR237128	AR237128 Sequence	507	61	10.7	3334	6	AX925268	AX925268 Sequence
C 435	61.2	10.7	789	6	AR237128	AR237128 Sequence	508	61	10.7	3334	6	AX925268	AX925268 Sequence
C 436	61.2	10.7	789	6	AR237128	AR237128 Sequence	509	61	10.7	3334	6	AX925268	AX925268 Sequence
C 437	61.2	10.7	789	6	AR237128	AR237128 Sequence	510	61	10.7	3334	6	AX925268	AX925268 Sequence
C 438	61.2	10.7	789	6	AR237128	AR237128 Sequence	511	61	10.7	3334	6	AX925268	AX925268 Sequence
C 439	61.2	10.7	789	6	AR237128	AR237128 Sequence	512	61	10.7	3334	6	AX925268	AX925268 Sequence
C 440	61.2	10.7	789	6	AR237128	AR237128 Sequence	513	61	10.7	3334	6	AX925268	AX925268 Sequence
C 441	61.2	10.7	789	6	AR237128	AR237128 Sequence	514	61	10.7	3334	6	AX925268	AX925268 Sequence
C 442	61.2	10.7	789	6	AR237128	AR237128 Sequence	515	61	10.7	3334	6	AX925268	AX925268 Sequence
C 443	61.2	10.7	789	6	AR237128	AR237128 Sequence	516	61	10.7	3334	6	AX925268	AX925268 Sequence
C 444	61.2	10.7	789	6	AR237128	AR237128 Sequence	517	61	10.7	3334	6	AX925268	AX925268 Sequence
C 445	61.2	10.7	789	6	AR237128	AR237128 Sequence	518	61	10.7	3334	6	AX925268	AX925268 Sequence
C 446	61.2	10.7	789	6	AR237128	AR237128 Sequence	519	61	10.7	3334	6	AX925268	AX925268 Sequence
C 447	61.2	10.7	789	6	AR237128	AR237128 Sequence	520	61	10.7	3334	6	AX925268	AX925268 Sequence
C 448	61.2	10.7	789	6	AR237128	AR237128 Sequence	521	61	10.7	3334	6	AX925268	AX925268 Sequence
C 449	61.2	10.7	789	6	AR237128	AR237128 Sequence	522	61	10.7	3334	6	AX925268	AX925268 Sequence
C 450	61.2	10.7	789	6	AR237128	AR237128 Sequence	523	61	10.7	3334	6	AX925268	AX925268 Sequence
C 451	61.2	10.7	789	6	AR237128	AR237128 Sequence	524	61	10.7	3334	6	AX925268	AX925268 Sequence
C 452	61.2	10.7	789	6	AR237128	AR237128 Sequence	525	61	10.7	3334	6	AX925268	AX925268 Sequence
C 453	61.2	10.7	789	6	AR237128	AR237128 Sequence	526	61	10.7	3334	6	AX925268	AX925268 Sequence
C 454	61.2	10.7	789	6	AR237128	AR237128 Sequence	527	61	10.7	3334	6	AX925268	AX925268 Sequence
C 455	61.2	10.7	789	6	AR237128	AR237128 Sequence	528	61	10.7	3334	6	AX925268	AX925268 Sequence
C 456	61.2	10.7	789	6	AR237128	AR237128 Sequence	529	61	10.7	3334	6	AX925268	AX925268 Sequence
C 457	61.2	10.7	789	6	AR237128	AR237128 Sequence	530	61	10.7	3334	6	AX925268	AX925268 Sequence



531	60.8	10.7	1779	6	AX251708	AX251708 Sequence	604	60.6	10.6	2820	6	CQ776753	CQ776753 Sequence
532	60.8	10.7	1882	10	BC017147	BC017147 Mus muscu	605	60.6	10.6	2820	9	BC025256	BC025256 Homo sapi
533	60.8	10.7	2084	10	BC058744	BC058744 Mus muscu	606	60.6	10.6	2968	10	BC058408	BC058408 Mus muscu
534	60.8	10.7	2084	10	BC062164	BC062164 Mus muscu	607	60.6	10.6	3099	10	BC055299	BC055299 Mus muscu
535	60.8	10.7	2116	9	BC031644	BC031644 Homo sapi	608	60.6	10.6	3581	9	BC038669	BC038669 Homo sapi
536	60.8	10.7	2131	6	AX364833	AX364833 Sequence	609	60.6	10.6	3724	9	HSM804529	HSM804529 Homo sapi
537	60.8	10.7	2173	9	BC063384	BC063384 Homo sapi	610	60.6	10.6	5135	10	BC061470	BC061470 Mus muscu
538	60.8	10.7	2533	5	BC064702	BC064702 Danio rer	611	60.6	10.6	6250	9	HSM807742	HSM807742 Homo sapi
539	60.8	10.7	2600	10	BC037001	BC037001 Mus muscu	612	60.6	10.6	6559	5	BC063724	BC063724 Xenopus 1
540	60.8	10.7	2628	9	BC034992	BC034992 Homo sapi	c 613	60.4	10.6	306	6	CQ423767	CQ423767 Sequence
541	60.8	10.7	3180	10	S79832	S79832 tianscripti	614	60.4	10.6	397	6	CQ517563	CQ517563 Sequence
542	60.8	10.7	3508	6	BD227241	BD227241 Secretd	c 615	60.4	10.6	407	6	CQ528868	CQ528868 Sequence
543	60.8	10.7	4128	10	AF022263	AF022263 Mus muscu	616	60.4	10.6	449	6	CQ526770	CQ526770 Sequence
544	60.8	10.7	4259	9	HSM805206	AL833900 Homo sapi	617	60.4	10.6	657	10	BC035943	BC035943 Mus muscu
545	60.8	10.7	6200	9	AF324064	AF324064 Homo sapi	c 618	60.4	10.6	731	6	CQ431866	CQ431866 Sequence
546	60.8	10.7	70705	2	AC101621	AC101621 Mus muscu	c 619	60.4	10.6	722	6	CQ431102	CQ431102 Sequence
547	60.8	10.7	153657	2	AC087145	AC087145 Mus muscu	620	60.4	10.6	792	10	BC006585	BC006585 Mus muscu
548	60.8	10.7	171260	2	CR812474	CR812474 Danio rer	621	60.4	10.6	944	9	BC018640	BC018640 Homo sapi
c 549	60.8	10.7	218010	2	AC116052	AC116052 Mus muscu	622	60.4	10.6	1048	3	AY069195	AY069195 Drosophill
c 550	60.8	10.7	223920	2	AC141733	AC141733 Apls mell	623	60.4	10.6	1051	9	BC070489	BC070489 Homo sapi
551	60.6	10.6	188	6	AR418867	AR418867 Sequence	624	60.4	10.6	1115	10	BC049678	BC049678 Mus muscu
552	60.6	10.6	188	6	AX979561	AX979561 Sequence	625	60.4	10.6	1358	9	AF022813	AF022813 Homo sapi
553	60.6	10.6	188	6	BD114420	BD114420 EST and e	626	60.4	10.6	1454	5	BC064706	BC064706 Danio rer
554	60.6	10.6	201	11	BV202595	BV202595 sqm20945	627	60.4	10.6	1524	5	BC067624	BC067624 Danio rer
555	60.6	10.6	267	6	CQ526755	CQ526755 Sequence	628	60.4	10.6	1561	9	AF217966	AF217966 Homo sapi
556	60.6	10.6	447	9	AK026855	AK026855 Homo sapi	629	60.4	10.6	1595	9	BC035626	BC035626 Homo sapi
557	60.6	10.6	458	10	BC061002	BC061002 Mus muscu	630	60.4	10.6	1627	10	BC043926	BC043926 Mus muscu
558	60.6	10.6	640	3	BT001518	BT001518 Drosophill	631	60.4	10.6	1630	9	BC029864	BC029864 Homo sapi
559	60.6	10.6	700	9	BC035864	BC035864 Homo sapi	632	60.4	10.6	1638	10	BC030439	BC030439 Mus muscu
560	60.6	10.6	766	6	I08319	I08319 Sequence 1	633	60.4	10.6	1702	10	BC057136	BC057136 Homo sapi
561	60.6	10.6	789	9	BC017112	BC017112 Homo sapi	634	60.4	10.6	1731	9	BC064395	BC064395 Mus muscu
562	60.6	10.6	805	10	BC063183	BC063183 Rattus no	635	60.4	10.6	1731	9	BC001554	BC001554 Homo sapi
563	60.6	10.6	860	6	BD260192	BD260192 50 human	636	60.4	10.6	1851	10	BC017684	BC017684 Mus muscu
564	60.6	10.6	1076	9	BC050446	BC050446 Homo sapi	637	60.4	10.6	1879	10	BC060146	BC060146 Mus muscu
565	60.6	10.6	1091	6	AR271010	AR271010 Sequence	638	60.4	10.6	1919	10	BC057964	BC057964 Mus muscu
566	60.6	10.6	1091	6	AX053122	AX053122 Sequence	639	60.4	10.6	1968	10	BC075618	BC075618 Mus muscu
567	60.6	10.6	1155	5	BC074027	BC074027 Danio rer	640	60.4	10.6	1956	9	HSM808069	HSM808069 Homo sapi
568	60.6	10.6	1157	6	BD233739	BD233739 31 human	641	60.4	10.6	2113	10	BC012405	BC012405 Homo sapi
569	60.6	10.6	1175	9	BC049386	BC049386 Homo sapi	642	60.4	10.6	2156	3	AK116789	AK116789 Mus muscu
570	60.6	10.6	1194	9	BC016139	BC016139 Homo sapi	643	60.4	10.6	2351	9	AB063077	AB063077 Mecaca fa
571	60.6	10.6	1234	6	AX092332	AX092332 Sequence	644	60.4	10.6	2701	9	HSM807920	HSM807920 Homo sapi
572	60.6	10.6	1234	6	AX376170	AX376170 Sequence	645	60.4	10.6	2722	9	HSM806004	HSM806004 Homo sapi
573	60.6	10.6	1234	9	AY358438	AY358438 Homo sapi	646	60.4	10.6	2739	10	BC055303	BC055303 Mus muscu
574	60.6	10.6	1339	9	BC048255	BC048255 Homo sapi	647	60.4	10.6	2990	10	AF185576	AF185576 Mus muscu
575	60.6	10.6	1445	5	BC020080	BC020080 Mus muscu	648	60.4	10.6	3204	10	BC075680	BC075680 Mus muscu
576	60.6	10.6	1480	5	BC066516	BC066516 Danio rer	649	60.4	10.6	3264	9	HSM805112	HSM805112 Homo sapi
577	60.6	10.6	1505	5	BC067601	BC067601 Danio rer	650	60.4	10.6	3327	10	BC028908	BC028908 Mus muscu
578	60.6	10.6	1638	10	BC057896	BC057896 Mus muscu	651	60.4	10.6	3520	9	BC037406	BC037406 Homo sapi
579	60.6	10.6	1643	10	BC008512	BC008512 Mus muscu	652	60.4	10.6	4077	5	BC075104	BC075104 Xenopus t
580	60.6	10.6	1684	9	BC034406	BC034406 Homo sapi	653	60.4	10.6	4452	9	BC051768	BC051768 Homo sapi
581	60.6	10.6	1788	5	BC084147	BC084147 Xenopus t	654	60.4	10.6	4857	10	BC030187	BC030187 Mus muscu
582	60.6	10.6	1807	10	BC081928	BC081928 Rattus no	655	60.4	10.6	5076	9	AB062750	AB062750 Homo sapi
583	60.6	10.6	1842	10	BC025589	BC025589 Mus muscu	656	60.4	10.6	5630	9	HSM806073	HSM806073 Homo sapi
584	60.6	10.6	1866	9	HSM800618	AL080110 Homo sapi	657	60.4	10.6	6702	9	AF378756	AF378756 Homo sapi
585	60.6	10.6	1904	9	HSM807438	BX647294 Homo sapi	c 658	60.4	10.6	130701	2	AC009889	AC009889 Homo sapi
586	60.6	10.6	1953	9	BC029049	BC029049 Homo sapi	c 659	60.4	10.6	160237	2	AC149065	AC149065 Mus muscu
587	60.6	10.6	1983	9	BC019338	BC019338 Homo sapi	c 660	60.4	10.6	175069	2	AC140895	AC140895 Homo sapi
588	60.6	10.6	2000	6	BD252089	BD252089 47 secrete	661	60.4	10.6	175785	2	AC016773	AC016773 Homo sapi
589	60.6	10.6	2040	5	BC026408	BC026408 Danio rer	662	60.4	10.6	189223	9	AC013897	AC013897 Homo sapi
590	60.6	10.6	2060	6	AR310262	AR310262 Sequence	663	60.4	10.6	202705	2	AC149065	AC149065 Mus muscu
591	60.6	10.6	2070	10	BC052830	BC052830 Mus muscu	664	60.4	10.6	211419	2	AC126760	AC126760 Homo sapi
592	60.6	10.6	2207	9	BC058880	BC058880 Homo sapi	c 665	60.4	10.6	235330	2	AC140522	AC140522 Homo sapi
593	60.6	10.6	2239	9	BC015555	BC015555 Homo sapi	c 666	60.4	10.6	291000	1	SC0939105	SC0939105 Streptomy
594	60.6	10.6	2307	9	BC032410	BC032410 Homo sapi	c 667	60.4	10.6	349980	6	AX344554	AX344554 Sequence
595	60.6	10.6	2320	9	BC033810	BC033810 Homo sapi	c 668	60.4	10.6	349980	6	AX344555	AX344555 Sequence
596	60.6	10.6	2403	9	HSM808752	BX648601 Homo sapi	669	60.2	10.6	153	6	CQ700107	CQ700107 Sequence
597	60.6	10.6	2429	9	BC001056	BC001056 Homo sapi	670	60.2	10.6	176	6	AR422406	AR422406 Sequence
598	60.6	10.6	2439	9	BC001823	BC001823 Homo sapi	671	60.2	10.6	176	6	AX983100	AX983100 Sequence
599	60.6	10.6	2438	10	BC075617	BC075617 Mus muscu	672	60.2	10.6	176	6	BD117959	BD117959 EST and e
600	60.6	10.6	2480	5	BC072229	BC072229 Xenopus 1	673	60.2	10.6	231	6	CQ526354	CQ526354 Sequence
601	60.6	10.6	2485	10	BC064470	BC064470 Mus muscu	674	60.2	10.6	261	6	CQ524617	CQ524617 Sequence
602	60.6	10.6	2514	9	BC044863	BC044863 Homo sapi	675	60.2	10.6	291	6	CQ488160	CQ488160 Sequence
603	60.6	10.6	2792	10	AF177401	AF177401 Spermophi	676	60.2	10.6	413	6	CQ517947	CQ517947 Sequence

677	60.2	10.6	471	6	COS22475	750	60.2	10.6	3308	9	BC035009	BC035009 Homo sapi
678	60.2	10.6	507	6	COS21478	751	60.2	10.6	3309	5	BC068420	BC068420 Danto rer
679	60.2	10.6	514	10	BC061178	752	60.2	10.6	3455	5	BC056871	BC056871 Homo sapi
680	60.2	10.6	515	6	COS26571	753	60.2	10.6	3492	5	BC078645	BC078645 Danto rer
681	60.2	10.6	527	6	COS27201	754	60.2	10.6	3830	5	BC071560	BC071560 Homo sapi
682	60.2	10.6	541	9	BC021886	755	60.2	10.6	4028	3	AF003106	AF003106 Homo sapi
683	60.2	10.6	542	9	BC040713	756	60.2	10.6	4135	9	HSM801979	ALJ3765 Homo sapi
684	60.2	10.6	556	6	COS23722	757	60.2	10.6	4660	6	AX211375	AX211375 Sequence
685	60.2	10.6	713	10	BC002008	758	60.2	10.6	4697	4	BTHROW2	X96540 B. laurus mr
686	60.2	10.6	806	9	BC071709	759	60.2	10.6	5137	10	BC065082	BC065082 Mus muscu
687	60.2	10.6	869	3	BT011554	760	60.2	10.6	5534	6	AX780181	AX780181 Sequence
688	60.2	10.6	903	3	AY118755	761	60.2	10.6	5536	10	BC060705	BC060705 Mus muscu
689	60.2	10.6	910	10	BC069266	762	60.2	10.6	5539	10	BC049182	BC049182 Mus muscu
690	60.2	10.6	1000	10	BC064816	763	60.2	10.6	163018	10	AC132254	AC132254 Mus muscu
691	60.2	10.6	1029	5	AK174142	764	60.2	10.6	189728	10	AC140223	AC140223 Mus muscu
692	60.2	10.6	1087	9	BC015905	765	60.2	10.6	267093	2	AC109408	AC109408 Rattus no
693	60.2	10.6	1092	10	BC005748	766	60.2	10.6	292100	1	SC093121	SC093121 Sequence
694	60.2	10.6	1104	6	AF047611	767	60.2	10.5	60	6	COS25290	COS25290 Sequence
695	60.2	10.6	1104	6	BD215254	768	60.2	10.5	155	5	COS22591	COS22591 Sequence
696	60.2	10.6	1164	6	AX098194	769	60.2	10.5	185	6	AX425282	AX425282 Sequence
697	60.2	10.6	1178	6	BD275922	770	60.2	10.5	185	6	AX985976	AX985976 Sequence
698	60.2	10.6	1208	4	AB090246	771	60.2	10.5	185	6	BD120835	BD120835 Sequence
699	60.2	10.6	1320	5	BC067193	772	60.2	10.5	201	11	BV200252	BV200252 Sequence
700	60.2	10.6	1320	5	BC067193	773	60.2	10.5	251	6	BD213305	BD213305 Novel hum
701	60.2	10.6	1510	5	BC037352	774	60.2	10.5	357	6	COS24729	COS24729 Sequence
702	60.2	10.6	1546	9	BC076399	775	60.2	10.5	357	6	COS24729	COS24729 Sequence
703	60.2	10.6	1572	9	BC044227	776	60.2	10.5	396	6	COS41648	COS41648 Sequence
704	60.2	10.6	1579	9	BC002809	777	60.2	10.5	418	6	COS26599	COS26599 Sequence
705	60.2	10.6	1697	10	AP165267	778	60.2	10.5	437	6	COS27330	COS27330 Sequence
706	60.2	10.6	1717	5	BC055558	779	60.2	10.5	442	6	COS502790	COS502790 Sequence
707	60.2	10.6	1718	9	BC073809	780	60.2	10.5	442	6	COS11647	COS11647 Sequence
708	60.2	10.6	1719	9	BC017498	781	60.2	10.5	484	6	COS27337	COS27337 Sequence
709	60.2	10.6	1722	9	BC047320	782	60.2	10.5	549	9	BC045165	BC045165 Homo sapi
710	60.2	10.6	1723	5	BC053112	783	60.2	10.5	559	9	BC043570	BC043570 Homo sapi
711	60.2	10.6	1769	6	BD205071	784	60.2	10.5	559	9	BC055580	BC055580 Danto rer
712	60.2	10.6	1769	6	BD205071	785	60.2	10.5	757	3	AY241961	AY241961 Demarcant
713	60.2	10.6	1769	6	AX014095	786	60.2	10.5	768	6	CQ432402	CQ432402 Sequence
714	60.2	10.6	1769	6	AX014203	787	60.2	10.5	814	10	RATPHGP	124896 Rattus norv
715	60.2	10.6	1877	10	BC064057	788	60.2	10.5	825	6	CQ430950	CQ430950 Sequence
716	60.2	10.6	1920	10	BC061765	789	60.2	10.5	873	6	AX780227	AX780227 Sequence
717	60.2	10.6	1928	9	BC014402	790	60.2	10.5	874	6	CQ414670	CQ414670 Sequence
718	60.2	10.6	1928	9	BC041625	791	60.2	10.5	875	9	BC001470	BC001470 Homo sapi
719	60.2	10.6	1930	9	BC062575	792	60.2	10.5	896	9	BC002491	BC002491 Homo sapi
720	60.2	10.6	1999	9	BC020684	793	60.2	10.5	1044	10	BC049565	BC049565 Mus muscu
721	60.2	10.6	2010	6	BD270044	794	60.2	10.5	1046	9	BC032585	BC032585 Homo sapi
722	60.2	10.6	2030	9	BC041637	795	60.2	10.5	1244	5	BC057444	BC057444 Homo sapi
723	60.2	10.6	2030	9	BC062592	796	60.2	10.5	1258	5	BC047862	BC047862 Danto rer
724	60.2	10.6	2088	9	BC001045	797	60.2	10.5	1263	6	AX546767	AX546767 Sequence
725	60.2	10.6	2089	6	CQ774671	798	60.2	10.5	1290	9	BC002975	BC002975 Homo sapi
726	60.2	10.6	2089	9	BC016840	799	60.2	10.5	1325	6	AR034830	AR034830 Sequence
727	60.2	10.6	2220	9	AF132730	800	60.2	10.5	1325	6	CQ875289	CQ875289 Sequence
728	60.2	10.6	2225	9	AB063079	801	60.2	10.5	1325	6	196214	196214 Sequence
729	60.2	10.6	2295	9	BC062628	802	60.2	10.5	1325	6	AX587540	AX587540 Sequence
730	60.2	10.6	2351	9	HSM80373	803	60.2	10.5	1325	6	AX695354	AX695354 Sequence
731	60.2	10.6	2369	9	BC051841	804	60.2	10.5	1325	6	BD079952	BD079952 Use relat
732	60.2	10.6	2409	9	AK074384	805	60.2	10.5	1325	6	HDMCYCD1	M63349 Human cycli
733	60.2	10.6	2409	9	BC034925	806	60.2	10.5	1423	10	109360	109360 Sequence
734	60.2	10.6	2446	9	BC039899	807	60.2	10.5	1470	10	BC082085	BC082085 Rattus no
735	60.2	10.6	2614	9	BC042629	808	60.2	10.5	1521	5	BC031399	BC031399 Homo sapi
736	60.2	10.6	2664	10	AY438023	809	60.2	10.5	1521	5	BC067689	BC067689 Danto rer
737	60.2	10.6	2699	9	AY438023	810	60.2	10.5	1625	9	BC004314	BC004314 Homo sapi
738	60.2	10.6	2699	10	CO801981	811	60.2	10.5	1625	9	AF089818	AF089818 Mus muscu
739	60.2	10.6	2725	5	BC077764	812	60.2	10.5	1625	10	BC033451	BC033451 Mus muscu
740	60.2	10.6	2809	9	BC032502	813	60.2	10.5	1633	10	BC024405	BC024405 Mus muscu
741	60.2	10.6	2872	10	BC045090	814	60.2	10.5	1633	10	BC057688	BC057688 Mus muscu
742	60.2	10.6	2920	5	BC063008	815	60.2	10.5	1749	9	BC052099	BC052099 Homo sapi
743	60.2	10.6	2953	5	AT719439	816	60.2	10.5	1842	9	AK026885	AK026885 Homo sapi
744	60.2	10.6	2989	9	HSM807541	817	60.2	10.5	1905	9	BC032703	BC032703 Homo sapi
745	60.2	10.6	3019	10	BC064821	818	60.2	10.5	1910	9	BC043519	BC043519 Homo sapi
746	60.2	10.6	3121	5	BC007903	819	60.2	10.5	1935	9	BC015582	BC015582 Homo sapi
747	60.2	10.6	3144	5	BC068213	820	60.2	10.5	1964	6	AX795328	AX795328 Sequence
748	60.2	10.6	3172	9	BC027998	821	60.2	10.5				
749	60.2	10.6	3220	9	BC064576	822	60.2	10.5				

823	60	10.5	2084	5	BC080960	BC080960 Xenopus t	896	59.8	10.5	1073	10	BC035490	BC035490 Mus muscu
824	60	10.5	2166	5	BC082654	BC082654 Xenopus 1	897	59.8	10.5	1091	9	BC044230	BC044230 Homo sapi
825	60	10.5	2293	9	BC043566	BC043566 Homo sapi	898	59.8	10.5	1092	9	BC064140	BC064140 Homo sapi
826	60	10.5	2296	9	BC044946	BC044946 Homo sapi	899	59.8	10.5	1116	9	BC039532	BC039532 Homo sapi
827	60	10.5	2247	9	BC025927	BC025927 Homo sapi	900	59.8	10.5	1126	9	BC009010	BC009010 Homo sapi
828	60	10.5	2489	10	BC031749	BC031749 Mus muscu	901	59.8	10.5	1152	6	BD191482	BD191482 Secretd
829	60	10.5	2649	9	BC063539	BC063539 Homo sapi	902	59.8	10.5	1171	9	AF245689	AF245689 Homo sapi
830	60	10.5	2776	9	BSM803693	AL832385 Homo sapi	903	59.8	10.5	1302	4	AF244915	AF244915 Canis fam
831	60	10.5	2849	9	BC027241	BC027241 Homo sapi	904	59.8	10.5	1302	6	BD211567	BD211567 Canine an
832	60	10.5	2977	9	BC067260	BC067260 Homo sapi	905	59.8	10.5	1302	6	BD211568	BD211568 Canine an
833	60	10.5	3010	6	AX358754	AX358754 Sequence	c 906	59.8	10.5	1302	6	AR241545	AR241545 Sequence
834	60	10.5	3010	6	AX362247	AX362247 Sequence	c 907	59.8	10.5	1302	6	AR241546	AR241546 Sequence
835	60	10.5	3010	6	AX358753	AX358753 Homo sapi	c 908	59.8	10.5	1302	6	AR254501	AR254501 Sequence
836	60	10.5	3072	3	AK116778	AK116778 Homo sapi	c 909	59.8	10.5	1302	6	AR254502	AR254502 Sequence
837	60	10.5	3067	10	BC081948	BC081948 Rattus no	c 910	59.8	10.5	1307	6	BC023632	BC023632 Homo sapi
838	60	10.5	3567	10	BC057551	BC057551 Mus muscu	911	59.8	10.5	1319	6	AX337799	AX337799 Sequence
839	60	10.5	3606	9	AY078404	AY078404 Homo sapi	912	59.8	10.5	1319	6	AX779892	AX779892 Sequence
840	60	10.5	3625	10	BC064810	BC064810 Mus muscu	913	59.8	10.5	1319	6	HMTRNSAL	HMTRNSAL Homo sapien
841	60	10.5	3658	9	BSM803139	AL831825 Homo sapi	914	59.8	10.5	1330	10	BC061713	BC061713 Rattus no
842	60	10.5	3669	9	BSM805593	AL834206 Homo sapi	915	59.8	10.5	1359	10	MUSHAP7GB	MUSHAP7GB Homo sapi
843	60	10.5	3702	9	BC071612	BC071612 Homo sapi	916	59.8	10.5	1371	9	BC005805	BC005805 Homo sapi
844	60	10.5	3797	5	BC063922	BC063922 Xenopus t	917	59.8	10.5	1455	10	BC062408	BC062408 Homo sapi
845	60	10.5	3844	10	BC056587	BC056587 Mus muscu	918	59.8	10.5	1480	5	BC062383	BC062383 Homo sapi
846	60	10.5	3851	9	BC035812	BC035812 Homo sapi	919	59.8	10.5	1516	6	E02253	E02253 human 'A my
847	60	10.5	3993	10	BC060090	BC060090 Mus muscu	920	59.8	10.5	1525	10	BC048821	BC048821 Mus muscu
848	60	10.5	4017	10	BC066066	BC066066 Mus muscu	921	59.8	10.5	1562	3	AK115546	AK115546 Homo sapi
849	60	10.5	4631	10	BC057342	BC057342 Mus muscu	922	59.8	10.5	1606	9	BSM800215	BSM800215 Homo sapi
850	60	10.5	88306	8	NCEBTK22	AL670543 Neurospor	923	59.8	10.5	1607	9	BC025369	BC025369 Homo sapi
c 851	60	10.5	193802	2	AC021133	AC021133 Homo sapi	924	59.8	10.5	1622	9	BC075857	BC075857 Homo sapi
852	60	10.5	292420	2	AC020873	AC020873 Mus muscu	925	59.8	10.5	1631	10	BC048821	BC048821 Mus muscu
853	59.8	10.5	135	6	AR419590	AR419590 Sequence	926	59.8	10.5	1635	9	BC017004	BC017004 Homo sapi
854	59.8	10.5	135	6	AX980284	AX980284 Sequence	927	59.8	10.5	1640	9	BC032422	BC032422 Homo sapi
855	59.8	10.5	135	6	BD115143	BD115143 EST and e	928	59.8	10.5	1641	9	BC017444	BC017444 Homo sapi
856	59.8	10.5	142	6	AR419304	AR419304 Sequence	929	59.8	10.5	1643	9	BC050730	BC050730 Homo sapi
857	59.8	10.5	142	6	AX979998	AX979998 Sequence	930	59.8	10.5	1658	5	BC047845	BC047845 Homo sapi
858	59.8	10.5	146	6	BD114857	BD114857 EST and e	931	59.8	10.5	1662	9	BSM805109	BSM805109 Homo sapi
859	59.8	10.5	160	6	AR418838	AR418838 Sequence	932	59.8	10.5	1663	9	BC006481	BC006481 Homo sapi
860	59.8	10.5	160	6	AX979532	AX979532 Sequence	933	59.8	10.5	1666	9	BC001128	BC001128 Homo sapi
861	59.8	10.5	160	6	BD114391	BD114391 EST and e	934	59.8	10.5	1711	10	RNH10SH1	X70685 R. norvegicu
862	59.8	10.5	163	6	AR418111	AR418111 Sequence	935	59.8	10.5	1768	9	BC073828	BC073828 Homo sapi
863	59.8	10.5	163	6	AX978805	AX978805 Sequence	936	59.8	10.5	1783	5	AF203473	AF203473 Salvelinu
864	59.8	10.5	163	6	BD113664	BD113664 EST and e	937	59.8	10.5	1795	5	BC064225	BC064225 Xenopus t
c 865	59.8	10.5	198	6	AX080530	AX080530 Sequence	938	59.8	10.5	1811	6	CO414890	CO414890 Sequence
866	59.8	10.5	220	6	CO488023	CO488023 Sequence	939	59.8	10.5	1820	9	BC065221	BC065221 Homo sapi
867	59.8	10.5	241	6	CO525819	CO525819 Sequence	940	59.8	10.5	1849	5	BC061396	BC061396 Homo sapi
868	59.8	10.5	274	6	CO522575	CO522575 Sequence	941	59.8	10.5	1897	5	BC049511	BC049511 Danio rer
869	59.8	10.5	304	6	CO487552	CO487552 Sequence	942	59.8	10.5	1920	3	AY061375	AY061375 Drosophill
870	59.8	10.5	315	6	CO517813	CO517813 Sequence	943	59.8	10.5	1942	10	BC071268	BC071268 Mus muscu
871	59.8	10.5	338	6	CO522686	CO522686 Sequence	944	59.8	10.5	1950	9	BC028206	BC028206 Homo sapi
c 872	59.8	10.5	360	6	CO427909	CO427909 Sequence	945	59.8	10.5	1990	9	AK000212	AK000212 Homo sapi
873	59.8	10.5	425	6	CO524522	CO524522 Sequence	946	59.8	10.5	2005	9	BSM803426	BSM803426 Homo sapi
874	59.8	10.5	479	9	BC040728	BC040728 Homo sapi	947	59.8	10.5	2054	9	BC058863	BC058863 Homo sapi
875	59.8	10.5	485	10	BC022770	BC022770 Mus muscu	948	59.8	10.5	2090	9	BC020565	BC020565 Homo sapi
c 876	59.8	10.5	541	6	CO411393	CO411393 Sequence	949	59.8	10.5	2127	5	BC071276	BC071276 Danio rer
877	59.8	10.5	589	10	BC002135	BC002135 Mus muscu	950	59.8	10.5	2170	9	AK074292	AK074292 Homo sapi
878	59.8	10.5	607	5	BC049055	BC049055 Danio rer	951	59.8	10.5	2174	10	BC004798	BC004798 Mus muscu
c 879	59.8	10.5	608	6	CO410246	CO410246 Sequence	952	59.8	10.5	2183	9	BC025699	BC025699 Homo sapi
c 880	59.8	10.5	664	6	CO378668	CO378668 Sequence	953	59.8	10.5	2208	10	BC052921	BC052921 Mus muscu
c 881	59.8	10.5	664	6	CO403965	CO403965 Sequence	954	59.8	10.5	2211	9	BC033795	BC033795 Homo sapi
882	59.8	10.5	716	9	BC044236	BC044236 Homo sapi	955	59.8	10.5	2220	5	BC067610	BC067610 Danio rer
883	59.8	10.5	732	6	BD191101	BD191101 186 human	956	59.8	10.5	2332	9	BSM803479	BSM803479 Homo sapi
884	59.8	10.5	732	6	AX924611	AX924611 Sequence	957	59.8	10.5	2366	9	BC017481	BC017481 Homo sapi
885	59.8	10.5	760	6	CO497632	CO497632 Sequence	958	59.8	10.5	2420	9	BC072670	BC072670 Homo sapi
886	59.8	10.5	780	5	BC076636	BC076636 Xenopus t	959	59.8	10.5	2435	6	AX780077	AX780077 Sequence
887	59.8	10.5	791	8	OSA004966	AJ0004966 Oryza sat	960	59.8	10.5	2446	9	BSM808753	BSM808753 Homo sapi
888	59.8	10.5	812	6	E15569	E15569 CDNA encodi	961	59.8	10.5	2475	3	AY296116	AY296116 Ixodes sc
889	59.8	10.5	812	6	AR222758	AR222758 Sequence	962	59.8	10.5	2522	10	BC065005	BC065005 Mus muscu
890	59.8	10.5	827	10	BC049739	BC049739 Mus muscu	963	59.8	10.5	2531	9	BC027040	BC027040 Homo sapi
891	59.8	10.5	883	10	BC049726	BC049726 Mus muscu	964	59.8	10.5	2534	10	BC066224	BC066224 Mus muscu
c 892	59.8	10.5	886	11	BV175306	BV175306 sqgm/8236	965	59.8	10.5	2575	6	BD140638	BD140638 36 human
c 893	59.8	10.5	911	9	BC004926	BC004926 Homo sapi	966	59.8	10.5	2575	6	AR409293	AR409293 Sequence
c 894	59.8	10.5	1066	6	AX285241	AX285241 Sequence	967	59.8	10.5	2584	6	BD140660	BD140660 36 human
895	59.8	10.5	1071	9	BC046244	BC046244 Homo sapi	968	59.8	10.5	2584	6	AR409315	AR409315 Sequence

969	59.8	10.5	2590	9	BC047315	1042	59.6	10.5	578	9	BC003052	BC003052 Homo sapi
970	59.8	10.5	2604	9	BC032396	c1043	59.6	10.5	645	9	CQ397628	CQ397628 Sequence
971	59.8	10.5	2652	3	AK174388	c1044	59.6	10.5	645	6	CQ403927	CQ403927 Sequence
972	59.8	10.5	2681	10	BC064454	1045	59.6	10.5	651	10	BC038494	BC038494 Mus muscu
973	59.8	10.5	2713	9	BC021912	1046	59.6	10.5	716	9	BC015172	BC015172 Homo sapi
974	59.8	10.5	2756	10	BC025980	1047	59.6	10.5	814	10	BC025933	BC025933 Mus muscu
975	59.8	10.5	2840	10	BC052769	1048	59.6	10.5	847	9	BC053571	BC053571 Mus muscu
976	59.8	10.5	2859	10	BC031850	1049	59.6	10.5	882	6	AR487879	AR487879 Homo sapi
977	59.8	10.5	2880	6	BD270054	1050	59.6	10.5	901	5	BC082363	BC082363 Mus muscu
978	59.8	10.5	2964	6	AR564552	1051	59.6	10.5	924	6	CQ769319	CQ769319 Sequence
979	59.8	10.5	2979	9	BSM803101	1052	59.6	10.5	1024	9	BSM806312	BSM806312 Homo sapi
980	59.8	10.5	2979	9	BSM803101	1053	59.6	10.5	1107	9	BC042635	BC042635 Homo sapi
981	59.8	10.5	3110	9	BSM803101	1054	59.6	10.5	1117	9	BC040937	BC040937 Homo sapi
982	59.8	10.5	3166	10	BC068331	1055	59.6	10.5	1137	3	AK116124	AK116124 Homo sapi
983	59.8	10.5	3186	5	BC068331	1056	59.6	10.5	1198	8	AR244677	AR244677 Sequence
984	59.8	10.5	3197	5	BC054582	1057	59.6	10.5	1198	8	AR244677	AR244677 Sequence
985	59.8	10.5	3197	5	BC054582	1058	59.6	10.5	1198	8	AR244677	AR244677 Sequence
986	59.8	10.5	3211	10	BC055403	1059	59.6	10.5	1198	8	AR244677	AR244677 Sequence
987	59.8	10.5	3216	9	BC070047	1060	59.6	10.5	1198	8	AR244677	AR244677 Sequence
988	59.8	10.5	3230	10	BC070047	1061	59.6	10.5	1198	8	AR244677	AR244677 Sequence
989	59.8	10.5	3245	9	BSM805849	1062	59.6	10.5	1198	8	AR244677	AR244677 Sequence
990	59.8	10.5	3260	10	BSM805849	1063	59.6	10.5	1198	8	AR244677	AR244677 Sequence
991	59.8	10.5	3273	10	BC023693	1064	59.6	10.5	1198	8	AR244677	AR244677 Sequence
992	59.8	10.5	3298	9	BC015928	1065	59.6	10.5	1198	8	AR244677	AR244677 Sequence
993	59.8	10.5	3371	9	AR453583	1066	59.6	10.5	1198	8	AR244677	AR244677 Sequence
994	59.8	10.5	3390	9	BC042068	1067	59.6	10.5	1198	8	AR244677	AR244677 Sequence
995	59.8	10.5	3421	10	BC067203	1068	59.6	10.5	1198	8	AR244677	AR244677 Sequence
996	59.8	10.5	3425	5	BC072233	1069	59.6	10.5	1198	8	AR244677	AR244677 Sequence
997	59.8	10.5	3596	9	BSM806341	1070	59.6	10.5	1198	8	AR244677	AR244677 Sequence
998	59.8	10.5	3596	9	BSM806341	1071	59.6	10.5	1198	8	AR244677	AR244677 Sequence
999	59.8	10.5	3788	10	BC022120	1072	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1000	59.8	10.5	3824	10	BSM805271	1073	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1001	59.8	10.5	3890	10	BSM805271	1074	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1002	59.8	10.5	4218	9	BSM807520	1075	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1003	59.8	10.5	4329	9	BC071579	1076	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1004	59.8	10.5	4407	10	BC048185	1077	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1005	59.8	10.5	4430	5	BC059794	1078	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1006	59.8	10.5	4513	10	BC057791	1079	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1007	59.8	10.5	4726	9	BC051030	1080	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1008	59.8	10.5	4755	10	BC054543	1081	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1009	59.8	10.5	4759	5	BC047162	1082	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1010	59.8	10.5	4915	5	HSZPHSL2	1083	59.6	10.5	1198	8	AR244677	AR244677 Sequence
1011	59.8	10.5	4915	5	HSZPHSL2	1084	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1012	59.8	10.5	8177	9	BSM805964	1085	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1013	59.8	10.5	8571	14	AB049089	1086	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1014	59.8	10.5	161375	2	AC068715	1087	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1015	59.8	10.5	163550	2	AC134958	1088	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1016	59.8	10.5	167741	10	AC124434	1089	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1017	59.8	10.5	169003	2	AC074197	1090	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1018	59.8	10.5	171834	10	AC145432	1091	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1019	59.8	10.5	182694	2	AC145595	1092	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1020	59.8	10.5	183648	3	AC112891	1093	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1021	59.8	10.5	184603	10	AC117081	1094	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1022	59.8	10.5	195802	2	AC121851	1095	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1023	59.8	10.5	216194	10	AC096051	1096	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1024	59.8	10.5	2252504	2	AC073815	1097	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1025	59.8	10.5	262198	2	AC106703	1098	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1026	59.6	10.5	112	6	BD190560	1099	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1027	59.6	10.5	112	6	BD190560	1100	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1028	59.6	10.5	112	6	BD190560	1101	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1029	59.6	10.5	112	6	BD190560	1102	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1030	59.6	10.5	112	6	BD190560	1103	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1031	59.6	10.5	112	6	BD190560	1104	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1032	59.6	10.5	112	6	BD190560	1105	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1033	59.6	10.5	112	6	BD190560	1106	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1034	59.6	10.5	112	6	BD190560	1107	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1035	59.6	10.5	112	6	BD190560	1108	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1036	59.6	10.5	112	6	BD190560	1109	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1037	59.6	10.5	112	6	BD190560	1110	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1038	59.6	10.5	112	6	BD190560	1111	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1039	59.6	10.5	112	6	BD190560	1112	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1040	59.6	10.5	112	6	BD190560	1113	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1041	59.6	10.5	112	6	BD190560	1114	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1042	59.6	10.5	112	6	BD190560	1115	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1043	59.6	10.5	112	6	BD190560	1116	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1044	59.6	10.5	112	6	BD190560	1117	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1045	59.6	10.5	112	6	BD190560	1118	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1046	59.6	10.5	112	6	BD190560	1119	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1047	59.6	10.5	112	6	BD190560	1120	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1048	59.6	10.5	112	6	BD190560	1121	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1049	59.6	10.5	112	6	BD190560	1122	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1050	59.6	10.5	112	6	BD190560	1123	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1051	59.6	10.5	112	6	BD190560	1124	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1052	59.6	10.5	112	6	BD190560	1125	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1053	59.6	10.5	112	6	BD190560	1126	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1054	59.6	10.5	112	6	BD190560	1127	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1055	59.6	10.5	112	6	BD190560	1128	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1056	59.6	10.5	112	6	BD190560	1129	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1057	59.6	10.5	112	6	BD190560	1130	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1058	59.6	10.5	112	6	BD190560	1131	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1059	59.6	10.5	112	6	BD190560	1132	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1060	59.6	10.5	112	6	BD190560	1133	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1061	59.6	10.5	112	6	BD190560	1134	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1062	59.6	10.5	112	6	BD190560	1135	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1063	59.6	10.5	112	6	BD190560	1136	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1064	59.6	10.5	112	6	BD190560	1137	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1065	59.6	10.5	112	6	BD190560	1138	59.6	10.5	1198	8	AR244677	AR244677 Sequence
c1066	59.6	10.5	112	6	BD190560	1139	59.6	10.5	1198	8	AR244677	

1115	59.4	10.4	146	6	AX385892	AX985892 Sequence	1188	59.4	10.4	2789	10	BC050830	BC050830 Mus muscu
1116	59.4	10.4	146	6	BD120742	BD120742 EST and e	1189	59.4	10.4	2841	10	BC045601	BC045601 Mus muscu
1117	59.4	10.4	146	6	BD120751	BD120751 EST and e	1190	59.4	10.4	2851	10	BC021117	BC021117 Homo sapi
1118	59.4	10.4	169	6	AR419752	AR419752 Sequence	1191	59.4	10.4	3004	9	BC064983	BC064983 Homo sapi
1119	59.4	10.4	169	6	AX980446	AX980446 Sequence	1192	59.4	10.4	3080	6	AR183238	AR183238 Sequence
1120	59.4	10.4	169	6	BD153305	BD153305 EST and e	1193	59.4	10.4	3080	6	AR205638	AR205638 Sequence
1121	59.4	10.4	179	6	AR418078	AR418078 Sequence	1194	59.4	10.4	3080	6	AR241240	AR241240 Sequence
1122	59.4	10.4	179	6	AX978772	AX978772 Sequence	1195	59.4	10.4	3080	6	AR256256	AR256256 Sequence
1123	59.4	10.4	179	6	BD113631	BD113631 EST and e	1196	59.4	10.4	3080	6	AR391603	AR391603 Sequence
1124	59.4	10.4	201	11	BV204551	BV204551 sqmm21558	1197	59.4	10.4	3080	6	AX082223	AX082223 Sequence
1125	59.4	10.4	237	6	AX284920	AX284920 Sequence	1198	59.4	10.4	3080	6	BD124002	BD124002 Novel mol
1126	59.4	10.4	244	6	AX201931	AX201931 Sequence	1199	59.4	10.4	3121	6	AX046405	AX046405 Sequence
1127	59.4	10.4	299	6	C0526545	C0526545 Sequence	1200	59.4	10.4	3143	9	BC014305	BC014305 Sequence
1128	59.4	10.4	341	6	C0522918	C0522918 Sequence	1201	59.4	10.4	3642	10	BC053385	BC053385 Mus muscu
1129	59.4	10.4	364	3	AF163972	AF163972 Taenia so	1202	59.4	10.4	3660	9	BC035683	BC035683 Sequence
1130	59.4	10.4	372	3	AF216695	AF216695 Taenia so	1203	59.4	10.4	4142	10	BC053026	BC053026 Sequence
1131	59.4	10.4	372	10	BC027531	BC027531 Mus muscu	1204	59.4	10.4	4158	9	HSW805995	HSW805995 Homo sapi
1132	59.4	10.4	383	6	C0525716	C0525716 Sequence	1205	59.4	10.4	4438	10	BC067016	BC067016 Sequence
1133	59.4	10.4	450	10	BC083104	BC083104 Mus muscu	1206	59.4	10.4	5309	6	HSW805828	HSW805828 Sequence
1134	59.4	10.4	476	6	C0410349	C0410349 Sequence	1207	59.4	10.4	6059	6	AX345714	AX345714 Sequence
1135	59.4	10.4	550	10	BC024397	BC024397 Mus muscu	1208	59.4	10.4	6577	6	AX351920	AX351920 Sequence
1136	59.4	10.4	664	6	BD231009	BD231009 49 human	1209	59.4	10.4	6577	6	AX346258	AX346258 Sequence
1137	59.4	10.4	664	6	AR337304	AR337304 Sequence	1210	59.4	10.4	6577	6	AX348993	AX348993 Sequence
1138	59.4	10.4	761	6	BD019227	BD019227 Novel gen	1211	59.4	10.4	7930	9	HSW808084	HSW808084 Sequence
1139	59.4	10.4	761	6	BD099165	BD099165 Novel gen	1212	59.4	10.4	87865	2	AC008477	AC008477 Homo sapi
1140	59.4	10.4	868	9	BC065714	BC065714 Homo sapi	1213	59.4	10.4	110000	3	AC116984_2	AC116984_2 Contnuation (3 of
1141	59.4	10.4	956	9	BC003637	BC003637 Homo sapi	1214	59.4	10.4	112643	2	AC009187	AC009187 Homo sapi
1142	59.4	10.4	965	6	C0776429	C0776429 Sequence	1215	59.4	10.4	118119	10	AL807243	AL807243 Mouse DNA
1143	59.4	10.4	996	10	BC032292	BC032292 Mus muscu	1216	59.4	10.4	166555	2	AC141826	AC141826 Apis mell
1144	59.4	10.4	1001	10	BC049605	BC049605 Mus muscu	1217	59.4	10.4	167120	10	AC110178	AC110178 Mus muscu
1145	59.4	10.4	1019	5	BC084449	BC084449 Xenopus t	1218	59.4	10.4	168721	9	AC136431	AC136431 Homo sapi
1146	59.4	10.4	1029	9	BC029872	BC029872 Homo sapi	1219	59.4	10.4	170861	2	AC025658	AC025658 Homo sapi
1147	59.4	10.4	1080	9	BC022354	BC022354 Homo sapi	1220	59.4	10.4	173113	2	AC138962	AC138962 Homo sapi
1148	59.4	10.4	1083	5	BC061302	BC061302 Xenopus t	1221	59.4	10.4	195740	2	AC141269	AC141269 Homo sapi
1149	59.4	10.4	1119	9	BC070137	BC070137 Homo sapi	1222	59.4	10.4	235592	2	AC110436	AC110436 Rattus no
1150	59.4	10.4	1131	9	BC004252	BC004252 Homo sapi	1223	59.4	10.4	244215	2	AC095004	AC095004 Rattus no
1151	59.4	10.4	1202	3	AY122189	AY122189 Drosophil	1224	59.4	10.4	250565	2	CR318655	CR318655 Dario rer
1152	59.4	10.4	1222	9	AF110329	AF110329 Homo sapi	1225	59.4	10.4	252504	2	AC073815	AC073815 Mus muscu
1153	59.4	10.4	1255	9	BC042461	BC042461 Homo sapi	1226	59.2	10.4	154	6	AX381214	AX381214 Sequence
1154	59.4	10.4	1259	6	E03348	E03348 CDNA sequen	1227	59.2	10.4	165	6	AR416630	AR416630 Sequence
1155	59.4	10.4	1358	5	BC044957	BC044957 Xenopus t	1228	59.2	10.4	165	6	AX977324	AX977324 Sequence
1156	59.4	10.4	1375	10	RN2P3PROT	Y10823 Rattus ratt	1229	59.2	10.4	165	6	BD112183	BD112183 EST and e
1157	59.4	10.4	1388	3	AY069347	AY069347 Drosophil	1230	59.2	10.4	176	6	C0527241	C0527241 Sequence
1158	59.4	10.4	1416	9	AF090943	AF090943 Homo sapi	1231	59.2	10.4	204	6	C0525707	C0525707 Sequence
1159	59.4	10.4	1426	5	BC054250	BC054250 Xenopus t	1232	59.2	10.4	209	6	C0525608	C0525608 Sequence
1160	59.4	10.4	1449	3	BT011495	BT011495 Drosophil	1233	59.2	10.4	212	6	C0677317	C0677317 Sequence
1161	59.4	10.4	1680	5	BC056749	BC056749 Dario rer	1234	59.2	10.4	224	6	C0526058	C0526058 Sequence
1162	59.4	10.4	1688	10	BC005523	BC005523 Mus muscu	1235	59.2	10.4	252	6	C0526702	C0526702 Sequence
1163	59.4	10.4	1692	5	BC045295	BC045295 Dario rer	1236	59.2	10.4	258	6	AR423856	AR423856 Sequence
1164	59.4	10.4	1733	10	BC083553	BC083553 Rattus no	1237	59.2	10.4	258	6	AX984550	AX984550 Sequence
1165	59.4	10.4	1749	10	BC046612	BC046612 Mus muscu	1238	59.2	10.4	258	6	BD119409	BD119409 EST and e
1166	59.4	10.4	1820	6	AX593406	AX593406 Sequence	1239	59.2	10.4	265	6	C0526081	C0526081 Sequence
1167	59.4	10.4	1831	6	BC080902	BC080902 Xenopus t	1240	59.2	10.4	267	6	C0410745	C0410745 Sequence
1168	59.4	10.4	1831	6	C0498497	C0498497 Sequence	1241	59.2	10.4	268	6	C0525997	C0525997 Sequence
1169	59.4	10.4	1844	6	C0412894	C0412894 Sequence	1242	59.2	10.4	268	6	C0526263	C0526263 Sequence
1170	59.4	10.4	1938	10	BC079260	BC079260 Rattus no	1243	59.2	10.4	274	6	C0526796	C0526796 Sequence
1171	59.4	10.4	1962	9	BC058882	BC058882 Homo sapi	1244	59.2	10.4	284	6	C0526203	C0526203 Sequence
1172	59.4	10.4	1999	9	BC006527	BC006527 Homo sapi	1245	59.2	10.4	284	6	C0526722	C0526722 Sequence
1173	59.4	10.4	2042	9	AK027146	AK027146 Homo sapi	1246	59.2	10.4	312	6	C0525834	C0525834 Sequence
1174	59.4	10.4	2051	6	AX780311	AX780311 Sequence	1247	59.2	10.4	323	6	C0524910	C0524910 Sequence
1175	59.4	10.4	2054	6	AX663299	AX663299 Sequence	1248	59.2	10.4	356	6	C0517353	C0517353 Sequence
1176	59.4	10.4	2130	10	BC062005	BC062005 Rattus no	1249	59.2	10.4	380	6	C0526811	C0526811 Sequence
1177	59.4	10.4	2155	9	BC056757	BC056757 Homo sapi	1250	59.2	10.4	391	6	C0524976	C0524976 Sequence
1178	59.4	10.4	2161	9	AB063084	AB063084 Macaca fa	1251	59.2	10.4	401	6	C0522425	C0522425 Sequence
1179	59.4	10.4	2195	9	BC042607	BC042607 Homo sapi	1252	59.2	10.4	402	6	C0411023	C0411023 Sequence
1180	59.4	10.4	2195	9	BC044936	BC044936 Homo sapi	1253	59.2	10.4	410	10	BC044054	BC044054 Mus muscu
1181	59.4	10.4	2235	9	BC017301	BC017301 Homo sapi	1254	59.2	10.4	426	9	HSW802848	HSW802848 Sequence
1182	59.4	10.4	2236	9	BC000317	BC000317 Homo sapi	1255	59.2	10.4	433	6	C0526050	C0526050 Sequence
1183	59.4	10.4	2230	9	BC036827	BC036827 Homo sapi	1256	59.2	10.4	436	6	C0522487	C0522487 Sequence
1184	59.4	10.4	2252	9	AB063071	AB063071 Macaca fa	1257	59.2	10.4	437	6	C0520397	C0520397 Sequence
1185	59.4	10.4	2570	10	BC037607	BC037607 Mus muscu	1258	59.2	10.4	444	6	BC002750	BC002750 Homo sapi
1186	59.4	10.4	2581	9	BC031820	BC031820 Homo sapi	1259	59.2	10.4	448	6	C0525199	C0525199 Sequence
1187	59.4	10.4	2584	9	HSW808543	EX648395 Homo sapi	1260	59.2	10.4	453	6	C0526678	C0526678 Sequence

1261	59.2	10.4	458	9	BSM806076	1334	59.2	10.4	2884	9	BSM807509	1406	59	10.4	1162	8	MMHRCBSA	MX6146 R. norvegicus
1262	59.2	10.4	476	6	CQ526175	1335	59.2	10.4	3021	9	BC033086	1405	59	10.4	1157	9	BC063544	BC030517 Homo sapi
1263	59.2	10.4	489	6	CQ524523	1336	59.2	10.4	3084	9	BC025782	1404	59	10.4	1139	9	BC030517	BC030517 Homo sapi
1264	59.2	10.4	490	6	CQ526663	1337	59.2	10.4	3255	5	BC068362	1403	59	10.4	1111	5	AP143806	AP143806 Gallus ga
1265	59.2	10.4	509	6	CQ522420	1338	59.2	10.4	3255	5	BC068362	1402	59	10.4	1060	5	AX053130	AX053130 Sequence
1266	59.2	10.4	510	6	CQ526266	1339	59.2	10.4	3479	9	BSM800673	1401	59	10.4	1059	6	AX053130	AX053130 Sequence
1267	59.2	10.4	532	6	CQ526534	1340	59.2	10.4	3532	9	BSM807375	1400	59	10.4	1044	5	BSM806003	BSM806003 Homo sapi
1268	59.2	10.4	541	6	BC038211	1341	59.2	10.4	3558	10	BC031301	1399	59	10.4	1032	8	AP043538	AP043538 Homo sapi
1269	59.2	10.4	549	6	CQ526150	1342	59.2	10.4	3559	9	BSM807375	1398	59	10.4	1014	6	AX070947	AX070947 Sequence
C1270	59.2	10.4	566	6	CQ410439	1343	59.2	10.4	4064	6	AR526951	1397	59	10.4	1011	6	AX070947	AX070947 Sequence
1271	59.2	10.4	579	6	CQ526139	1344	59.2	10.4	4295	10	AP4338405	1396	59	10.4	1011	6	AX070947	AX070947 Sequence
1272	59.2	10.4	585	6	CQ526139	1345	59.2	10.4	4295	10	AP4338405	1395	59	10.4	1011	6	AX070947	AX070947 Sequence
1273	59.2	10.4	627	10	BC061005	1346	59.2	10.4	4518	10	BSM805210	1394	59	10.4	942	6	AX070947	AX070947 Sequence
1274	59.2	10.4	645	6	CQ769291	1347	59.2	10.4	4518	10	BSM805210	1393	59	10.4	898	10	BC026633	BC026633 Homo sapi
1275	59.2	10.4	704	10	BC069749	1348	59.2	10.4	4636	10	BSM802971	1392	59	10.4	882	9	BC005002	BC005002 Homo sapi
1276	59.2	10.4	722	6	BD192304	1349	59.2	10.4	4779	3	AB120954	1391	59	10.4	857	9	BSM808731	BSM808731 Homo sapi
1277	59.2	10.4	779	5	BC076202	1350	59.2	10.4	5359	8	BC054082	1390	59	10.4	811	7	BD269361	BD269361 Gene show
1278	59.2	10.4	837	9	878214	1351	59.2	10.4	65076	10	NCB13020	1389	59	10.4	700	5	BD269361	BD269361 Gene show
1279	59.2	10.4	975	10	BC012263	1352	59.2	10.4	126611	10	AL928592	1388	59	10.4	687	9	IR0821087	IR0821087 Homo sapi
1280	59.2	10.4	982	9	BC022482	1353	59.2	10.4	134218	9	HS17085	1387	59	10.4	617	9	IR0821087	IR0821087 Homo sapi
1281	59.2	10.4	1014	9	BC016845	1354	59.2	10.4	170655	2	AP001012	1386	59	10.4	572	10	BC049701	BC049701 Mus muscu
1282	59.2	10.4	1048	9	BC016845	1355	59.2	10.4	170655	2	AP001012	1385	59	10.4	511	6	CQ524260	CQ524260 Sequence
1283	59.2	10.4	1065	10	BC026521	1356	59.2	10.4	196754	2	BC019223	1384	59	10.4	505	6	CQ523774	CQ523774 Sequence
1284	59.2	10.4	1122	9	BC046132	1357	59.2	10.4	200441	2	AC022130	1383	59	10.4	438	6	CQ523774	CQ523774 Sequence
1285	59.2	10.4	1128	9	BC071732	1358	59.2	10.4	216410	2	AC027321	1382	59	10.4	438	6	CQ523774	CQ523774 Sequence
1286	59.2	10.4	1160	9	BC035911	1359	59.2	10.4	260	6	CQ524964	1381	59	10.4	446	6	CQ522677	CQ522677 Sequence
1287	59.2	10.4	1178	10	BC018244	1360	59	10.4	260	6	CQ524964	1380	59	10.4	446	6	CQ522677	CQ522677 Sequence
1288	59.2	10.4	1204	6	AX040958	1361	59	10.4	270	6	AR425430	1379	59	10.4	446	6	CQ522677	CQ522677 Sequence
1289	59.2	10.4	1324	10	BC013526	1362	59	10.4	270	6	AR425430	1378	59	10.4	446	6	CQ522677	CQ522677 Sequence
1290	59.2	10.4	1409	10	BC013526	1363	59	10.4	270	6	AR425430	1377	59	10.4	446	6	CQ522677	CQ522677 Sequence
1291	59.2	10.4	1425	5	BC074593	1364	59	10.4	285	6	BD121983	1376	59	10.4	446	6	CQ522677	CQ522677 Sequence
1292	59.2	10.4	1464	9	BC021958	1365	59	10.4	285	6	BD121983	1375	59	10.4	446	6	CQ522677	CQ522677 Sequence
1293	59.2	10.4	1497	9	BC042061	1366	59	10.4	291	6	CQ522677	1374	59	10.4	446	6	CQ522677	CQ522677 Sequence
1294	59.2	10.4	1513	8	AP169799	1367	59	10.4	305	6	CQ522677	1373	59	10.4	446	6	CQ522677	CQ522677 Sequence
1295	59.2	10.4	1513	8	AP169799	1368	59	10.4	305	6	CQ522677	1372	59	10.4	446	6	CQ522677	CQ522677 Sequence
1296	59.2	10.4	1530	9	BSM803698	1369	59	10.4	313	6	CQ523441	1371	59	10.4	446	6	CQ522677	CQ522677 Sequence
1297	59.2	10.4	1530	9	BSM803698	1370	59	10.4	313	6	CQ523441	1370	59	10.4	446	6	CQ522677	CQ522677 Sequence
1298	59.2	10.4	1530	9	BSM803698	1371	59	10.4	313	6	CQ523441	1369	59	10.4	446	6	CQ522677	CQ522677 Sequence
1299	59.2	10.4	1530	9	BSM803698	1372	59	10.4	313	6	CQ523441	1368	59	10.4	446	6	CQ522677	CQ522677 Sequence
1300	59.2	10.4	1530	9	BSM803698	1373	59	10.4	313	6	CQ523441	1367	59	10.4	446	6	CQ522677	CQ522677 Sequence
1301	59.2	10.4	1530	9	BSM803698	1374	59	10.4	313	6	CQ523441	1366	59	10.4	446	6	CQ522677	CQ522677 Sequence
1302	59.2	10.4	1530	9	BSM803698	1375	59	10.4	313	6	CQ523441	1365	59	10.4	446	6	CQ522677	CQ522677 Sequence
1303	59.2	10.4	1530	9	BSM803698	1376	59	10.4	313	6	CQ523441	1364	59	10.4	446	6	CQ522677	CQ522677 Sequence
1304	59.2	10.4	1530	9	BSM803698	1377	59	10.4	313	6	CQ523441	1363	59	10.4	446	6	CQ522677	CQ522677 Sequence
1305	59.2	10.4	1530	9	BSM803698	1378	59	10.4	313	6	CQ523441	1362	59	10.4	446	6	CQ522677	CQ522677 Sequence
1306	59.2	10.4	1530	9	BSM803698	1379	59	10.4	313	6	CQ523441	1361	59	10.4	446	6	CQ522677	CQ522677 Sequence
1307	59.2	10.4	1530	9	BSM803698	1380	59	10.4	313	6	CQ523441	1360	59	10.4	446	6	CQ522677	CQ522677 Sequence
1308	59.2	10.4	1530	9	BSM803698	1381	59	10.4	313	6	CQ523441	1359	59	10.4	446	6	CQ522677	CQ522677 Sequence
1309	59.2	10.4	1530	9	BSM803698	1382	59	10.4	313	6	CQ523441	1358	59	10.4	446	6	CQ522677	CQ522677 Sequence
1310	59.2	10.4	1530	9	BSM803698	1383	59	10.4	313	6	CQ523441	1357	59	10.4	446	6	CQ522677	CQ522677 Sequence
1311	59.2	10.4	1530	9	BSM803698	1384	59	10.4	313	6	CQ523441	1356	59	10.4	446	6	CQ522677	CQ522677 Sequence
1312	59.2	10.4	1530	9	BSM803698	1385	59	10.4	313	6	CQ523441	1355	59	10.4	446	6	CQ522677	CQ522677 Sequence
1313	59.2	10.4	1530	9	BSM803698	1386	59	10.4	313	6	CQ523441	1354	59	10.4	446	6	CQ522677	CQ522677 Sequence
1314	59.2	10.4	1530	9	BSM803698	1387	59	10.4	313	6	CQ523441	1353	59	10.4	446	6	CQ522677	CQ522677 Sequence
1315	59.2	10.4	1530	9	BSM803698	1388	59	10.4	313	6	CQ523441	1352	59	10.4	446	6	CQ522677	CQ522677 Sequence
1316	59.2	10.4	1530	9	BSM803698	1389	59	10.4	313	6	CQ523441	1351	59	10.4	446	6	CQ522677	CQ522677 Sequence
1317	59.2	10.4	1530	9	BSM803698	1390	59	10.4	313	6	CQ523441	1350	59	10.4	446	6	CQ522677	CQ522677 Sequence
1318	59.2	10.4	1530	9	BSM803698	1391	59	10.4	313	6	CQ523441	1349	59	10.4	446	6	CQ522677	CQ522677 Sequence
1319	59.2	10.4	1530	9	BSM803698	1392	59	10.4	313	6	CQ523441	1348	59	10.4	446	6	CQ522677	CQ522677 Sequence
1320	59.2	10.4	1530	9	BSM803698	1393	59	10.4	313	6	CQ523441	1347	59	10.4	446	6	CQ522677	CQ522677 Sequence
1321	59.2	10.4	1530	9	BSM803698	1394	59	10.4	313	6	CQ523441	1346	59	10.4	446	6	CQ522677	CQ522677 Sequence
1322	59.2	10.4	1530	9	BSM803698	1395	59	10.4	313	6	CQ523441	1345	59	10.4	446	6	CQ522677	CQ522677 Sequence
1323	59.2	10.4	1530	9	BSM803698	1396	59	10.4	313	6	CQ523441	1344	59	10.4	446	6	CQ522677	CQ522677 Sequence
1324	59.2	10.4	1530	9	BSM803698	1397	59	10.4	313	6	CQ523441	1343	59	10.4	446	6	CQ522677	CQ522677 Sequence
1325	59.2	10.4	1530	9	BSM803698	1398	59	10.4	313	6	CQ523441	1342	59	10.4	446	6	CQ522677	CQ522677 Sequence
1326	59.2	10.4	1530	9	BSM803698	1399	59	10.4	313	6	CQ523441	1341	59	10.4	446	6	CQ522677	CQ522677 Sequence
1327	59.2	10.4	1530	9	BSM803698	1400	59	10.4	313	6	CQ523441	1340	59	10.4	446	6	CQ522677	CQ522677 Sequence
1328	59.2	10.4	1530	9	BSM803698	1401	59	10.4	313	6	CQ523441	1339	59	10.4	446	6	CQ522677	CQ522677 Sequence
1329	59.2	10.4	1530	9	BSM803698	1402	59	10.4	313	6	CQ523441	1338	59	10.4	446	6	CQ522677	CQ522677 Sequence
1330	59.2	10.4	1530	9	BSM803698	1403	59	10.4	313	6	CQ523441	1337	5					

1407	59	10.4	1200	10	BC028327	BC028327 Mus muscu
1408	59	10.4	1208	10	BC025539	BC025539 Mus muscu
1409	59	10.4	1223	9	BC051848	BC051848 Homo sapi
1410	59	10.4	1229	9	BC033827	BC033827 Homo sapi
1411	59	10.4	1239	9	BC018639	BC018639 Homo sapi
1412	59	10.4	1271	5	BC053296	BC053296 Danto rer
1413	59	10.4	1277	9	AB096984	AB096984 Macaca fa
1414	59	10.4	1310	9	BC065197	BC065197 Homo sapi
1415	59	10.4	1334	9	BC009311	BC009311 Homo sapi
1416	59	10.4	1366	10	BC029450	BC029450 Mus muscu
1417	59	10.4	1376	3	AK174695	AK174695 Clona int
1418	59	10.4	1376	5	BC053263	BC053263 Danto rer
1419	59	10.4	1436	9	BSM804685	BSM804685 Homo sapi
1420	59	10.4	1444	9	BC053609	BC053609 Homo sapi
1421	59	10.4	1495	5	BC046652	BC046652 Xenopus t
1422	59	10.4	1507	10	BC069967	BC069967 Mus muscu
1423	59	10.4	1510	9	BC062585	BC062585 Homo sapi
1424	59	10.4	1555	6	BD133511	BD133511 Method fo
1425	59	10.4	1555	9	AB077880	AB077880 Homo sapi
1426	59	10.4	1560	9	BC073173	BC073173 Homo sapi
1427	59	10.4	1564	9	AB125186	AB125186 Macaca fa
1428	59	10.4	1621	9	BC004530	BC004530 Homo sapi
1429	59	10.4	1638	9	BC034291	BC034291 Homo sapi
1430	59	10.4	1672	3	AY070492	AY070492 Drosophi1
1431	59	10.4	1672	5	BC053184	BC053184 Danto rer
1432	59	10.4	1680	10	BC010314	BC010314 Mus muscu
1433	59	10.4	1720	5	BC056713	BC056713 Danto rer
1434	59	10.4	1744	9	BC019265	BC019265 Homo sapi
1435	59	10.4	1792	10	BC027065	BC027065 Mus muscu
1436	59	10.4	1795	10	BC052654	BC052654 Mus muscu
1437	59	10.4	1806	10	BC056619	BC056619 Mus muscu
1438	59	10.4	1814	3	AY118710	AY118710 Drosophi1
1439	59	10.4	1818	10	BC023454	BC023454 Mus muscu
1440	59	10.4	1847	6	AX795332	AX795332 Sequence
1441	59	10.4	1875	10	BC058247	BC058247 Mus muscu
1442	59	10.4	1877	9	BSM804687	BSM804687 Homo sapi
1443	59	10.4	1884	9	AF086921	AF086921 Homo sapi
1444	59	10.4	1900	9	BC073959	BC073959 Homo sapi
1445	59	10.4	1926	10	BC049784	BC049784 Mus muscu
1446	59	10.4	1930	5	BC046873	BC046873 Danto rer
1447	59	10.4	1935	9	BC030246	BC030246 Homo sapi
1448	59	10.4	1940	5	BC067673	BC067673 Danto rer
1449	59	10.4	1943	5	BC054628	BC054628 Danto rer
1450	59	10.4	1977	5	BC074690	BC074690 Xenopus t
1451	59	10.4	1988	10	BC026978	BC026978 Mus muscu
1452	59	10.4	2021	5	BC074652	BC074652 Xenopus t
1453	59	10.4	2022	9	AB061793	AB061793 Homo sapi
1454	59	10.4	2064	9	BC033388	BC033388 Homo sapi
1455	59	10.4	2066	9	BSM807857	BSM807857 Homo sapi
1456	59	10.4	2071	5	BC056843	BC056843 Xenopus t
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1458	59	10.4	2095	3	AY069487	AY069487 Drosophi1
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1461	59	10.4	2148	5	BC081110	BC081110 Xenopus t
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1465	59	10.4	2195	10	BC053752	BC053752 Mus muscu
1466	59	10.4	2237	3	AK112710	AK112710 Clona int
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1468	59	10.4	2278	6	C0413227	C0413227 Sequence
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1470	59	10.4	2330	9	BC006555	BC006555 Homo sapi
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1473	59	10.4	2394	5	BC063911	BC063911 Xenopus t
1474	59	10.4	2435	9	BC051753	BC051753 Homo sapi
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1486	59	10.4	2957	10	AJ609635	AJ609635 Mus muscu
1487	59	10.4	3149	10	BC040763	BC040763 Homo sapi
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1500	59	10.4	9699	9	BC063633	BC063633 Homo sapi

## ALIGNMENTS

RESULT 1	AR252648	AR252648	570 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	Sequence 407 from patent US 6478825.					
DEFINITION	AR252648					
ACCESSION	AR252648					
VERSION	AR252648.1	GI:27300556				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 570)					
AUTHORS	Wintersbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.					
TITLE	Implant, method of making same and use of the implant for the					
JOURNAL	treatment of bone defects					
FEATURES	Patent: US 6478825-A 407 12-NOV-2002;					
source	Location/Qualifiers					
	1..570					
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ORIGIN						
Query Match	100.0%; Score 570; DB 6; Length 570;					
Best Local Similarity	100.0%; Pred. No. 6-9e-86;					
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1 GCGAGGACCGGGATPAGAGCCTCGTGGCTTCCCGGCGAGCCGACAGTTCCCGCGC	60				
DB	1 GCGAGGACCGGGATPAGAGCCTCGTGGCTTCCCGGCGAGCCGACAGTTCCCGCGC	60				
QY	61 GCCCGAGCGCCCGCGCGATGAAGCTCGCGGCTCTCTGGGGCTCTGGGTGGCGCTGC	120				
DB	61 GCCCGAGCGCCCGCGCGATGAAGCTCGCGGCTCTCTGGGGCTCTGGGTGGCGCTGC	120				
QY	121 TCAGAGTCGCTGCTGCTTTCTTAAGTGGGCTGGCGACCTGTGGCCGACGCTGTGCT	180				
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QY	301 TCCAGAGTGTGTGCTGAGTGGTCCCGAGGCGGTGGGCGCGTGAAGCGCTGAAG	360				
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LOCUS Sequence 407 from Patent WO0073454.  
DEFINITION AX403520  
ACCESSION AX403520.1 GI:21437002  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Ashkenazi, A.J., Baker, K.P., Boctstein, D., Desnyers, L., Eaton, D.,  
Ferrara, N., Gerber, H., Gertsen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Kijavich, I., Nessler, M.A., Pan, J.,  
Paoli, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0073454-A 407 07-DEC-2000;  
Genentech Inc. (US)  
JOURNAL

TITLE  
JOURNAL  
FEATURES  
source  
1. .570  
/organism="Homo sapiens"  
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ORIGIN

Query Match 100.0%; Score 570; DB 6; Length 570;  
Best Local Similarity 100.0%; Pred. No. 6.9e-86;  
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGAGAGCCGGTATTAAGAGCTGCTGAGCCCTTGCAGGAGCCGAGCTTCCCGGAGC 60  
Db 1 GCGAGAGCCGGTATTAAGAGCTGCTGAGCCCTTGCAGGAGCCGAGCTTCCCGGAGC 60  
Qy 61 GCCCGAGCCCGCGAGCATGAAGCTGCGGCGCTCTGGGGCTCTGGGTGAGCCCTGTC 120  
Db 61 GCCCGAGCCCGCGAGCATGAAGCTGCGGCGCTCTGGGGCTCTGGGTGAGCCCTGTC 120  
Qy 121 TGAAGCTCCGCTGCTCTTTCTTAAGTGGCTGCGCAAGCCCTGAGCCAGCTGTGCT 180  
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Qy 361 GCCCTGCTGGGGGCCCTGAGAGTGTGTGCTGAGCCGAGACTGAGAGATCTACACTGAG 420  
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Db 541 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 570

RESULT 3  
AY359064 570 bp mRNA linear PRI 03-OCT-2003  
LOCUS Homo sapiens clone DNA64884 SCGB3A1 (UNQ629) mRNA, complete cds.  
DEFINITION AY359064  
ACCESSION AY359064.1 GI:37183245  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Clark, H.P., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,  
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, O., Hase, P.B.,  
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,  
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,  
Schoenfeld, J., Seshagiri, S., Simons, U., Singh, J., Smith, V.,  
Stinson, J., Vagstad, A., Vanden, R., Watanabe, C., Wiesend, D., Woods, K.,  
Xie, M.H., Yensura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,  
Goddard, A., Wood, W.I. and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
JOURNAL

TITLE  
JOURNAL  
FEATURES  
source  
1. .570  
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ORIGIN

Query Match 100.0%; Score 570; DB 9; Length 570;  
Best Local Similarity 100.0%; Pred. No. 6.9e-86;  
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGAGAGCCGGTATTAAGAGCTGCTGAGCCCTTGCAGGAGCCGAGCTTCCCGGAGC 60  
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Qy 121 TGAAGCTCCGCTGCTCTTTCTTAAGTGGCTGCGCAAGCCCTGAGCCAGCTGTGCT 180  
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Qy 181 GCGCTGAGTGGCGCGAGGCGCGGAGCGCGGAGCCCTGAGCAACCCCTTGGAGCCCTC 240  
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Qy 241 AACCCGCTGAAGCTCTGCTGAGAGCTGAGAGCTTCCCGTGAACCACTCATAGAGGCG 300  
Db 241 AACCCGCTGAAGCTCTGCTGAGAGCTTCCCGTGAACCACTCATAGAGGCG 300  
Qy 301 TCCAGAAAGTGTGTGCTGAGCTGGGTCCCAAGCCGTGGGGCCCTGAAGCCCTGAAG 360  
Db 301 TCCAGAAAGTGTGTGCTGAGCTGGGTCCCAAGCCGTGGGGCCCTGAAGCCCTGAAG 360

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FH Key Location/Qualifiers  
FT source 1..543  
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ORIGIN

Query Match 92.8%; Score 529; DB 6; Length 543;  
Best Local Similarity 100.0%; Pred. No. 5.1e-79;  
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAGGACCGGGTATTAAGAAAGCTCGTGCTTCCCGGAGCCGAGATTCCCGCGC 60  
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QY 421 GACAAAGCGCTGCGCACCGCGGAGGCTGAAAAACCGCGGAGGAGGAGCGTCCATCC 480  
DB 435 GACAAAGCGCTGCGCACCGCGGAGGCTGAAAAACCGCGGAGGAGGAGCGTCCATCC 494  
QY 481 CTTTCCCGCGCCCTCTCAATTAACGTGTTAAGCAAAAAA 529  
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RESULT 6  
BD26775 543 bp DNA linear PAT 17-JUL-2003  
LOCUS A novel method of diagnosing, monitoring and staging lung cancer.  
DEFINITION BD26775  
ACCESSION BD26775.1 GI:33036545  
VERSION JP 2002515262-A/6.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 543)  
Yang,F., Macina,R.A. and Sun,Y.  
A novel method of diagnosing, monitoring and staging lung cancer  
Patent: JP 2002515262-A 6 28-MAY-2002;  
DIADEXUS INC  
OS Homo sapiens (human)  
PN JP 2002515262-A/6  
PD 28-MAY-2002 JP 2000549766  
PR 12-MAY-1999 JP 2000549766  
PR 21-MAY-1998 US 60/086212

PI FRI YANG, ROBERTO A MACINA, YONGMING SUN  
PC C12N15/09, C12Q1/68, G01N33/50, C12N15/00  
CC A novel method of diagnosing, monitoring and staging lung CC  
FH Key Location/Qualifiers  
FT source 1..543  
FT Location/Qualifiers  
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ORIGIN

Query Match 92.8%; Score 529; DB 6; Length 543;  
Best Local Similarity 100.0%; Pred. No. 5.1e-79;  
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAGGACCGGGTATTAAGAAAGCTCGTGCTTCCCGGAGCCGAGATTCCCGCGC 60  
DB 15 GCGAGGACCGGGTATTAAGAAAGCTCGTGCTTCCCGGAGCCGAGATTCCCGCGC 74  
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RESULT 7  
BD082142 519 bp DNA linear PAT 27-AUG-2002  
LOCUS Reagents and methods useful for detecting diseases of the lung.  
DEFINITION BD082142  
ACCESSION BD082142.1 GI:22627752  
VERSION JP 2001522225-A/6.  
KEYWORDS Zea mays  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 519)  
Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,  
Granados,E.N., Hodges,S.C., Klags,M.R., Kratochvil,J.D., Rapp,L.R.,  
Rusnell,J.C. and Stroupe,S.D.  
Reagents and methods useful for detecting diseases of the lung  
Patent: JP 2001522225-A 6 13-NOV-2001;

QY 1 GCGAGACCGGGTATAGAGCCTCGTGGCTTCCCGGACGCCAGGTTCCCGCGC 60  
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 QY 541 AAAAAAAAAAAAAAAAAAAAAA 569  
 Db 541 AAAAAAAAAAAAAAAAAAAAAA 569

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 LOCUS AX201348 569 bp DNA linear PAT 30-AUG-2001  
 DEFINITION Sequence 27 from Patent WO0153486.  
 ACCESSION AX201348  
 VERSION AX201348.1 GI:15391167  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Aghkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,  
 Hillan, K.J., Marsters, S.A., Pan, J., Pitt, R.M., Roy, M.A., Smith, V.,  
 Stone, D.M., Watanabe, C.K., and Wood, W.I.  
 TITLE Human signal peptide-containing protein  
 JOURNAL Patent: WO 0153486-A 27 26-JUL-2001;  
 Genentech, Inc. (US)  
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 source Location/Qualifiers  
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RESULT 5  
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 DEFINITION Human signal peptide-containing protein.  
 ACCESSION BD222719  
 VERSION BD222719.1 GI:33032489  
 KEYWORDS JP 2002519030-A/65.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 543)  
 AUTHORS Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J.,  
 Raughn, M.R., Akredom, I.E., Young, J.A., Yue, H., Patterson, C.,  
 Reddy, R., Hillman, J.D., and Bandman, O.  
 TITLE Human signal peptide-containing protein  
 JOURNAL Patent: JP 2002519030-A 65 02-JUL-2002;  
 INCYTE PHARMACEUTICALS INC  
 OS Homo sapiens (human)  
 PN JP 2002519030-A/65  
 PD 02-JUL-2002  
 PR 25-JUN-1999 JP 2000557363  
 PR 26-JUN-1998 US 60/090762, 31-JUL-1998 US 60/094983 PR  
 01-OCT-1998 US 60/102686, 11-DEC-1998 US 60/112129 PI PREETI  
 LAL, Y TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER,  
 PI MARIAN R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE,  
 PI CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN  
 PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61P9/00, A61P15/00,  
 PC A61P25/00,  
 PC A61P29/00, A61P35/00, A61P43/00, C07K14/47, C07K16/18, C12N1/15, PC  
 C12N1/19,  
 PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//C12P21/08, PC  
 C12N15/00,  
 PC A61K37/02, C12N5/00

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COMMENT ABBOTT LABORATORIES  
PN JP 2001522225-A/6  
PD 13-NOV-2001  
PF 30-JAN-1998 JP 1998533078  
PR 31-JAN-1997 US 08/7917710  
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA  
PI N FRIEDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
KLASS,  
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
PI STROUPE  
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
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CC Topology: Linear;  
FH Key Location/Qualifiers.  
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RESULT 8  
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DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082141  
VERSION BD082141.1 GI:22627751  
KEYWORDS JP 2001522225-A/5.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT ABBOTT LABORATORIES  
PN JP 2001522225-A/5  
PD 13-NOV-2001  
PF 30-JAN-1998 JP 1998533078  
PR 31-JAN-1997 US 08/7917710  
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PI N FRIEDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
KLASS,  
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
PI STROUPE  
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
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CC Topology: Linear;  
FH Key Location/Qualifiers.  
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Query Match 91.0%; Score 518.6; DB 6; Length 562;  
Best Local Similarity 99.8%; Pred. No. 2.8e-77;  
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RESULT 9  
BC072673  
LOCUS  
DEFINITION BC072673 Homo sapiens secretoglobin, family 3A, member 1, mRNA (cDNA clone MGC:87867 IMAGE:5753142), complete cds.  
ACCESSION BC072673  
VERSION  
KEYWORDS  
SOURCE MGC.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Weller K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Du X., Gibbs R.A., Sanchez A., Whitting M., Madan A., Young A.C., Rodriguez S., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Butcherfield Y.S., Rodriguez A.C., Gilmwood J., Schultz J., Myers R.M., Schermer A., Schein J.E., Jones S.J., Skalska U., Smalls D.E., human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
TITLE  
JOURNAL  
PUBMED  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
REMARK  
COMMENT  
NHL-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland.  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@hgrl.nih.gov](mailto:nisc_mgc@hgrl.nih.gov)  
Aklter, N., Ayala K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooke, S., Distcher, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lari, C.P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mestrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripp, S., Thomas, P.J., Touchman, J.W., Tsurugon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.  
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16418366.  
Location/Qualifiers  
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418 GAGGACGAGTGTGGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 477  
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538 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 570  
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RESULT 10  
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LOCUS  
DEFINITION BC029176 Homo sapiens secretoglobin, family 3A, member 1, mRNA (cDNA clone MGC:34758 IMAGE:5180304), complete cds.  
ACCESSION BC029176  
VERSION BC029176.1 GI:20809672  
KEYWORDS  
SOURCE MGC.  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 503)

TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
JOURNAL

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheaf C.F., Bhat N.K., Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stabile T.E., Soares M.B., Bonaldo M.F., Casavant T.L., Scherz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M., Butlerfield Y.S., Krzywinski M.I., Skalski U., Smalins D.E., Scherch A., Schein J.E., Jones S.J. and Marra M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 503)  
Strausberg R.  
Direct Submission  
Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-rc@mail.nih.gov](mailto:cgabbs-rc@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsges, H., Kowls, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

## FEATURES

## source

## gene

## CDS

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAK Plate: 50 Row: b Column: 24  
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RESULT 11  
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ACCESSION AF086152  
VERSION AF086152.1 GI:3483497  
KEYWORDS FLI CDNA.  
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ORGANISM Homo sapiens  
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1 (bases 1 to 471)  
REFERENCE  
AUTHORS Moesener, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J., March, G., Bowles, J., Wylie, T., Bowers, Y., Steptoe, M., Theising, B., Geisel, S., Allen, M., Underwood, K., Chappell, J., Peterson, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Swaller, T., Behner, K., Hillier, L., Wilson, R. and Waterston, R.  
Full Clone Sequencing of the Longest Available Member from Each Unigene Cluster  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 471)  
AUTHORS Waterston, R.  
TITLE Direct Submission

JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
COMMENT SUBMITTED BY: Washington University  
Department of Genetics  
St. Louis MO 63108, USA  
http://genome.wustl.edu/gsc  
mailto:est@wustl.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

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DEFINITION

11/20/01  
ACCESSION AF436839.1 GI:33315289  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
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AUTHORS  
TITLE  
JOURNAL

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ACCESSION CQ776781  
VERSION CQ776781.1 GI:45380171  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuahara,K.  
TITLE Methods of testing for bronchial asthma or chronic obstructive  
pulmonary disease  
JOURNAL Patent: EP 1394274-A 467 03-MAR-2004;  
Genex Research, Inc. (JP)  
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KEYWORDS  
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REFERENCE  
AUTHORS Krop,I.E., Sgroi,D., Porter,D.A., Lunetta,K.L., LeVangie,R.,

Seth,P., Kaelin,C.M., Rhei,E., Rosenberg,M., Schmitt,S.,  
Marks,J.R., Pagon,Z., Belina,D., Razumovic,U. and Polyak,K.  
HIN-1, a putative cytokine highly expressed in normal but not  
cancerous mammary epithelial cells  
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9796-9801 (2001)  
JOURNAL  
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PUBMED 11481438  
REFERENCE  
AUTHORS Polyak,K., Krop,I. and Sgroi,D.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUN-2001) Adult Oncology, Dana-Farber Cancer  
Institute, 44 Binney St. D740C, Boston, MA 02115, USA  
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Best Local Similarity 99.6%; Pred. No. 4.3e-67;  
Matches 459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DEFINITION Homo sapiens UGRP2 mRNA, complete cds.  
ACCESSION AF313458  
VERSION AF313458.1 GI:16565421

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE

JOURNAL  
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Search completed: March 8, 2005, 07:46:36  
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C 261	66.4	11.6	164	2	BE963918	BE963918	C 334	65.8	11.5	368	4	BI491351
C 262	66.4	11.6	189	7	CF145452	UI--HF-C80	C 335	65.8	11.5	382	2	AM089640
C 263	66.4	11.6	195	2	BF817402	MM2-C1012	C 336	65.8	11.5	394	1	AI678843
C 264	66.4	11.6	204	4	BG996016	MR4-HT127	C 337	65.8	11.5	421	1	AI623810
C 265	66.4	11.6	208	4	BI001891	MR3--HN014	C 338	65.8	11.5	485	6	CB409310
C 266	66.4	11.6	214	4	BI018957	MR3--MT032	C 339	65.8	11.5	549	2	BF526693
C 267	66.4	11.6	244	4	BI001653	MR3--HN014	C 340	65.8	11.5	647	2	BF159647
C 268	66.4	11.6	247	1	AV670281	AV670281	C 341	65.8	11.5	707	7	CO873430
C 269	66.4	11.6	252	1	AI683240	tz39d03.x	C 342	65.8	11.5	721	2	AM029102
C 270	66.4	11.6	295	1	AA807015	OC29d09.s	C 343	65.8	11.5	750	9	CNS047762
C 271	66.4	11.6	348	1	BF150129	uy82b08.y	C 344	65.8	11.5	845	5	BU169841
C 272	66.4	11.6	398	2	AI5200931	to96f01.x	C 345	65.8	11.5	855	5	BU521925
C 273	66.4	11.6	384	6	CB703043	AMGNCC.N	C 346	65.8	11.5	866	6	CB197254
C 274	66.4	11.6	391	1	CK428913	1aj19b06.	C 347	65.8	11.5	886	7	CV069286
C 275	66.4	11.6	393	1	AI678021	wc81g12.x	C 348	65.8	11.5	913	9	CNS055MY
C 276	66.4	11.6	411	2	BF781925	602105876	C 349	65.8	11.5	931	7	CV069499
C 277	66.4	11.6	420	7	CF320317	HD--11-cl	C 350	65.8	11.5	957	4	BM415074
C 278	66.4	11.6	432	4	BI697437	603348180	C 351	65.8	11.5	961	5	BU532923
C 279	66.4	11.6	491	5	BO525482	NISC_no10	C 352	65.8	11.5	992	7	CF578886
C 280	66.4	11.6	517	6	CB052733	NISC_g109	C 353	65.8	11.5	1393	4	BI519451
C 281	66.4	11.6	523	6	CB409712	NC06	C 354	65.8	11.5	1394	3	CF122616
C 282	66.4	11.6	530	1	AI539042	CP76f09.x	C 355	65.6	11.5	276	5	BM888453
C 283	66.4	11.6	558	7	CNS263399	AGENCY	C 356	65.6	11.5	296	5	BX255325
C 284	66.4	11.6	569	7	CO872400	Bovgen_00	C 357	65.6	11.5	206	4	BG956193
C 285	66.4	11.6	591	6	CB443252	694122_MA	C 358	65.6	11.5	250	1	AI922365
C 286	66.4	11.6	665	7	CO873254	Bovgen_01	C 359	65.6	11.5	260	7	CO877337
C 287	66.4	11.6	784	2	BE964538	601658651	C 360	65.6	11.5	276	5	BM887899
C 288	66.4	11.6	794	4	BU529833	AGENCY	C 361	65.6	11.5	276	5	BM888453
C 289	66.4	11.6	814	4	BI697359	603348288	C 362	65.6	11.5	296	5	BX255325
C 290	66.4	11.6	911	2	BE731275	601567175	C 363	65.6	11.5	329	1	AI559737
C 291	66.4	11.6	912	5	BU843541	AGENCY	C 364	65.6	11.5	359	4	BG109810
C 292	66.4	11.6	928	4	BM415733	OP20814 M	C 365	65.6	11.5	548	1	AI571049
C 293	66.4	11.6	945	4	BM415029	OP20085 M	C 366	65.6	11.5	584	4	BI832039
C 294	66.4	11.6	1181	2	BE962759	601656155	C 367	65.6	11.5	592	5	BP271839
C 295	66.2	11.6	181	4	BG382625	298592 MA	C 368	65.6	11.5	679	7	CNS28978
C 296	66.2	11.6	190	1	AI250856	AI220856	C 369	65.6	11.5	693	5	BU075511
C 297	66.2	11.6	206	1	BF753023	RC3--BN042	C 370	65.6	11.5	716	8	AZ197151
C 298	66.2	11.6	226	5	BU584561	550026H1	C 371	65.6	11.5	864	7	CV069405
C 299	66.2	11.6	230	2	BF814333	MM2-C1012	C 372	65.6	11.5	957	4	BM415792
C 300	66.2	11.6	230	4	BG988222	MM3--HT120	C 373	65.6	11.5	4952	3	AP447875
C 301	66.2	11.6	310	1	AI282602	uy82b05.x	C 374	65.4	11.5	173	2	BF191537
C 302	66.2	11.6	419	6	CB410568	NISC_nc12	C 375	65.4	11.5	202	1	AI926878
C 303	66.2	11.6	592	6	CD770942	AGENCY	C 376	65.4	11.5	209	1	AI686002
C 304	66.2	11.6	771	5	BU567350	AGENCY	C 377	65.4	11.5	263	1	AI568765
C 305	66.2	11.6	822	7	CK796075	AGENCY	C 378	65.4	11.5	273	1	AI627748
C 306	66.2	11.6	913	8	BM154234	ENVT85TF	C 379	65.4	11.5	321	2	AM085667
C 307	66.2	11.6	951	8	AZ672893	ENVTU74TF	C 380	65.4	11.5	337	4	BG732598
C 308	66.2	11.6	1465	5	BQ219618	AGENCY	C 381	65.4	11.5	349	1	AI432813
C 309	66.2	11.6	196	6	BI490163	603031924	C 382	65.4	11.5	352	1	AI623796
C 310	66.2	11.6	1773	2	BE260634	601146135	C 383	65.4	11.5	393	5	AM1667198
C 311	66.2	11.6	198	2	AM148356	xt13607.x	C 384	65.4	11.5	416	2	AM656975
C 312	66	11.6	199	6	CD671493	FG05B07.x	C 385	65.4	11.5	430	2	BF724157
C 313	66	11.6	261	2	AM335117	543D4 AGS	C 386	65.4	11.5	542	4	BG824636
C 314	66	11.6	355	1	AI554516	tg22e08.x	C 387	65.4	11.5	552	4	BI521946
C 315	66	11.6	377	5	BQ527000	NC019	C 388	65.4	11.5	604	2	AM644921
C 316	66	11.6	405	1	AI570142	tc075d05.x	C 389	65.4	11.5	676	2	BB794802
C 244	66.8	11.7	1202	5	BU903646	AGENCY	C 317	66	11.6	515	7	CF332909
C 245	66.6	11.7	163	2	BE964512	BE964512	C 318	66	11.6	519	5	BP157240
C 246	66.6	11.7	178	2	BE963286	BE963286	C 319	66	11.6	929	4	BG287670
C 247	66.6	11.7	186	2	AM346369	27839 MAR	C 320	66	11.6	962	4	BM415326
C 248	66.6	11.7	190	7	CF330394	NACL--06-	C 321	66	11.6	1013	4	BM416113
C 249	66.6	11.7	288	7	CF328884	NACL--03-	C 322	65.8	11.5	193	4	BG988931
C 250	66.6	11.7	308	6	CB051558	NISC_g101	C 323	65.8	11.5	197	1	AT620302
C 251	66.6	11.7	326	2	BE664835	BE664835	C 324	65.8	11.5	199	4	BI053615
C 252	66.6	11.7	376	7	CF317110	HD--06-K2	C 325	65.8	11.5	205	7	CK377129
C 253	66.6	11.7	417	4	BI467777	389550 MA	C 326	65.8	11.5	225	5	BX480526
C 254	66.6	11.7	481	5	BO526610	NISC_no17	C 327	65.8	11.5	254	7	CF301655
C 255	66.6	11.7	561	6	CB952214	AGENCY	C 328	65.8	11.5	277	2	AM196037
C 256	66.6	11.7	643	2	BE964576	BE964576	C 329	65.8	11.5	282	2	AM241016
C 257	66.6	11.7	800	4	BG780621	SEADWC00	C 330	65.8	11.5	288	2	AM150453
C 258	66.6	11.7	908	4	BM416110	OP21196 M	C 331	65.8	11.5	292	7	CF320682
C 259	66.6	11.7	947	9	CNS00034	AL075868	C 332	65.8	11.5	345	4	BG980484
C 260	66.6	11.7	976	2	BE965034	601658817	C 333	65.8	11.5	365	1	AI912533
C 261	66.4	11.6	164	2	BE963918	BE963918	C 334	65.8	11.5	368	4	BI491351
C 262	66.4	11.6	189	7	CF145452	UI--HF-C80	C 335	65.8	11.5	382	2	AM089640
C 263	66.4	11.6	195	2	BF817402	MM2-C1012	C 336	65.8	11.5	394	1	AI678843
C 264	66.4	11.6	204	4	BG996016	MR4-HT127	C 337	65.8	11.5	421	1	AI623810
C 265	66.4	11.6	208	4	BI001891	MR3--HN014	C 338	65.8	11.5	485	6	CB409310
C 266	66.4	11.6	214	4	BI018957	MR3--MT032	C 339	65.8	11.5	549	2	BF526693
C 267	66.4	11.6	244	4	BI001653	MR3--HN014	C 340	65.8	11.5	647	2	BF159647
C 268	66.4	11.6	247	1	AV670281	AV670281	C 341	65.8	11.5	707	7	CO873430
C 269	66.4	11.6	252	1	AI683240	tz39d03.x	C 342	65.8	11.5	721	2	AM029102
C 270	66.4	11.6	295	1	AA807015	OC29d09.s	C 343	65.8	11.5	750	9	CNS047762
C 271	66.4	11.6	348	1	BF150129	uy82b08.y	C 344	65.8	11.5	845	5	BU169841
C 272	66.4	11.6	398	2	AI5200931	to96f01.x	C 345	65.8	11.5	855	5	BU521925
C 273	66.4	11.6	384	6	CB703043							

[illegible]

536	64.6	11.3	461	6	CB844257	CB844257	M15E--5213	C 609	64.2	11.3	420	1	AJ485582	AJ485582
C 537	64.6	11.3	467	6	CB052899	CB052899	N15C_g110	C 610	64.2	11.3	434	7	BJ333677	BJ333677
C 538	64.6	11.3	468	4	BI492374	BI492374	df23rd3.w	C 611	64.2	11.3	441	4	BG574118	BG574118
539	64.6	11.3	473	4	BM553962	BM553962	AGENCOURT	C 612	64.2	11.3	445	7	CK988611	CK988611
540	64.6	11.3	506	7	CK484235	CK484235	a1_F001.4	C 613	64.2	11.3	448	6	CD239708	CD239708
541	64.6	11.3	516	7	CN783044	CN783044	a1_S003.4	C 614	64.2	11.3	453	7	CO881716	CO881716
542	64.6	11.3	523	4	BM281946	BM281946	k123c05.y	C 615	64.2	11.3	460	5	BQ387565	BQ387565
C 543	64.6	11.3	614	8	BM166902	BM166902	ENTRO90TR	C 616	64.2	11.3	472	6	CB343321	CB343321
544	64.6	11.3	824	4	BM415861	BM415861	OP0943.M	C 617	64.2	11.3	476	9	CNS02R01	CNS02R01
545	64.6	11.3	824	7	CF784510	CF784510	AGENCOURT	C 618	64.2	11.3	484	5	BQ395565	BQ395565
546	64.6	11.3	857	5	BU954681	BU954681	AGENCOURT	C 619	64.2	11.3	500	3	CR640278	CR640278
C 547	64.6	11.3	877	2	BE964755	BE964755	601658407	C 620	64.2	11.3	503	7	CO874516	CO874516
C 548	64.6	11.3	910	7	CV069478	CV069478	WPAEhux15	C 621	64.2	11.3	515	6	CB084196	CB084196
C 549	64.6	11.3	940	2	BE963809	BE963809	601657460	C 622	64.2	11.3	526	6	CD678874	CD678874
550	64.6	11.3	1016	5	BO718364	BO718364	AGENCOURT	C 623	64.2	11.3	526	7	CK776971	CK776971
551	64.6	11.3	1615	9	AG311072	AG311072	Mus_muscu	C 624	64.2	11.3	544	6	CB053489	CB053489
C 552	64.4	11.3	179	4	BG168185	BG168185	602341586	C 625	64.2	11.3	550	5	BP372967	BP372967
C 553	64.4	11.3	250	7	CK407161	CK407161	AUF_ILFvr	C 626	64.2	11.3	553	1	AI683714	AI683714
554	64.4	11.3	250	7	CK407161	CK407161	AUF_ILFvr	C 627	64.2	11.3	556	7	CF319654	CF319654
555	64.4	11.3	263	6	CB048444	CB048444	N15C_g104	C 628	64.2	11.3	572	5	BP306440	BP306440
556	64.4	11.3	263	6	CB048444	CB048444	N15C_g104	C 629	64.2	11.3	585	1	AI539847	AI539847
C 557	64.4	11.3	278	6	CB052708	CB052708	N15C_g109	C 630	64.2	11.3	588	1	AI952114	AI952114
558	64.4	11.3	288	6	BE754450	BE754450	207961.MA	C 631	64.2	11.3	604	7	CO877670	CO877670
C 559	64.4	11.3	305	2	AM007309	AM007309	wf54h02.x	C 632	64.2	11.3	608	5	BQ397388	BQ397388
C 560	64.4	11.3	337	2	AM151970	AM151970	xf71a07.x	C 633	64.2	11.3	627	7	CF314054	CF314054
C 561	64.4	11.3	349	6	CD723632	CD723632	0124f02.y	C 634	64.2	11.3	637	7	CF549772	CF549772
C 562	64.4	11.3	367	1	AI857760	AI857760	w121g04.x	C 635	64.2	11.3	745	7	CO872976	CO872976
563	64.4	11.3	368	3	AF116644	AF116644	Homo_sapi	C 636	64.2	11.3	750	2	BE886858	BE886858
C 564	64.4	11.3	435	7	CF320474	CF320474	HD--11-G0	C 637	64.2	11.3	792	7	CO960760	CO960760
565	64.4	11.3	439	5	BQ802093	BQ802093	WHE2822.A	C 638	64.2	11.3	846	2	BE963818	BE963818
566	64.4	11.3	441	2	AM953817	AM953817	EST936607	C 639	64.2	11.3	882	4	BG828051	BG828051
C 567	64.4	11.3	523	7	CF316038	CF316038	HD--05-C2	C 640	64.2	11.3	897	4	BF983626	BF983626
C 568	64.4	11.3	789	5	BU414617	BU414617	6036567993	C 641	64.2	11.3	924	8	BM415316	BM415316
C 569	64.4	11.3	789	4	BG474227	BG474227	602516846	C 642	64.2	11.3	932	8	AZ542647	AZ542647
C 570	64.4	11.3	879	2	BE969452	BE969452	601649669	C 643	64.2	11.3	934	4	BM415897	BM415897
C 571	64.4	11.3	932	2	BE965022	BE965022	601658805	C 644	64.2	11.3	937	7	CF581299	CF581299
C 572	64.4	11.3	1077	5	BM907650	BM907650	AGENCOURT	C 645	64.2	11.3	944	2	BE536909	BE536909
C 573	64.4	11.3	1165	4	BG488803	BG488803	602534774	C 646	64.2	11.3	949	7	CF581465	CF581465
C 574	64.4	11.3	1206	4	BM009429	BM009429	603628937	C 647	64.2	11.3	986	7	CF581387	CF581387
C 575	64.4	11.3	1271	2	BE964600	BE964600	601658526	C 648	64.2	11.3	989	7	CV069665	CV069665
576	64.4	11.3	2129	3	BC0033579	BC0033579	Homo_sapi	C 649	64.2	11.3	1014	2	BE965471	BE965471
C 577	64.2	11.3	112	4	BI0013345	BI0013345	MR2--HN012	C 650	64.2	11.3	1023	2	BE964045	BE964045
C 578	64.2	11.3	137	2	BF811802	BF811802	MR2--CI018	C 651	64.2	11.3	1227	7	CF579397	CF579397
C 579	64.2	11.3	155	4	BI015381	BI015381	MR4--ET024	C 652	64.2	11.3	1246	5	BO433823	BO433823
C 580	64.2	11.3	179	2	BF921092	BF921092	MR2--NT013	C 653	64.2	11.3	1258	4	BM394234	BM394234
C 581	64.2	11.3	233	4	AI587121	AI587121	cf53e03.x	C 654	64.2	11.3	1844	2	BE962888	BE962888
C 582	64.2	11.3	257	2	BG956916	BG956916	OVO--C7073	C 655	64.2	11.3	3169	3	HSM808852	HSM808852
583	64.2	11.3	257	4	AM656503	AM656503	108790.MA	C 656	64.2	11.3	318	4	BG996119	BG996119
584	64.2	11.3	259	4	BI539149	BI539149	451338.MA	C 657	64.2	11.3	318	4	BG996119	BG996119
C 585	64.2	11.3	272	1	AJ799419	AJ799419	WA72902.x	C 658	64.2	11.3	141	5	BU584043	BU584043
C 586	64.2	11.3	277	1	AI952360	AI952360	WA72902.x	C 659	64.2	11.3	144	5	BX558864	BX558864
C 587	64.2	11.3	279	1	AI863411	AI863411	cf240h07.x	C 660	64.2	11.3	150	1	AI859464	AI859464
C 588	64.2	11.3	313	1	AI624668	AI624668	cf43d06.x	C 661	64.2	11.3	176	4	BG996113	BG996113
C 589	64.2	11.3	313	1	AI824444	AI824444	cf70c10.x	C 662	64.2	11.3	178	5	BM905125	BM905125
C 590	64.2	11.3	318	6	CA501316	CA501316	WHE4032.B	C 663	64.2	11.3	185	7	CR630621	CR630621
C 591	64.2	11.3	330	1	AI285732	AI285732	QUB14D02.x	C 664	64.2	11.3	224	6	CA803744	CA803744
C 592	64.2	11.3	332	7	CF328738	CF328738	NACL--03-	C 665	64.2	11.3	252	2	BE012414	BE012414
C 593	64.2	11.3	335	7	CN840208	CN840208	AGENCOURT	C 666	64.2	11.3	266	4	BM548955	BM548955
C 594	64.2	11.3	336	7	CF317484	CF317484	HD--07-D0	C 667	64.2	11.3	276	1	AI564290	AI564290
C 595	64.2	11.3	338	4	CF330404	CF330404	NACL--06-	C 668	64.2	11.3	279	4	BM025387	BM025387
C 596	64.2	11.3	343	4	BM445435	BM445435	11111D1.x	C 669	64.2	11.3	301	5	BU584940	BU584940
C 597	64.2	11.3	345	1	AI682837	AI682837	w669a01.x	C 670	64.2	11.3	307	4	BI440945	BI440945
598	64.2	11.3	347	5	BU679066	BU679066	UT--CF-DU1	C 671	64.2	11.3	307	7	CF321592	CF321592
C 599	64.2	11.3	349	1	AI339388	AI339388	qf02a12.x	C 672	64.2	11.3	308	7	CO081924	CO081924
C 600	64.2	11.3	353	6	CB050372	CB050372	N15C_gj16	C 673	64.2	11.3	311	7	CF331006	CF331006
601	64.2	11.3	366	5	BM925639	BM925639	AGENCOURT	C 674	64.2	11.3	312	1	AI933518	AI933518
C 602	64.2	11.3	369	2	AM168296	AM168296	x662907.x	C 675	64.2	11.3	320	1	BF904178	BF904178
C 603	64.2	11.3	386	4	BI898861	BI898861	480651.MA	C 676	64.2	11.3	320	1	AI706784	AI706784
C 604	64.2	11.3	391	2	AI887221	AI887221	wm37d11.x	C 677	64.2	11.3	328	7	CF298861	CF298861
C 605	64.2	11.3	394	2	AM090494	AM090494	xc84b11.x	C 678	64.2	11.3	329	1	AI949510	AI949510
C 606	64.2	11.3	394	6	CD105470	CD105470	AGENCOURT	C 679	64.2	11.3	337	2	BF812516	BF812516
C 607	64.2	11.3	412	2	AM130584	AM130584	xf54c09.x	C 680	64.2	11.3	353	7	CF584273	CF584273
608	64.2	11.3	413	7	CK467628	CK467628	938943.MA	C 681	64.2	11.3	364	4	BG3191700	BG3191700



C 682	64	11.2	374	7	CF310089	CF310089	ABF--04-J	C 755	63.8	11.2	608	1	AA465953
C 683	64	11.2	389	7	CO891668	CO891668	BoyGen.19	C 756	63.8	11.2	641	1	AA648546
C 684	64	11.2	391	2	AM084812	AM084812	xc63d0e.x	C 757	63.8	11.2	662	1	B1858668
C 685	64	11.2	403	5	BO524385	BO524385	NISC.nc04	C 758	63.8	11.2	688	6	CD108918
C 686	64	11.2	424	1	AA790256	AA790256	vw16d09.t	C 759	63.8	11.2	721	7	CN165144
C 687	64	11.2	438	6	CD672592	CD672592	fg13h05.x	C 760	63.8	11.2	840	7	BE965071
C 688	64	11.2	439	7	CO876707	CO876707	BoyGen.05	C 761	63.8	11.2	939	7	CV068729
C 689	64	11.2	454	5	BO397624	BO397624	NISC.ng28	C 762	63.8	11.2	952	7	CK403655
C 690	64	11.2	464	7	CF332023	CF332023	NACL--08-	C 763	63.8	11.2	956	2	BE964759
C 691	64	11.2	469	5	BO525723	BO525723	NISC.no12	C 764	63.8	11.2	1003	4	B1258565
C 692	64	11.2	476	7	CF312501	CF312501	ABF--08-R	C 765	63.8	11.2	1005	4	BM416485
C 693	64	11.2	489	5	BF104582	BF104582	UI--M-FPO	C 766	63.8	11.2	1034	2	BE966775
C 694	64	11.2	495	7	CF122597	CF122597	UI--HR-CH0	C 767	63.8	11.2	1090	2	BE966775
C 695	64	11.2	500	6	CB285207	CB285207	CO91911.x	C 768	63.8	11.2	1280	2	BE966570
C 696	64	11.2	514	5	BE013956	BE013956	BM204F06	C 769	63.8	11.2	1382	4	BE734492
C 697	64	11.2	515	6	CB716451	CB716451	AMGNNUC.S	C 770	63.8	11.2	1801	2	BE734492
C 698	64	11.2	538	1	AL727686	AL727686	AL727686	C 771	63.8	11.2	1801	2	BE734492
C 700	64	11.2	545	5	BO527470	BO527470	NISC.no22	C 772	63.6	11.2	127	7	CF321991
C 701	64	11.2	564	7	CF313743	CF313743	HD--01-P1	C 773	63.6	11.2	143	5	BM534646
C 702	64	11.2	575	1	AJ746726	AJ746726	NISC.g107	C 774	63.6	11.2	164	2	AM129271
C 703	64	11.2	575	4	BM123450	BM123450	LO525C01-	C 775	63.6	11.2	167	1	AM1251830
C 704	64	11.2	575	6	CB052407	CB052407	NISC.mq09	C 776	63.6	11.2	171	4	B1001534
C 705	64	11.2	646	5	BO389769	BO389769	NISC.mq09	C 777	63.6	11.2	175	4	BE993627
C 706	64	11.2	646	7	CF175945	CF175945	799960.MA	C 778	63.6	11.2	180	1	AM144590
C 707	64	11.2	738	2	BE974632	BE974632	601680655	C 779	63.6	11.2	193	5	BM536365
C 708	64	11.2	752	7	CO876882	CO876882	BoyGen.05	C 780	63.6	11.2	200	1	AM1467537
C 709	64	11.2	754	1	AV716495	AV716495	AV716495	C 781	63.6	11.2	204	1	AM1467537
C 710	64	11.2	760	9	CNS02171	CNS02171	reticodon	C 782	63.6	11.2	210	2	AM438793
C 711	64	11.2	825	2	BE884441	BE884441	601510725	C 783	63.6	11.2	210	7	CR557393
C 712	64	11.2	825	5	BU587899	BU587899	AGENCOURT	C 784	63.6	11.2	219	5	BU844285
C 713	64	11.2	921	4	BE965731	BE965731	603175821	C 785	63.6	11.2	222	5	BU844285
C 714	64	11.2	939	2	BE965731	BE965731	601659790	C 786	63.6	11.2	242	7	CF329593
C 715	64	11.2	965	2	BE965731	BE965731	601659790	C 787	63.6	11.2	242	7	CF329593
C 716	64	11.2	1006	3	BE965731	BE965731	601659790	C 788	63.6	11.2	242	7	CF329593
C 717	64	11.2	1006	3	BE965731	BE965731	601659790	C 789	63.6	11.2	242	7	CF329593
C 718	64	11.2	1006	3	BE965731	BE965731	601659790	C 790	63.6	11.2	242	7	CF329593
C 719	64	11.2	1006	3	BE965731	BE965731	601659790	C 791	63.6	11.2	242	7	CF329593
C 720	64	11.2	1006	3	BE965731	BE965731	601659790	C 792	63.6	11.2	242	7	CF329593
C 721	64	11.2	1006	3	BE965731	BE965731	601659790	C 793	63.6	11.2	242	7	CF329593
C 722	64	11.2	1006	3	BE965731	BE965731	601659790	C 794	63.6	11.2	242	7	CF329593
C 723	64	11.2	1006	3	BE965731	BE965731	601659790	C 795	63.6	11.2	242	7	CF329593
C 724	64	11.2	1006	3	BE965731	BE965731	601659790	C 796	63.6	11.2	242	7	CF329593
C 725	64	11.2	1006	3	BE965731	BE965731	601659790	C 797	63.6	11.2	242	7	CF329593
C 726	64	11.2	1006	3	BE965731	BE965731	601659790	C 798	63.6	11.2	242	7	CF329593
C 727	64	11.2	1006	3	BE965731	BE965731	601659790	C 799	63.6	11.2	242	7	CF329593
C 728	64	11.2	1006	3	BE965731	BE965731	601659790	C 800	63.6	11.2	242	7	CF329593
C 729	64	11.2	1006	3	BE965731	BE965731	601659790	C 801	63.6	11.2	242	7	CF329593
C 730	64	11.2	1006	3	BE965731	BE965731	601659790	C 802	63.6	11.2	242	7	CF329593
C 731	64	11.2	1006	3	BE965731	BE965731	601659790	C 803	63.6	11.2	242	7	CF329593
C 732	64	11.2	1006	3	BE965731	BE965731	601659790	C 804	63.6	11.2	242	7	CF329593
C 733	64	11.2	1006	3	BE965731	BE965731	601659790	C 805	63.6	11.2	242	7	CF329593
C 734	64	11.2	1006	3	BE965731	BE965731	601659790	C 806	63.6	11.2	242	7	CF329593
C 735	64	11.2	1006	3	BE965731	BE965731	601659790	C 807	63.6	11.2	242	7	CF329593
C 736	64	11.2	1006	3	BE965731	BE965731	601659790	C 808	63.6	11.2	242	7	CF329593
C 737	64	11.2	1006	3	BE965731	BE965731	601659790	C 809	63.6	11.2	242	7	CF329593
C 738	64	11.2	1006	3	BE965731	BE965731	601659790	C 810	63.6	11.2	242	7	CF329593
C 739	64	11.2	1006	3	BE965731	BE965731	601659790	C 811	63.6	11.2	242	7	CF329593
C 740	64	11.2	1006	3	BE965731	BE965731	601659790	C 812	63.6	11.2	242	7	CF329593
C 741	64	11.2	1006	3	BE965731	BE965731	601659790	C 813	63.6	11.2	242	7	CF329593
C 742	64	11.2	1006	3	BE965731	BE965731	601659790	C 814	63.6	11.2	242	7	CF329593
C 743	64	11.2	1006	3	BE965731	BE965731	601659790	C 815	63.6	11.2	242	7	CF329593
C 744	64	11.2	1006	3	BE965731	BE965731	601659790	C 816	63.6	11.2	242	7	CF329593
C 745	64	11.2	1006	3	BE965731	BE965731	601659790	C 817	63.6	11.2	242	7	CF329593
C 746	64	11.2	1006	3	BE965731	BE965731	601659790	C 818	63.6	11.2	242	7	CF329593
C 747	64	11.2	1006	3	BE965731	BE965731	601659790	C 819	63.6	11.2	242	7	CF329593
C 748	64	11.2	1006	3	BE965731	BE965731	601659790	C 820	63.6	11.2	242	7	CF329593
C 749	64	11.2	1006	3	BE965731	BE965731	601659790	C 821	63.6	11.2	242	7	CF329593
C 750	64	11.2	1006	3	BE965731	BE965731	601659790	C 822	63.6	11.2	242	7	CF329593
C 751	64	11.2	1006	3	BE965731	BE965731	601659790	C 823	63.6	11.2	242	7	CF329593
C 752	64	11.2	1006	3	BE965731	BE965731	601659790	C 824	63.6	11.2	242	7	CF329593
C 753	64	11.2	1006	3	BE965731	BE965731	601659790	C 825	63.6	11.2	242	7	CF329593
C 754	64	11.2	1006	3	BE965731	BE965731	601659790	C 826	63.6	11.2	242	7	CF329593
C 755	64	11.2	1006	3	BE965731	BE965731	601659790	C 827	63.6	11.2	242	7	CF329593

BM923875 AGENCOURT

C 828	63.6	11.2	406	5	B0526114	NISC_nol4	901	63.6	11.2	772	1	AV758339	AV758339
C 829	63.6	11.2	411	1	A1811845	tw45c12.x	902	63.6	11.2	777	6	CB985960	CB985960
830	63.6	11.2	412	1	AL597750	DKF5c113B	903	63.6	11.2	784	1	AI541048	AI541048
831	63.6	11.2	413	5	BP368161	BP368161	904	63.6	11.2	790	5	B0957936	B0957936
832	63.6	11.2	413	5	BP368309	BP368309	905	63.6	11.2	797	1	AV757205	AV757205
833	63.6	11.2	414	1	AV681639	AV681639	906	63.6	11.2	816	6	CB310550	CB310550
C 834	63.6	11.2	414	6	CB217992	NISC_nb06	C 907	63.6	11.2	818	8	AZ538703	ENTDNA9TR
835	63.6	11.2	414	6	CB839976	MI5E--0084	C 908	63.6	11.2	822	2	BF204483	BF204483
836	63.6	11.2	423	7	CK662119	LP22103.5	909	63.6	11.2	832	7	CK128668	CK128668
837	63.6	11.2	427	5	B0564291	AGENCOURT	910	63.6	11.2	833	5	B0564378	B0564378
838	63.6	11.2	428	7	CR753607	DKF2p469f	911	63.6	11.2	843	4	BG109959	BG109959
839	63.6	11.2	429	6	CD238001	FNPASER10	912	63.6	11.2	846	1	AV757362	AV757362
840	63.6	11.2	431	6	CD106183	AGENCOURT	913	63.6	11.2	847	4	BI759832	BI759832
841	63.6	11.2	434	7	CR629072	DKF2p4681	914	63.6	11.2	856	4	BI524056	BI524056
842	63.6	11.2	435	7	CR832270	AGENCOURT	915	63.6	11.2	870	5	B0958052	B0958052
843	63.6	11.2	436	6	CD175136	AGENCOURT	C 916	63.6	11.2	897	8	BH162937	BH162937
844	63.6	11.2	441	4	BI761192	603043418	917	63.6	11.2	900	4	BI255205	BI255205
845	63.6	11.2	444	6	CD173669	AGENCOURT	918	63.6	11.2	901	5	BU181433	BU181433
846	63.6	11.2	445	5	BY393726	BY393726	919	63.6	11.2	905	4	BG575878	BG575878
847	63.6	11.2	446	6	CD238662	FNPBD07	C 920	63.6	11.2	913	4	BM416526	BM416526
848	63.6	11.2	449	6	CD239598	FNPBD09	C 921	63.6	11.2	917	2	BE964089	BE964089
849	63.6	11.2	449	6	CD239647	FNPBDH10	C 922	63.6	11.2	919	5	BU533717	BU533717
850	63.6	11.2	450	5	BP327554	BP327554	923	63.6	11.2	930	6	CD389750	CD389750
851	63.6	11.2	450	6	CD239723	FNPBXG09	924	63.6	11.2	932	9	CNS0070E	CNS0070E
C 852	63.6	11.2	455	5	BU587776	AGENCOURT	925	63.6	11.2	932	6	CD507735	CD507735
853	63.6	11.2	456	6	CB044455	NISC_gc04	926	63.6	11.2	933	6	CD388765	CD388765
854	63.6	11.2	457	6	CD386558	AGENCOURT	C 928	63.6	11.2	940	6	BM415207	BM415207
855	63.6	11.2	458	4	BG108189	BG108189	C 929	63.6	11.2	940	6	CD386618	CD386618
856	63.6	11.2	460	5	BP367883	BP367883	930	63.6	11.2	941	5	BU540230	BU540230
857	63.6	11.2	464	7	CN842303	AGENCOURT	931	63.6	11.2	948	6	CD390144	CD390144
858	63.6	11.2	471	7	CK349199	CK349199	932	63.6	11.2	949	6	CD387866	CD387866
859	63.6	11.2	472	5	B0627411	rc779g03.y	933	63.6	11.2	950	6	CD389726	CD389726
860	63.6	11.2	473	6	CA337220	NISC_lv10	934	63.6	11.2	951	6	CD386657	CD386657
861	63.6	11.2	473	6	CD640969	AGENCOURT	935	63.6	11.2	951	6	CD389712	CD389712
C 862	63.6	11.2	476	2	AM080357	AGENCOURT	936	63.6	11.2	962	6	CD386074	CD386074
863	63.6	11.2	482	7	CK128725	AGENCOURT	937	63.6	11.2	963	6	CD387343	CD387343
864	63.6	11.2	483	6	CD639284	AGENCOURT	938	63.6	11.2	965	5	BQ276670	BQ276670
865	63.6	11.2	486	5	BQ526855	NISC_nol8	C 939	63.6	11.2	969	5	BU503863	BU503863
866	63.6	11.2	492	4	BG574039	BG574039	940	63.6	11.2	971	6	CD055074	CD055074
C 867	63.6	11.2	492	4	CO873678	BOVGEn_02	941	63.6	11.2	978	6	CD051220	CD051220
C 868	63.6	11.2	497	5	BQ523971	NISC_no02	942	63.6	11.2	978	6	CD388087	CD388087
869	63.6	11.2	503	1	AV756451	AV756451	943	63.6	11.2	980	6	CD243153	CD243153
870	63.6	11.2	518	1	AV756566	AV756566	944	63.6	11.2	986	6	CB193687	CB193687
871	63.6	11.2	526	1	A1476086	t197903.x	945	63.6	11.2	988	6	CD246455	CD246455
C 872	63.6	11.2	534	5	BQ395278	NISC_ng14	946	63.6	11.2	992	6	CD579612	CD579612
873	63.6	11.2	550	5	BM919518	BM919518	947	63.6	11.2	998	6	CD050633	CD050633
874	63.6	11.2	555	5	BX550071	BX550071	948	63.6	11.2	1003	2	BE967251	BE967251
C 875	63.6	11.2	582	5	BP367580	BP367580	C 949	63.6	11.2	1003	2	BE967251	BE967251
876	63.6	11.2	582	5	BE56257	601117687	C 950	63.6	11.2	1007	5	BQ233647	BQ233647
877	63.6	11.2	589	1	AV714347	AV714347	951	63.6	11.2	1010	5	CD049879	CD049879
878	63.6	11.2	602	1	AV734425	AV734425	952	63.6	11.2	1016	6	CD050745	CD050745
879	63.6	11.2	603	1	AV732976	AV732976	953	63.6	11.2	1020	6	BE965997	BE965997
880	63.6	11.2	605	1	AV714341	AV714341	C 954	63.6	11.2	1032	2	BE965997	601659891
881	63.6	11.2	616	2	BE964260	601657952	955	63.6	11.2	1041	6	CD2498041	CD2498041
C 882	63.6	11.2	622	1	A15696829	AGENCOURT	956	63.6	11.2	1043	6	CD249756	CD249756
883	63.6	11.2	624	6	CD771403	AGENCOURT	957	63.6	11.2	1056	6	CD385652	CD385652
884	63.6	11.2	628	7	CO877522	BOVGEn_05	C 958	63.6	11.2	1065	5	BM907561	BM907561
C 885	63.6	11.2	652	4	BG169501	BG169501	959	63.6	11.2	1083	6	CD243051	CD243051
C 886	63.6	11.2	654	2	BF682593	602117218	C 960	63.6	11.2	1084	7	CK230695	ILLUMIGEN
887	63.6	11.2	660	1	A1256022	u176f04.x	961	63.6	11.2	1088	4	CD048594	CD048594
C 888	63.6	11.2	670	2	AM166977	xg69c11.x	962	63.6	11.2	1100	4	BG108233	BG108233
C 889	63.6	11.2	684	6	CD237052	FNPAGB05	963	63.6	11.2	1111	2	BE286899	BE286899
890	63.6	11.2	685	1	AV733869	AV733869	964	63.6	11.2	1117	4	BM460752	BM460752
C 892	63.6	11.2	702	5	BU803007	SJFPAQ09	C 965	63.6	11.2	1156	5	BQ688321	AGENCOURT
893	63.6	11.2	707	1	AV681884	AV681884	966	63.6	11.2	1158	6	CD389915	CD389915
894	63.6	11.2	709	6	CD639498	AGENCOURT	967	63.6	11.2	1200	5	BM920102	AGENCOURT
895	63.6	11.2	716	4	BG113863	602284313	C 968	63.6	11.2	1307	7	CO390224	AGENCOURT
896	63.6	11.2	726	6	CD638566	AGENCOURT	C 969	63.6	11.2	1349	4	BG120046	602353402
897	63.6	11.2	736	6	CD638562	AGENCOURT	C 970	63.6	11.2	1349	4	BI490160	603031918
898	63.6	11.2	737	6	AV758146	AV758146	C 971	63.6	11.2	1446	4	BI490258	603032068
899	63.6	11.2	741	1	AV760340	AV760340	C 972	63.6	11.2	1603	3	BF983779	602307390
900	63.6	11.2	748	1	AV757984	AV757984	973	63.6	11.2	2146	3	BC027965	Homo sapi

C 974	63.4	11.1	168	7	CF307645	CF307645	ABF--01-C	C1047	63.2	11.1	186	4	BG97864
C 975	63.4	11.1	176	4	BI001620	BI001620	MR3--HN014	1048	63.2	11.1	186	6	CG522269
C 976	63.4	11.1	176	5	BQ636470	BQ636470	hdi0a12.y	1048	63.2	11.1	206	7	CK454091
C 977	63.4	11.1	189	7	CK622931	CK622931	mj03b07.y	1050	63.2	11.1	212	1	AA904121
C 978	63.4	11.1	191	5	BK951840	BK951840	DKFPD7818	1051	63.2	11.1	216	1	AI208112
C 979	63.4	11.1	201	4	BM190413	BM190413	POSM01000	1052	63.2	11.1	220	4	BG96137
C 980	63.4	11.1	204	5	BK951289	BK951289	DKFPD8661	1053	63.2	11.1	221	1	BP987714
C 981	63.4	11.1	205	4	BG957418	BG957418	nph1b09	1054	63.2	11.1	231	2	AM426349
C 982	63.4	11.1	216	5	CFJ13061	CFJ13061	HD--01-A2	1055	63.2	11.1	231	2	AM426349
C 983	63.4	11.1	242	5	BK563001	BK563001	EXS63001	1056	63.2	11.1	232	2	BF904253
C 984	63.4	11.1	256	4	BI001686	BI001686	MR3--HN014	1057	63.2	11.1	232	2	AM103893
C 985	63.4	11.1	269	4	BG980699	BG980699	MR4--HT127	1058	63.2	11.1	241	4	BI490962
C 986	63.4	11.1	272	4	BG995967	BG995967	MR3--CN014	1059	63.2	11.1	242	6	CA376650
C 987	63.4	11.1	294	6	CB522658	CB522658	UI-M-GK0-	1060	63.2	11.1	250	1	AI563578
C 988	63.4	11.1	317	1	AI628292	AI628292	lU87b02.x	1061	63.2	11.1	253	1	AI503174
C 989	63.4	11.1	324	4	BM117156	BM117156	LO847A02-	1062	63.2	11.1	257	1	AI503174
C 990	63.4	11.1	347	6	CB523220	CB523220	UI-M-GK0-	1063	63.2	11.1	259	6	CPD32647
C 991	63.4	11.1	352	2	AM183621	AM183621	xg66910.x	1064	63.2	11.1	268	4	BI056298
C 992	63.4	11.1	367	7	BI847951	BI847951	470215.MA	1065	63.2	11.1	270	1	AI922216
C 993	63.4	11.1	367	7	CFJ298661	CFJ298661	7LBNP--02	1066	63.2	11.1	282	6	CH424357
C 994	63.4	11.1	368	1	AI133692	AI133692	mq28a09.x	1067	63.2	11.1	284	2	AI679358
C 995	63.4	11.1	385	7	CFJ38493	CFJ38493	HD--08-K0	1068	63.2	11.1	296	2	BE683816
C 996	63.4	11.1	389	7	CK374907	CK374907	1a142a05.	1069	63.2	11.1	302	2	AM084440
C 997	63.4	11.1	390	2	BE904691	BE904691	1a149811	1070	63.2	11.1	305	7	EX473779
C 998	63.4	11.1	402	1	AI610822	AI610822	lp38h08.x	1071	63.2	11.1	305	5	CO083659
C 999	63.4	11.1	402	6	BI647950	BI647950	470214.MA	1072	63.2	11.1	309	2	AM059737
C 1000	63.4	11.1	418	6	CD672135	CD672135	fg10b01.x	1073	63.2	11.1	311	2	AM189268
C 1001	63.4	11.1	423	5	CB523074	CB523074	UI-M-GK0-	1074	63.2	11.1	313	6	CB052707
C 1002	63.4	11.1	445	2	BF499456	BF499456	AT14017.5	1075	63.2	11.1	313	5	CP457289
C 1003	63.4	11.1	451	1	AI590781	AI590781	tw25d08.x	1076	63.2	11.1	314	1	AI680280
C 1004	63.4	11.1	453	1	AI627896	AI627896	ly20d07.x	1077	63.2	11.1	328	1	AI250848
C 1005	63.4	11.1	459	4	BI377034	BI377034	BFLG3--000	1078	63.2	11.1	328	2	AM081653
C 1006	63.4	11.1	489	4	AJ747892	AJ747892	UI-R-G00-	1079	63.2	11.1	343	3	BG060256
C 1007	63.4	11.1	513	6	CD371875	CD371875	UI-R-G00-	1080	63.2	11.1	343	7	CO091671
C 1008	63.4	11.1	525	4	BG181066	BG181066	602329181	1081	63.2	11.1	347	7	CK415146
C 1009	63.4	11.1	547	3	CR733854	CR733854	TEtredodn	1082	63.2	11.1	357	1	AI891157
C 1010	63.4	11.1	557	7	CR978761	CR978761	TEtredodn	1083	63.2	11.1	362	1	AI891157
C 1011	63.4	11.1	565	3	CR734714	CR734714	TEtredodn	1084	63.2	11.1	380	1	AI912091
C 1012	63.4	11.1	595	3	CR673874	CR673874	TEtredodn	1085	63.2	11.1	380	2	AM104145
C 1013	63.4	11.1	599	5	BP742823	BP742823	TEtredodn	1086	63.2	11.1	388	4	BM541202
C 1014	63.4	11.1	620	1	AI953803	AI953803	wx81f03.x	1087	63.2	11.1	396	4	BI538821
C 1015	63.4	11.1	622	1	AI923034	AI923034	UI-M-BZ1-	1088	63.2	11.1	399	6	CD673835
C 1016	63.4	11.1	669	6	BE939267	BE939267	UI-M-BZ1-	1089	63.2	11.1	405	1	AI872051
C 1017	63.4	11.1	716	2	CB634293	CB634293	AG044147	1090	63.2	11.1	407	2	BE033090
C 1018	63.4	11.1	808	9	AG044147	AG044147	pan t09l	1091	63.2	11.1	424	1	AI8002625
C 1019	63.4	11.1	834	5	BU938828	BU938828	AG044147	1092	63.2	11.1	426	6	CM521867
C 1020	63.4	11.1	849	5	BU961032	BU961032	AG044147	1093	63.2	11.1	448	2	AM117907
C 1021	63.4	11.1	849	5	BU961032	BU961032	AG044147	1094	63.2	11.1	449	2	AM117907
C 1022	63.4	11.1	849	5	BU961032	BU961032	AG044147	1095	63.2	11.1	449	2	AM117907
C 1023	63.4	11.1	853	1	AI613492	AI613492	AG044147	1096	63.2	11.1	449	2	AM117907
C 1024	63.4	11.1	853	1	AI613492	AI613492	AG044147	1097	63.2	11.1	449	2	AM117907
C 1025	63.4	11.1	854	5	BU938806	BU938806	AG044147	1098	63.2	11.1	449	2	AM117907
C 1026	63.4	11.1	871	2	BE964571	BE964571	AG044147	1099	63.2	11.1	449	2	AM117907
C 1027	63.4	11.1	880	6	CA494582	CA494582	AG044147	1100	63.2	11.1	449	2	AM117907
C 1028	63.4	11.1	915	4	BM415836	BM415836	AG044147	1101	63.2	11.1	449	2	AM117907
C 1029	63.4	11.1	933	4	BM415836	BM415836	AG044147	1102	63.2	11.1	449	2	AM117907
C 1030	63.4	11.1	959	4	BM415836	BM415836	AG044147	1103	63.2	11.1	449	2	AM117907
C 1031	63.4	11.1	979	4	BM415836	BM415836	AG044147	1104	63.2	11.1	449	2	AM117907
C 1032	63.4	11.1	1020	2	BE964420	BE964420	AG044147	1105	63.2	11.1	449	2	AM117907
C 1033	63.4	11.1	1059	7	CK162692	CK162692	AG044147	1106	63.2	11.1	449	2	AM117907
C 1034	63.4	11.1	1288	4	BG105187	BG105187	AG044147	1107	63.2	11.1	449	2	AM117907
C 1035	63.4	11.1	1450	4	BG297378	BG297378	AG044147	1108	63.2	11.1	449	2	AM117907
C 1036	63.4	11.1	5124	3	BC041101	BC041101	AG044147	1109	63.2	11.1	449	2	AM117907
C 1037	63.4	11.1	112	4	BG956245	BG956245	AG044147	1110	63.2	11.1	449	2	AM117907
C 1038	63.2	11.1	144	7	CR854513	CR854513	AG044147	1111	63.2	11.1	449	2	AM117907
C 1039	63.2	11.1	144	7	CR854513	CR854513	AG044147	1112	63.2	11.1	449	2	AM117907
C 1040	63.2	11.1	159	4	BE996109	BE996109	AG044147	1113	63.2	11.1	449	2	AM117907
C 1041	63.2	11.1	162	4	BE996109	BE996109	AG044147	1114	63.2	11.1	449	2	AM117907
C 1042	63.2	11.1	162	5	BE996109	BE996109	AG044147	1115	63.2	11.1	449	2	AM117907
C 1043	63.2	11.1	174	1	BI890806	BI890806	AG044147	1116	63.2	11.1	449	2	AM117907
C 1044	63.2	11.1	175	4	BE980736	BE980736	AG044147	1117	63.2	11.1	449	2	AM117907
C 1045	63.2	11.1	180	2	CD520960	CD520960	AG044147	1118	63.2	11.1	449	2	AM117907
C 1046	63.2	11.1	181	4	AM193134	AM193134	AG044147	1119	63.2	11.1	449	2	AM117907
C 974	63.4	11.1	168	7	CF307645	CF307645	ABF--01-C	C1047	63.2	11.1	186	4	BG97864
C 975	63.4	11.1	176	4	BI001620	BI001620	MR3--HN014	1048	63.2	11.1	186	6	CG522269
C 976	63.4	11.1	176	5	BQ636470	BQ636470	hdi0a12.y	1048	63.2	11.1	206	7	CK454091
C 977	63.4	11.1	189	7	CK622931	CK622931	mj03b07.y	1050	63.2	11.1	212	1	AA904121
C 978	63.4	11.1	191	5	BK951840	BK951840	DKFPD7818	1051	63.2	11.1	216	1	AI208112
C 979	63.4	11.1	201	4	BM190413	BM190413	POSM01000	1052	63.2	11.1	220	4	BG96137
C 980	63.4	11.1	204	5	BK951289	BK951289	DKFPD8661	1053	63.2	11.1	221	1	BP987714
C 981	63.4	11.1	205	4	BG957418	BG957418	nph1b09	1054	63.2	11.1	231	2	AM426349
C 982	63.4	11.1	216	5	CFJ13061	CFJ13061	HD--01-A2	1055	63.2	11.1	231	2	AM426349
C 983	63.4	11.1	242	5	BK563001	BK563001	EXS63001	1056	63.2	11.1	232	2	BF904253
C 984	63.4	11.1	256	4	BI001686	BI001686	MR3--HN014	1057	63.2	11.1	232	2	AM103893
C 985	63.4	11.1	269	4	BG980699	BG980699	MR4--HT127	1058	63.2	11.1	241	4	BI490962
C 986	63.4	11.1	272	4	BG995967	BG995967	MR3--CN014	1059	63.2	11.1	242	6	CA376650
C 987	63.4	11.1	294	6	CB522658	CB522658	UI-M-GK0-	1060	63.2	11.1	250	1	AI563578
C 988	63.4	11.1	317	1	AI628292	AI628292	lU87b02.x	1061	63.2	11.1	253	1	AI503174
C 989	63.4	11.1	324	4	BM117156	BM117156	LO847A02-	1062	63.2	11.1	257	1	AI503174
C 990	63.4	11.1	347	6	CB523220	CB523220	UI-M-GK0-	1063	63.2	11.1	259	6	CPD32647
C 991	63.4	11.1	352	2	AM183621	AM183621	xg66910.x	1064	63.2	11.1	268	4	BI056298
C 992	63.4	11.1	367	7	BI847951	BI847951	470215.MA	1065	63.2	11.1	270	1	AI922216
C 993	63.4	11.1	3										

1120	63.2	11.1	666	7	CK653872	CK653872	AGENCYCOURT	c1193	63	11.1	448	9	CR062536	CR062536	Forward	9
c1121	63.2	11.1	666	7	CK0874611	CK0874611	Boysen_02	c1194	63	11.1	449	6	CB742907	CB742907	AMGNNC:S	5
c1122	63.2	11.1	737	1	AA643038	AA643038	nt57c04_8	c1195	63	11.1	453	5	BU608169	BU608169	UI-CF-FNO	5
c1123	63.2	11.1	744	7	CK999006	CK999006	438409.b	c1196	63	11.1	459	5	BM904780	BM904780	AGENCYCOURT	5
1124	63.2	11.1	747	6	CD299778	CD299778	AGENCYCOURT	c1197	63	11.1	468	6	CB840902	CB840902	M15E-1331	1
c1126	63.2	11.1	786	9	CNS00609	CNS00609	AV725134	c1198	63	11.1	479	6	CB044200	CB044200	NISC_gc03	3
1127	63.2	11.1	787	9	AV698583	AV698583	Drosophila	c1199	63	11.1	483	1	AI687068	AI687068	lp212.1.x	1
c1128	63.2	11.1	796	9	CNS0118D	CNS0118D	AL065615	c1200	63	11.1	488	6	CB217912	CB217912	NISC_nb05	5
c1129	63.2	11.1	808	1	AI811509	AI811509	Drosophila	c1201	63	11.1	491	6	CB857450	CB857450	NISC_na07	7
1130	63.2	11.1	825	1	BU600219	BU600219	tw43f08.x	c1202	63	11.1	492	4	BM320215	BM320215	r88606.y	7
c1131	63.2	11.1	828	5	BU958119	BU958119	AGENCYCOURT	c1203	63	11.1	496	5	BO524185	BO524185	NISC_mo03	3
c1132	63.2	11.1	848	7	CK199711	CK199711	FGAS00821	c1204	63	11.1	496	6	CB049017	CB049017	NISC_g108	8
1133	63.2	11.1	885	5	BU533661	BU533661	AGENCYCOURT	c1205	63	11.1	500	4	BM566217	BM566217	r997b12.y	7
c1134	63.2	11.1	880	7	CV070569	CV070569	WPABHux15	c1206	63	11.1	504	7	CV172531	CV172531	CS6017034	4
c1135	63.2	11.1	889	2	BE974614	BE974614	601680620	c1207	63	11.1	508	5	BU507079	BU507079	AGENCYCOURT	7
c1136	63.2	11.1	892	2	BE965281	BE965281	60169386	c1208	63	11.1	518	1	AI860546	AI860546	w114c08.x	8
c1137	63.2	11.1	892	4	BM416250	BM416250	OP21338 M	c1209	63	11.1	533	3	CR711595	CR711595	Tetradon	3
c1138	63.2	11.1	893	8	AZ538835	AZ538835	ENTDQ54TF	c1210	63	11.1	550	6	CB051646	CB051646	NISC_g102	10
c1139	63.2	11.1	912	2	BE963960	BE963960	601657727	c1211	63	11.1	568	2	AW957086	AW957086	EST369156	6
c1140	63.2	11.1	912	7	CV070007	CV070007	WPABHux15	c1212	63	11.1	575	7	CF284471	CF284471	AGENCYCOURT	7
c1141	63.2	11.1	918	4	BM415367	BM415367	OP20441 M	c1213	63	11.1	582	7	CO879551	CO879551	Boysen_05	7
c1142	63.2	11.1	928	4	BM415124	BM415124	OP20196 M	c1214	63	11.1	629	7	CO876814	CO876814	Boysen_07	7
c1143	63.2	11.1	931	4	BM416456	BM416456	OP21550 M	c1215	63	11.1	675	7	CK654848	CK654848	AGENCYCOURT	7
c1144	63.2	11.1	934	7	CV069353	CV069353	WPABHux15	c1216	63	11.1	682	7	CV200553	CV200553	KN05604.y	7
c1145	63.2	11.1	948	2	BE965430	BE965430	601659149	c1217	63	11.1	690	7	CN842486	CN842486	AGENCYCOURT	7
1146	63.2	11.1	951	5	BU927697	BU927697	AGENCYCOURT	c1218	63	11.1	736	4	BI523076	BI523076	603175614	4
c1147	63.2	11.1	965	5	BU230407	BU230407	AGENCYCOURT	c1219	63	11.1	749	9	AG056308	AG056308	Pan trogl	1
1148	63.2	11.1	1022	9	AG031648	AG031648	Pan trogl	c1220	63	11.1	750	4	BG281986	BG281986	602403172	2
c1149	63.2	11.1	1032	9	BM415979	BM415979	OP21061 M	c1221	63	11.1	758	2	BE254113	BE254113	601113971	7
c1150	63.2	11.1	1104	4	BF982923	BF982923	602306313	c1222	63	11.1	793	7	CF784736	CF784736	AGENCYCOURT	7
c1151	63.2	11.1	1121	2	BE964617	BE964617	601658543	c1223	63	11.1	794	5	BU945019	BU945019	AGENCYCOURT	7
c1152	63.2	11.1	1132	2	CR676528	CR676528	601888324	c1224	63	11.1	811	6	CA465023	CA465023	AGENCYCOURT	7
1153	63.2	11.1	1136	2	BE967014	BE967014	601660745	c1225	63	11.1	819	7	CF784519	CF784519	AGENCYCOURT	7
c1154	63.2	11.1	1234	2	BE967014	BE967014	601660745	c1226	63	11.1	827	5	BU960656	BU960656	AGENCYCOURT	7
c1155	63.2	11.1	1359	2	BE620384	BE620384	601483575	c1227	63	11.1	841	6	CA465886	CA465886	AGENCYCOURT	7
c1156	63.2	11.1	1495	4	BI489115	BI489115	603021183	c1228	63	11.1	897	7	CF783590	CF783590	AGENCYCOURT	7
c1157	63.2	11.1	1526	2	BE964665	BE964665	601658595	c1229	63	11.1	906	7	CN323797	CN323797	AGENCYCOURT	7
c1158	63.2	11.1	1503	4	BI519227	BI519227	603061958	c1230	63	11.1	932	7	CV069725	CV069725	WPABHux15	5
1159	63.2	11.1	1734	3	CR749861	CR749861	Homo sapi	c1231	63	11.1	943	6	CD049386	CD049386	AGENCYCOURT	7
c1160	63.2	11.1	2494	3	BC042109	BC042109	Homo sapi	c1232	63	11.1	949	8	AZ6899021	AZ6899021	ENTUS61TR	7
1161	63.2	11.1	2494	3	BC042109	BC042109	Homo sapi	c1233	63	11.1	955	5	BU843979	BU843979	AGENCYCOURT	7
c1162	63.2	11.1	4883	3	BC051164	BC051164	Mus muscu	c1234	63	11.1	964	5	BQ890200	BQ890200	AGENCYCOURT	7
c1163	63	11.1	138	4	BM541161	BM541161	6169409.b	c1235	63	11.1	964	6	CD106471	CD106471	601866531	7
1164	63	11.1	186	5	BU564879	BU564879	AGENCYCOURT	c1237	63	11.1	1020	2	BF204434	BF204434	602297092	2
1165	63	11.1	257	7	CN226037	CN226037	WLA084C02	c1238	63	11.1	1044	4	BG029532	BG029532	602297092	2
c1167	63	11.1	263	7	CO886356	CO886356	Boysen_14	c1239	63	11.1	1048	4	BG826633	BG826633	602748947	7
c1168	63	11.1	294	4	BI491125	BI491125	6044009.w	c1240	63	11.1	1053	4	BM415599	BM415599	OP20676 M	7
c1169	63	11.1	300	4	BI495345	BI495345	601658545	c1241	63	11.1	1106	5	BM907699	BM907699	AGENCYCOURT	7
1170	63	11.1	310	4	BM154701	BM154701	601888324	c1242	63	11.1	1135	9	CNS03360	CNS03360	AGENCYCOURT	7
c1171	63	11.1	311	4	BM154695	BM154695	601888324	c1243	63	11.1	1139	2	BE965380	BE965380	601658293	3
c1172	63	11.1	330	5	BU709836	BU709836	601888324	c1244	63	11.1	1308	5	BU415948	BU415948	603666734	7
c1173	63	11.1	334	5	CO880999	CO880999	Boysen_09	c1245	63	11.1	1375	2	BE965727	BE965727	601659786	7
1174	63	11.1	340	2	BE750641	BE750641	202125_MA	c1246	63	11.1	1446	4	BI489271	BI489271	603021591	7
c1175	63	11.1	351	5	BU779776	BU779776	601888324	c1247	63	11.1	1566	2	BF343790	BF343790	602015455	7
c1176	63	11.1	354	7	CK313270	CK313270	SB02037A2	c1248	62.8	11.0	125	4	BG576072	BG576072	602598431	7
c1177	63	11.1	355	1	AI358455	AI358455	q19d12.x	c1250	62.8	11.0	130	7	CF641337	CF641337	D38_R07_F	7
1178	63	11.1	356	1	AA537492	AA537492	v447909.x	c1251	62.8	11.0	143	7	CF651657	CF651657	04_L02058	8
c1179	63	11.1	359	1	AI619781	AI619781	601888324	c1252	62.8	11.0	157	6	CD638752	CD638752	AGENCYCOURT	7
c1180	63	11.1	360	1	AI697236	AI697236	601888324	c1253	62.8	11.0	177	4	BU679544	BU679544	601888324	7
c1181	63	11.1	363	5	BO521565	BO521565	NISC_n111	c1254	62.8	11.0	201	1	AI823980	AI823980	601888324	7
1182	63	11.1	374	4	BM154585	BM154585	601888324	c1255	62.8	11.0	209	1	AI858997	AI858997	601888324	7
c1183	63	11.1	379	6	CA684690	CA684690	w1m96.pk0	c1256	62.8	11.0	211	6	BY525196	BY525196	601888324	7
c1184	63	11.1	391	7	CV199373	CV199373	601888324	c1257	62.8	11.0	221	1	BI001657	BI001657	MK3-HN015	7
c1185	63	11.1	392	1	AI690480	AI690480	601888324	c1258	62.8	11.0	222	1	AI868831	AI868831	w58h03.x	7
c1186	63	11.1	393	5	AI282319	AI282319	601888324	c1259	62.8	11.0	231	6	CA779266	CA779266	601888324	7
1187	63	11.1	403	5	BM933621	BM933621	601888324	c1260	62.8	11.0	234	7	CN005680	CN005680	603057818	7
c1188	63	11.1	405	7	CO881030	CO881030	Boysen_09	c1261	62.8	11.0	241	4	BI766585	BI766585	603057818	7
1189	63	11.1	408	7	CF285752	CF285752	AGENCYCOURT	c1262	62.8	11.0	243	3	CO894508	CO894508	Boysen_22	7
c1190	63	11.1	419	5	BO924177	BO924177	AGENCYCOURT	c1263	62.8	11.0	244	4	BU677078	BU677078	601888324	7
1191	63	11.1	420	5	BM938846	BM938846	UI-M-BZ1-	c1264	62.8	11.0	248	1	AI224992	AI224992	601888324	7
1192	63	11.1	439	4	BM529006	BM529006	601888324	c1265	62.8	11.0	255	2	AM426344	AM426344	601888324	7

1266	62.8	11.0	263	4	BG894579	355249	MA	1339	62.8	11.0	1266	5	BO433927	BO433927	AGENCY
1267	62.8	11.0	270	1	AI446605	CJ25B06.x		1340	62.8	11.0	1352	2	BE735370	BE735370	AGENCY
1268	62.8	11.0	271	4	BI539105	451270	MA	1341	62.8	11.0	1456	2	BI490278	BI490278	AGENCY
1269	62.8	11.0	301	6	CA825339	R57C06	MA	1342	62.8	11.0	2042	3	HSM80381	HSM80381	AGENCY
1270	62.8	11.0	304	4	BM572662	FX56A06.y		1343	62.8	11.0	3233	3	HSM803971	HSM803971	AGENCY
1271	62.8	11.0	316	4	BI073294	BI073294		1344	62.6	11.0	120	4	BI775433	BI775433	AGENCY
1272	62.8	11.0	316	7	CA316162	CA316162		1345	62.6	11.0	133	4	BI775433	BI775433	AGENCY
1273	62.8	11.0	317	1	AI642173	AI642173		1346	62.6	11.0	160	4	BI042317	BI042317	AGENCY
1274	62.8	11.0	322	7	CO876326	CO876326		1347	62.6	11.0	167	7	CF968987	CF968987	AGENCY
1275	62.8	11.0	332	7	CK859774	CK859774		1348	62.6	11.0	179	4	BE987113	BE987113	AGENCY
1276	62.8	11.0	339	1	AI609594	AI609594		1349	62.6	11.0	182	2	BE061389	BE061389	AGENCY
1277	62.8	11.0	339	1	AI872139	AI872139		1350	62.6	11.0	186	1	AI918449	AI918449	AGENCY
1278	62.8	11.0	339	1	AI872139	AI872139		1351	62.6	11.0	187	1	AI863191	AI863191	AGENCY
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1284	62.8	11.0	388	4	BG834442	BG834442		1357	62.6	11.0	211	7	CF301886	CF301886	AGENCY
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1322	62.8	11.0	780	6	CB962815	CB962815		1395	62.6	11.0	372	7	CO882559	CO882559	AGENCY
1323	62.8	11.0	795	4	BG396473	BG396473		1396	62.6	11.0	377	6	CB045096	CB045096	AGENCY
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C1418	62.6	11.0	455	7	CF309960	ABF--04-F	
C1419	62.6	11.0	473	5	BUS89899	AGENCOURT	
C1420	62.6	11.0	477	2	BF074766	BR074766	222302.MA
C1421	62.6	11.0	479	5	BQ394664	NISC_ng10	
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C1423	62.6	11.0	483	5	BX744466	BX744466	
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C1435	62.6	11.0	528	5	BQ396638	NISC_ng22	
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C1461	62.6	11.0	782	1	AV755529	AV755529	
C1462	62.6	11.0	786	5	BUS35863	AGENCOURT	
C1463	62.6	11.0	787	5	BUS32114	AGENCOURT	
C1464	62.6	11.0	789	5	BUS67214	AGENCOURT	
C1465	62.6	11.0	818	2	BE964743	601658288	
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DEFINITION							
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EST.							
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NIH-MGC http://mgc.nci.nih.gov/							
Unpublished (1999)							
Contact: Robert Strausberg, Ph.D.							
Email: cgaabs-r@mail.nih.gov							
Tissue Procurement: Life Technologies, Inc.							
CDNA Library Preparation: Life Technologies, Inc.							
DNA Sequencing by: Incyte Genomics, Inc.							
Clone distribution: MGC clone distribution information can be							
found through the I.M.A.G.E. Consortium/LNLT at:							
http://image.lnlt.gov							
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male lung, age 27; and 1 male testis, age 69. Library is							
oligo-dT primed and directionally cloned (EcoRV site is							
destroyed upon cloning). Average insert size 1.8 kb,							
insert size range 1-3 kb. Library is normalized and							
enriched for full-length clones and was constructed by C.							
Gruber (Invitrogen). Research Genetics tracking code							
021. Note: this is a NIH_MGC Library."							
ORIGIN							
Query Match							
Best Local Similarity							
Matches 501; Conservative							
85.6%; Score 488.2; DB 4; Length 875;							
Pred. No. 6,4e-83;							
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Qy 125 GCTCCCTGCTGCTTTCTTTAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGGCTGGC 184  
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Qy 365 TGCTGGGGGGCCCTCAAGTGTGTGGCTGAGCCGAGACTGAGGATCTACACCTGAGGACA 424  
Db 300 TGCTGGGGGGCCCTCAAGTGTGTGGCTGAGCCGAGACTGAGGATCTACACCTGAGGACA 359  
Qy 425 AGAGCTGTGGCCACCGCGAGAGGCTGAAACCCCGCGCGGAGAGACGCTGCATCCCTT 484  
Db 360 AGAGCTGTGGCCACCGCGAGAGGCTGAAACCCCGCGCGGAGAGACGCTGCATCCCTT 419  
Qy 485 CCGCGGCGCGCTCTCAATTAACGTGTGTAAGCAAAAAAAAAAAAAAAAAAAAAA 544  
Db 420 CCGCGGCGCGCTCTCAATTAACGTGTGTAAGCAAAAAAAAAAAAAAAAAAAAAA 479  
Qy 545 AAAAAAAAAAAAAAAAAAAAAA 569  
Db 480 AAAAAAAAAAAAAAAAAAAAAA 504

RESULT 2  
BI818715 496 bp mRNA linear EST 04-OCT-2001  
LOCUS 60303735F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5178608 5',  
DEFINITION mRNA sequence.  
BI818715  
VERSION BI818715.1 GI:15930265  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 496)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strauberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
DNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LLM11445 row: e column: 09  
High quality sequence stop: 471.  
Location/Qualifiers  
1..496  
/organism="Homo sapiens"  
/mol\_type="RNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5178608"  
/lab\_host="DH10B"  
/clone\_1="NIH\_MGC\_115"  
/note="Organ: pooled brain, lung, testis; Vector:  
pCMV-SPORT6; site\_1: NotI; site\_2: EcoRV (destroyed); RNA

## FEATURES

Source

source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."

Query Match 85.1%; Score 485; DB 4; Length 496;  
Best Local Similarity 99.0%; Pred. No. 2,6e-82;  
Matches 488; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 56 CGGCGCGCCCGAGCCCGCCGCAATGAAGCTGCGCCGCTCTGGGGCTGTGCTGGCC 115  
Db 1 CGGCGCGCCCGAGCCCGCCGCAATGAAGCTGCGCCGCTCTGGGGCTGTGCTGGCC 60  
Qy 116 TGTCTGAGCACTCCGCTGCTTTCTTTAGTGGGCTGGCCAAAGCTGTGGCCAGCTG 175  
Db 61 TGTCTGAGCACTCCGCTGCTTTCTTTAGTGGGCTGGCCAAAGCTGTGGCCAGCTG 120  
Qy 176 TGTCTGAGCACTCCGCTGCTTTCTTTAGTGGGCTGGCCAAAGCTGTGGCCAGCTG 235  
Db 121 TGTCTGAGCACTCCGCTGCTTTCTTTAGTGGGCTGGCCAAAGCTGTGGCCAGCTG 180  
Qy 236 CCGTCAACCGCTGAAGCTCTGCTGAGCAAGCTGTGGCACTCCCGTGAACCACTCATAG 295  
Db 181 CCGTCAACCGCTGAAGCTCTGCTGAGCAAGCTGTGGCACTCCCGTGAACCACTCATAG 240  
Qy 296 AGGCTCCGAGAGTGTGTGAGCTGAGCTGTGGTCCCGAGCGCGTGGGGGCGCTGAAGGCC 355  
Db 241 AGGCTCCGAGAGTGTGTGAGCTGAGCTGTGGTCCCGAGCGCGTGGGGGCGCTGAAGGCC 300  
Qy 356 TGAAGGCTGCTGTGGGGGCGCTGAGCACTGTGTGGCTGAGCCGAGACTGAGCATCTAC 415  
Db 301 TGAAGGCTGCTGTGGGGGCGCTGAGCACTGTGTGGCTGAGCCGAGACTGAGCATCTAC 360  
Qy 416 CTGAGGCAAGAGCTGTGGCCACCGCGAGAGGCTGAAACCCCGCGCGGAGAGACGCTC 475  
Db 361 CTGAGGCAAGAGCTGTGGCCACCGCGAGAGGCTGAAACCCCGCGCGGAGAGACGCTC 420  
Qy 476 CATCCCTTCCCGCGCGCGCTCTCAATTAACGTGTGTAAGCAAAAAAAAAAAAAA 535  
Db 421 CATCCCTTCCCGCGCGCGCTCTCTCAATTAACGTGTGTAAGCAAAAAAAAAAAAAA 480  
Qy 536 AAAAAAAAAAAAAA 548  
Db 481 ATTAACAACAAACA 493

RESULT 3  
BM977626/c 490 bp mRNA linear EST 21-FEB-2003  
LOCUS BM977626  
DEFINITION UI-CF-EN1-aef-o-13-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
BM977626  
VERSION BM977626.1 GI:1596235  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 490)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548

Contact: McCray, PB  
McCray Lab  
University of Iowa



2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
The following repetitive elements were found in this CDNA  
sequence: 459-484. >GC rich#low\_complexity  
Seq primer: M13 FORWARD  
POLYA=yes.

## FEATURES

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/mol\_type="mRNA"  
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Cells"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EN1"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-CF-EN1 is a normalized CDNA library containing the  
following tissue(s): Primary Lung Cystic Fibrosis  
Epithelial Cells. The library was constructed according to  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into pT73-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CTGCTCAGGT.  
TAG\_TISSUE=Human Lung Epithelial Cell lines untreated LPS  
6hr to LPS 24h  
TAG\_LIB=UI-CF-EN1  
TAG\_SEQ=CTGCTCAGGT"

## ORIGIN

Query Match 84.6%; Score 482; DB 5; Length 490;  
Best Local Similarity 100.0%; Pred. No. 9, 7e-82;  
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
55 CCGCGCGCCCGGAGCCCGGCGATGAGCTGCGGCTCTGCGTGGCC 114  
|||  
482 CCGCGGCGCCCGGAGCCCGGCGATGAGCTGCGGCTCTGCGTGGCC 423  
|||  
115 CTGTCGTGAGAGCTCCGCTGCTCTTCTTATGAGGAGCGGCAAGCCTGAGCCAGCC 174  
|||  
422 CTGTCGTGAGAGCTCCGCTGCTCTTCTTATGAGGAGCGGCAAGCCTGAGCCAGCC 353  
|||  
175 GTGCTGCGCTGAGAGCTGCGGCGGAGGCGGCGGAGCCTGAGCCAGCCCTCGGC 234  
|||  
362 GTGCTGCGCTGAGAGCTGCGGCGGAGGCGGCGGAGCCTGAGCCAGCCCTCGGC 303  
|||  
235 ACCCTCAACCCGCTGAAAGCTCTGCTGAGAGCCTGGGCAATCCCGTGAACCACTCAT 294  
|||  
302 ACCCTCAACCCGCTGAAAGCTCTGCTGAGAGCCTGGGCAATCCCGTGAACCACTCAT 243  
|||  
295 GAGGGCTCCCGAGAGGTGTGCTGAGAGCTGGGTCCCGAGGCGTGGGGGCGGAGAGGCC 354  
|||  
242 GAGGGCTCCCGAGAGGTGTGCTGAGAGCTGGGTCCCGAGGCGTGGGGGCGGAGAGGCC 183  
|||  
355 CTGAAGGCTCTGCTGAGGAGCCTGACAGTGTGCTGAGCCGAGACTGGAGCATCTACA 414  
|||  
182 CTGAAGGCTCTGCTGAGGAGCCTGACAGTGTGCTGAGCCGAGACTGGAGCATCTACA 123

QY 415 CCTGAGACAGAGCGTGGCCACCCGCGAGGGCTGAAAAACCCGCGCGGGAGAGACCGT 474  
|||  
DB 122 CCTGAGACAGAGCGTGGCCACCCGCGAGGGCTGAAAAACCCGCGCGGGAGAGACCGT 63  
|||  
QY 475 CCATCCCTTCCCGCGGCGCCCTCTCAATTAAGCTGTTAAGACAAAAA 534  
|||  
DB 62 CCATCCCTTCCCGCGGCGCCCTCTCAATTAAGCTGTTAAGACAAAAA 3  
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QY 535 AA 536  
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DB 2 AA 1

RESULT 4  
BI489765 880 bp mRNA 1linear EST 28-AUG-2001  
LOCUS 603032283F1 NIH\_MGC\_115 Homo sapiens CDNA clone IMAGE:5173268 5',  
DEFINITION mRNA sequence.  
ACCESSION BI489765 GI:15328993  
VERSION BI489765.1 GI:15328993  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 880)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cga@rs-remail.nih.gov](mailto:cga@rs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA library preparation: Life Technologies, Inc.  
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM11431 row: F column: 21  
High quality sequence stop: 464.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:5173268"  
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/clone\_lib="NIH\_MGC\_115"  
/note="Organ: pooled brain, lung, testis; Vector:  
pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."

## FEATURES

source  
Location/Qualifiers  
1. .880  
/organism="Homo sapiens"  
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/clone\_lib="NIH\_MGC\_115"  
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pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 83.9%; Score 478.4; DB 4; Length 880;  
Best Local Similarity 97.6%; Pred. No. 1, 7e-81;  
Matches 496; Conservative 0; Mismatches 11; Indels 1; Gaps 1;  
63 CCGAGACCCCGGCGCATGAGCTGCGGCGCTCTGAGGAGCTGTGCGCCCTGCTG 122  
|||  
DB 7 CCGAGACCCCGGCGCATGAGCTGCGGCGCTCTGAGGAGCTGTGCGCCCTGCTG 65  
|||  
QY 123 CAGCTCGCTGCTGCTTTCTTATGAGGAGCTGGCGCAAGCTGTGCGCCAGCTGTGCTGC 182  
|||  
DB 66 CAGCTCGCTGCTGCTTTCTTATGAGGAGCTGGCGCAAGCTGTGCGCCAGCTGTGCTGC 125  
|||

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QY 183 GCTGAGTGGGCGGAGAGCCGGGCGCGGACCCCTGGCCAAACCCCTCGGCAACCCCTCAA 242
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Db 126 GCTGAGTGGGCGGAGAGCCGGGCGCGGACCCCTGGCCAAACCCCTCGGCAACCCCTCAA 185
QY 243 CCCGCTGAAGCTCCTGCTGAGCAGCCTGGGATCCCGGTGAACCACTCATAGAGGCTC 302
    |||
Db 186 CCCGCTGAAGCTCCTGCTGAGCAGCCTGGGATCCCGGTGAACCACTCATAGAGGCTC 245
QY 303 CCAGAAAGTGTGGCTGAGCTGGTCCCAAGCCGCTGGGGCCGTGAAGCCCTGAAGGC 362
    |||
Db 246 CCAAGAGTGTGGCTGAGCTGGTCCCAAGCCGCTGGGGCCGTGAAGCCCTGAAGGC 305
QY 363 CCTGCTGGGGGCGCTGACAGTGTGGCTGAGCCGAGACTGAGAGCATTAACCTGAAGA 422
    |||
Db 306 CCTGCTGGGGGCGCTGACAGTGTGGCTGAGCCGAGACTGAGAGCATTAACCTGAAGA 365
QY 423 CAAGACCTGCGCCACCCGCGAGGGCTGAACCCCGCGCGGGAGAGACCTGTCAATCCC 482
    |||
Db 366 CAAGACCTGCGCCACCCGCGAGGGCTGAACCCCGCGCGGGAGAGACCTGTCAATCCC 425
QY 483 TTCCCTCGGCGCTCTCAATTAACGTGTGAAGAGCAAAAAAAGAAAAAAGAAAAA 542
    |||
Db 426 TTCCCTCGGCGCTCTCAATTAACGTGTGAAGAGCAAAAAAAGAAAAAAGAAAAA 485
QY 543 AAAAAAAAAAAAAAAAAAAAAA 570
    |||
Db 486 AAAAAAGCAAAAACATAGTAAAAACAA 513

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RESULT 5
BM920793 473 bp mRNA linear EST 12-MAR-2002
LOCUS BM920793 5', mRNA sequence.
DEFINITION AGENCOURT 6705933 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752038
ACCESSION BM920793
VERSION BM920793.1 GI:19371172
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12785 row: j column: 07
High quality sequence stop: 474.
Location/Qualifiers
1..473
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
/clone_1fb="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code

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ORIGIN
Query Match 82.8%; Score 472; DB 5; Length 473;
Best Local Similarity 100.0%; Pred. No. 7.7e-80;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

021. Note: this is a NIH_MGC Library."

QY 73 GCGGCATGAAAGCTCGCCGCTCCCTGAGGGGCTGTGGGAGCCCTTCTGACGCTCGCT 132
    |||
Db 1 GCGGCATGAAAGCTCGCCGCTCCCTGAGGGGCTGTGGGAGCCCTTCTGACGCTCGCT 60
QY 133 GCTGCTTTCTAGTGGGCTCGGCTCAAGCTGTGGCCAGCCCTGTGCGCTGAGAGTGT 192
    |||
Db 61 GCTGCTTTCTAGTGGGCTCGGCTCAAGCTGTGGCCAGCCCTGTGCGCTGAGAGTGT 120
QY 193 GCGGCGAGGCGCGGGGCGCGGACCTGCGCAACCCCGGACCCGCTGAAG 252
    |||
Db 121 GCGGCGAGGCGCGGGGCGCGGACCTGCGCAACCCCGCTGAAG 180
QY 253 CTCCTGCTGAGGAGGCTGGGCTATCCCGTGAACCACTCATAGAGGCTCCAGAAAGTGT 312
    |||
Db 181 CTCCTGCTGAGGAGGCTGGGCTATCCCGTGAACCACTCATAGAGGCTCCAGAAAGTGT 240
QY 313 GTGCTGAGCTGGGTCCCAAGCCGTGGGGCGGTGAAGGCTCTGCTGGGG 372
    |||
Db 241 GTGCTGAGCTGGGTCCCAAGCCGTGGGGCGGTGAAGGCTCTGCTGGGG 300
QY 373 GCCCTGACAGTGTGGCTGAGCTGAGACTGAGACTTCAACCTGAGAGCAAGAGCTGT 432
    |||
Db 301 GCCCTGACAGTGTGGCTGAGCTGAGACTGAGACTTCAACCTGAGAGCAAGAGCTGT 360
QY 433 CCAACCCGCGAGGCTGAACCCCGCGGGGAGAGACCTGTCCCTTCCCGCGG 492
    |||
Db 361 CCAACCCGCGAGGCTGAACCCCGCGGGGAGAGACCTGTCCCTTCCCGCGG 420
QY 493 CCTCTCAATTAACGTGTGAAGCAAAAAAAGAAAAAAGAAAAA 544
    |||
Db 421 CCTCTCAATTAACGTGTGAAGCAAAAAAAGAAAAAAGAAAAA 472

RESULT 6
BM920794 473 bp mRNA linear EST 12-MAR-2002
LOCUS BM920794 5', mRNA sequence.
DEFINITION AGENCOURT 6705953 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752039
ACCESSION BM920794
VERSION BM920794.1 GI:19371173
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12785 row: j column: 08
High quality sequence stop: 474.
Location/Qualifiers
1..473
/organism="Homo sapiens"
/mol_type="mRNA"
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/lab.host="EDH08"
/clone.lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SpRites; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

```

## ORIGIN

Query Match	82.5%	Score 470.4	DB 5	Length 473
Best Local Similarity	99.8%	Pred. No. 1.6e-79		
Matches 471	Conservative	0	Mismatches 1	Indels 0
			Gaps 0	
QY	73	CGCGCCATGAAGACTGCGCGCCCTCCTGCGGGGCTGTGCGGCGCTTGTCTCTGCAAGCTCCCT	132	
Db	1	CGCGCCATGAAGACTGCGCGCCCTCCTGCGGGGCTGTGCGGCGCTTGTCTCTGCAAGCTCCCT	60	
QY	133	GCTGCTTTCTTAAGTGGGCTCGGCCCAAGCCTGTGGCCAGCCTGTGCTCGCGCTGAGTCG	192	
Db	61	GCTGCTTTCTTAAGTGGGCTCGGCCCAAGCCTGTGGCCAGCCTGTGCTCGCGCTGAGTCG	120	
QY	193	GCGGCGAGGCGCGGGGCGGGAGCCTTGCGCAACCCCTTGCGCACTTAACCCGCTGAAG	252	
Db	121	GCGGCGAGGCGCGGGGCGGGAGCCTTGCGCAACCCCTTGCGCACTTAACCCGCTGAAG	180	
QY	253	CTCCGTGCAACAAGCTGCGGCACTCCCGGTGAACCAACTATGAGGGCTCCCAAGAGAT	312	
Db	181	CTCCGTGCAACAAGCTGCGGCACTCCCGGTGAACCAACTATGAGGGCTCCCAAGAGAT	240	
QY	313	GTGCGTAGCTGGGTCCTCCAGAGCGTGGGGGCGGTGAAGCCCTGAAGACCTGCTGGAG	372	
Db	241	GTGCGTAGCTGGGTCCTCCAGAGCGTGGGGGCGGTGAAGCCCTGCTGGAG	300	
QY	373	GCCCTGAACAGTGTGTTGGCTGAGCCGAGACTGGAGCATTAACACTGAAGACAAGACGTG	432	
Db	301	GCCCTGAACAGTGTGTTGGCTGAGCCGAGACTGGAGCATTAACACTGAAGACAAGACGTG	360	
QY	433	CCCAACCGCGAGGGGTGAAGAACCCCGCGCGGGAGGACCGTCATCCCTTTCCCGGAC	492	
Db	361	CCCAACCGCGAGGGGTGAAGAACCCCGCGCGGGAGGACCGTCATCCCTTTCCCGGAC	420	
QY	493	CCCTCTCAATAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	544	
Db	421	CCCTCTCAATAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	472	

RESULT 7				
B1819795				
LOCUS	B1819795	496 bp	mRNA	linear EST 04-OCT-2001
DEFINITION	603041303F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182081 5', mRNA sequence.			
ACCESSION	B1819795			
VERSION	B1819795.1	GI:15931345		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 496)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-r@mail.nih.gov			
	Tissue Procurement: Life Technologies, Inc.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.W.A.G.E. Consortium (ULNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM1454 row: f column: 02  
High quality sequence start: 6  
High quality sequence stop: 496.

## FEATURES

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/organism="Homo sapiens"
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/clone_lib="NH_MGC_115"
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pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
cligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NH_MGC Library."

```

## ORIGIN

Query Match	Similarity	82.0%	Score	467.4	DB 4	Length	496
Best Local	Similarity	99.4%	Pred.	5.8e-79			
Matches	490	Conservative	0	Mismatches	1	Indels	2
Qy	55	CCGCGCGCCCCGAGACCCCCCGGCCATGAGAGCTCGCCGCTCTCTGGGGCTCTGCTGGCC	114				
Db	1	CCGCGCGCCCCGAGACCCCCCGGCCATGAGAGCTCGCCGCTCTCTGGGGCTCTGCTGGCC	59				
Qy	115	CTGCTCTGGAGCTCCGCTGCTCTTCTTCTAGTGGGCTCGGCCAAGCCGTGTGGCCAGGCT	174				
Db	60	CTGCTCTGGAGCTCCGCTGCTCTTCTTCTAGTGGGCTCGGCCAAGCCGTGTGGCCAGGCT	119				
Qy	175	GTCGCTGCGCTGAGAGTCGCGCGGCGGAGGCGGGGCGGGACCTTGCCAAACCCCTCGGC	234				
Db	120	GTCGCTGCGCTGAGAGTCGCGCGGCGGAGGCGGGGCGGGACCTTGCCAAACCCCTCGGC	179				
Qy	235	ACCTCTCAACCCGCTGGAAGCTCTGCTGAGGAGCTCTGGGCAATCCCGCTGAACCACTCAT	294				
Db	180	ACCTCTCAACCCGCTGGAAGCTCTGCTGAGGAGCTCTGGGCAATCCCGCTGAACCACTCAT	239				
Qy	295	GAGGGCTCCCGAAGTGTGTGGCTGAGGCTGGGATCCCGAGGCGGTGGGGGCGTGGAAGCC	354				
Db	240	GAGGGCTCCCGAAGTGTGTGGCTGAGGCTGGGATCCCGAGGCGGTGGGGGCGTGGAAGCC	299				
Qy	355	CTGAAGGCGCTGTGGGGGCGCTTGAAGATGTTTGGCTGAGCGGAGACTGAGACATCTACA	414				
Db	300	CTGAAGGCGCTGTGGGGGCGCTTGAAGATGTTTGGCTGAGCGGAGACTGAGACATCTACA	359				
Qy	415	CGTGAAGACAAAGAGCTGCGCCACCGCGGAGGGCTGAAAACCCCGCGGGGGAGGACCGT	474				
Db	360	CGTGAAGACAAAGAGCTGCGCCACCGCGGAGGGCTGAAAACCCCGCGGGGGAGGACCGT	418				
Qy	475	CCATCCCTTCCCGCGGCGCTCTCAATTAACGTGTGAAGACAAAAAAAAAAAAAAAAAAAA	534				
Db	419	CCATCCCTTCCCGCGGCGCTCTCAATTAACGTGTGAAGACAAAAAAAAAAAAAAAAAAAA	478				
Qy	535	AAAAAAAAAAAAA 547					
Db	479	AAAAAAAAAAAAA 491					
RESULT 8							
LOCUS	B0067622	1059 bp	mRNA	linear	EST 02-APR-2007		
DEFINITION	AGNENOCURT_6759083 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:575192						
ACCESSION	B0067622						

VERSION B0067622.1 GI:19896668  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS 1 (bases 1 to 1059)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM12793 row: m column: 17  
High quality sequence stop: 343.  
Location/Qualifiers  
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/clone="IMAGE:5755192"  
/lab\_host="DH10B"  
/clone\_11b="NIH\_MGC\_115"  
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 81.1%; Score 462.4; DB 5; Length 1059;  
Best Local Similarity 99.8%; Pred. No. 5.2e-78;  
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 57 GCGGCCCCGAGCCCGCCGCAATGAGCTCGCCGCTCTGAGGCTGAGGCTCTT 116  
DB 1 GCGGCCCCGAGCCCGCCGCAATGAGCTCGCCGCTCTGAGGCTGAGGCTCTT 116  
QY 117 GTCCTGAGCTCGGCTGCTCTTTTAACTGAGGCTGAGGCTGAGGCTGAGGCTG 176  
DB 61 GTCCTGAGCTCGGCTGCTCTTTTAACTGAGGCTGAGGCTGAGGCTGAGGCTG 120  
QY 177 GCGTGGCTGAGTGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 236  
DB 121 GCGTGGCTGAGTGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 180  
QY 237 CCTCAACCGGCTGAGCTCTGCTGAGGAGCTGGGCAATCCCGTGAACCACTCATAGA 296  
DB 181 CCTCAACCGGCTGAGCTCTGCTGAGGAGCTGGGCAATCCCGTGAACCACTCATAGA 240  
QY 297 GGGCTCCCAAGAGTGTGTGAGCTGAGCTGGGTCCTCCAGGCGGAGGAGGCGGAGGAGG 356  
DB 241 GGGCTCCCAAGAGTGTGTGAGCTGAGCTGGGTCCTCCAGGCGGAGGAGGCGGAGGAGG 300  
QY 357 GAAGGCGGCTGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 416  
DB 301 GAAGGCGGCTGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 360  
QY 417 TGAGGACAAGAGCTGCCCAACCGGAGGAGGCTGAAGAAACCCCGCGGAGGAGGAGACGGTCC 476  
DB 361 TGAGGACAAGAGCTGCCCAACCGGAGGAGGCTGAAGAAACCCCGCGGAGGAGGAGACGGTCC 420

QY 477 ATCCCTTCCCCCGGCGCCCTCTCAATPAACGTGTGAAGGCA 520  
DB 421 ATCCCTTCCCCCGGCGCCCTCTCAATPAACGTGTGAAGGCA 464

RESULT 9  
LOCUS BM921624  
DEFINITION BM921624 1093 bp mRNA linear EST 12-MAR-2002  
AGENCOURT\_6707854 NIH\_MGC\_115 Homo sapiens CDNA clone IMAGE:5753142  
5', mRNA sequence.  
BM921624  
BM921624.1 GI:19372003  
EST.  
VERSION BM921624  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS 1 (bases 1 to 1083)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM12788 row: h column: 07  
High quality sequence stop: 486.  
Location/Qualifiers  
1..1083  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5753142"  
/lab\_host="DH10B"  
/clone\_11b="NIH\_MGC\_115"  
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 80.9%; Score 461; DB 5; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 9.6e-78;  
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GCGGCCCCGAGCCCGCCGCAATGAGCTCGCCGCTCTGAGGCTGAGGCTCTT 117  
DB 20 GCGGCCCCGAGCCCGCCGCAATGAGCTCGCCGCTCTGAGGCTGAGGCTCTT 79  
QY 118 TCTTCAGCTCCGCTGCTCTTTTAACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 177  
DB 80 TCTTCAGCTCCGCTGCTCTTTTAACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 139  
QY 178 GCTGGCTGAGTGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 237  
DB 140 GCTGGCTGAGTGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 199  
QY 238 CTCAACCGGCTGAGGCTCTGCTGAGGAGCTGGGCAATCCCGTGAACCACTCATAGA 297  
DB 200 CTCAACCGGCTGAGGCTCTGCTGAGGAGCTGGGCAATCCCGTGAACCACTCATAGA 259  
QY 298 GGTCCCAAGAGTGTGTGAGCTGAGGTCCTCCAGGCGGAGGAGGCGGAGGAGGCGGAGG 357

Db	260	GGCTCCAGAAAGTGTGTGCTGAGCTGGGTCCCAAGCCGTGTGGGGCCGTAAAGGCCCTTG	319
QY	358	AAGGCCCTGTGGGGGCCCTTGACAGTGTGTTGGCTTGAGCCGAGACTGAGACATCTACACT	417
Db	320	AAGGCCCTGTGGGGGCCCTTGACAGTGTGTTGGCTTGAGCCGAGACTGAGACATCTACACT	379
QY	418	GAGACAAAGACGCTGGCCCAACCCCGAGGGCTGAAAAACCCCGCGGGGAGAGACGCTCCA	477
Db	380	GAGACAAAGACGCTGGCCCAACCCCGAGGGCTGAAAAACCCCGCGGGGAGAGACGCTCCA	439
QY	478	TTCCCTTCCCCCGGCCCTCTCAATTAACGTTGAAGC	518
Db	440	TTCCCTTCCCCCGGCCCTCTCAATTAACGTTGAAGC	480
RESULT 10			
LOCUS	AM974727	550 bp	mRNA linear EST 02-JUN-2000
DEFINITION	EST386817 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.		
ACCESSION	AM974727		
VERSION	AM974727.1	GI:8165915	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Hedde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, T.E., Speed, A.T., Shatov, V., Lee, N.H., Yeatman, T.J. and Assenbush, J.		
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 338		
FEATURES	Seq primer: Reverse.		
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone_id="MAGE resequences, MAGN"		
	/note="Vector: pBluescriptSKm"		
ORIGIN			
Query Match	80.3%	Score 457.6;	DB 2; Length 550;
Best Local Similarity	99.1%	Pred. No. 4.3e-77;	
Matches 460;	Conservative	0; Mismatches	4; Indels 0; Gaps 0
QY	55	CCGGCGCGCCCGAGGCCCGCGGCATGAAGCTCGCGGCTCTCTGGGCTCTGCGTGGCC	114
Db	1	CCTTGCGCGCCGAGGCCCGCGGCATGAAGCTCGCGGCTCTCTGGGCTCTGCGTGGCC	60
QY	115	CTGTCTCTGAGTCCGCTGCTGCTCTTTCTTAATGTTGGGCTGGCCAAAGCTGTGGCCAGCTT	174
Db	61	CTGTCTCTGAGTCCGCTGCTGCTCTTTCTTAATGTTGGGCTGGCCAAAGCTGTGGCCAGCTT	120
QY	175	GTCGCTGGCTGGAGTTCGGCGCGGAGGCCGGGAGGCCGGAACCTTGAGCCAAACCCCTCGGC	234
Db	121	GTCGCTGGCTGGAGTTCGGCGCGGAGGCCGGGAGGCCGGAACCTTGAGCCAAACCCCTCGGC	180
QY	235	ACCTCAACCCGCTGAAGCTCTCTGCTGAGCAGCTTGAGGATCCCGTGAACCACTCATTA	294
Db	181	ACCTCAACCCGCTGAAGCTCTCTGCTGAGCAGCTTGAGGATCCCGTGAACCACTCATTA	240
QY	295	GAGGCTCCCAAGATGTGTGCTGAGCTGGTCCCAAGCCGTGGGGCGCTGAAGGCC	354

Db	241	GAGGGCTCCAGAAAGTGATGAGCTGAGCTGAGGTCCCAAGGCGGTG66GGCCGTGAAGGCC	300
Qy	355	CTGAAGGCGCTGCTGGGGGGCCCTGACAGCTGTTTGCTGAGCCGACGACTGTGAAGCTCTTACA	414
Db	301	CTGAAGGCGCTGCTGGGGGGCCCTGACAGCTGTTTGCTGAGCCGACGACTGTGAAGCTCTTACA	360
Qy	415	CTGAGAGCAAGAGCTGCTGCCACCCGGGAGGGGCTGAAGAACCCGCGCGGGAGAGACCGT	474
Db	361	CTGAGAGCAAGAGCTGCTGCCACCCGGGAGGGGCTGAAGAACCCGCGCGGGAGAGACCGT	420
Qy	475	CCATCCCGCTTCCCCCGGCGCCCTCTCAATTAACGTGTGTTAAGAGC	518
Db	421	CCATCCCGCTTCCCCCGGCGCCCTCTCAATTAACGTGTGTTAAGAGC	464
RESULT 11			
Bi819014		491 bp	mRNA
LOCUS	603033130F1	NIH_MGC_115	Homo sapiens cDNA clone IMAGE:5174526 5',
DEFINITION	mRNA sequence.		
ACCESSION	Bi819014		
VERSION	Bi819014.1	GI:15930564	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 491)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-rc@mail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: LLNL1434 row: k column: 07		
FEATURES	High quality sequence stop: 470.		
source	Location/Qualifiers		
	1..491		
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	/clone="IMAGE:5174526"		
	/lab_host="DH10B"		
	/clone_id="NIH_MGC_115"		
	/note="Organ: pooled brain, lung, testis; Vector: pCMW-SORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA male lung, age 27; and 1 male testis, age 65. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	80.1%;	Score 456.4;	DB 4; Length 491;
Best Local Similarity	97.5%;	Pred. No. 7.2e-77;	
Matches	474;	Conservative 0;	Mismatches 11; Indels 1; Gaps 1;
Qy	58	CGCGCCCCGAGCCCCCGGCCATGAAGCTGCGCCGCTCTGCGGGCTCTGCGTGGCCCTG	117
Db	1	CGCGCCCCGAGCCCCCGGCCATGAAGCTGCGCG-CTCTCGGGGCTCTGCGTGGCCCTG	59
Qy	118	TTCGCGAGCTCCGCTGCTGCTTTCTTAGTGAGGCTCGGCAAGCCTGTGGCCCAAGCTCTGTC	177
Db	60	TTCGCGAGCTCCGCTGCTGCTTTCTTAGTGAGGCTCGGCAAGCCTGTGGCCCAAGCTCTG	119

RESULT 12	
LOCUS	BI821791
DEFINITION	BI821791 680 bp mRNA
ACCESSION	60305866F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176672 5',
VERSION	BI821791
KEYWORDS	BI821791.1 GI:15933341
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	1 (bases 1 to 680)
	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
COMMENT	Contract. Robert Stenmark

## FEATURES

```

1. 680
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:5176672"
/lab_host="DH10B"
/clone_1fb="NH MGC 115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27, and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 Kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C

```

	Gruber (Invitrogen). Research Genetics tracking code	
ORIGIN	021. Note: this is a NTH_MGC Library."	
Query Match	80.0%; Score 456.2; DB 4;	Length 680;
Best Local Similarity	95.2%; Pstd. No. 7.9e-77;	
Matches 492; Conservative 0;	Mismatches 23;	Indels 2; Gaps 2
Dn	CGCGGCGCCGAGGCCCGCGGGCATGAGTGTCGCGCCCTTCTGGGGCTTCGTGGGCC	115
Dn	1 CGCGCGCCCCGAGGCCCGCGGGCATGAGTGTCGCGCCCTTCTGGGGCTTCGTGGGCC	115
Dn	116 TGTCGTACACTCCGCTGCTGCTTTCTTAATGAGGCTCGGCCAAGCCTGGGCCAGCTG	175
Dn	61 TGTCTTGAAGTCCGCTGCTGCTTTCTTAATGAGGCTCGGCCAAGCCTGGGCCAGCTG	120
Dn	176 TCGTGTGCTGAGTGGGCGGCG - GAGCGCGGGGCGGGACCCTGGCCAACTCCCTTG	234
Dn	121 TCGGTGGCTGAGTGGGCGGCGTAGGCGCGGAGCCCGGAGACCTGGCCAACTCCCTTG	180
Dn	235 ACCCTCAACCCGCTGAGTCTCTGCTGAGCAAGCTGGGCATCCCCTGAAACAACCTCAT	294
Dn	181 ACCTCAACCCGCTGAGTCTCTGCTGAGCAAGCTGGGCATCCCCTGAAACAACCTCAT	240
Dn	295 GAGGCTCCAGAGTGTGTGCTGAGTGGGATCCCGAGGCGGTGGGGGCGCGTGAAGCC	354
Dn	241 GAGGCTCCAGAGTGTGTGCTGAGTGGGATCCCGAGGCGGTGGGGGCGCGTGAAGCC	300
Dn	355 CTGAAGGCCCTGCTGGGGGCCCTGACATGTTTTGGCTGAGCCGAGAATGAGCATCTACA	414
Dn	301 CTGAAGGCCCTGCTGGGGGCCCTGACATGTTTTGGCTGAGCCGAGAATGAGCATCTACA	360
Dn	415 CTTGAGGACAGAGCTGTCACACCGGAGGGCTGAAAAACCGCGCGCGGGAGGACCGT	474
Dn	361 CTTGAGGACAGAGCTGTCACACCGGAGGGCTGAAAAACCGCGCGCGGGAGGACCGT	420
Dn	475 CCATCCCTTCCCGGCGCCCTCTCAA - TTAAGTGTTTAAGGCAAAAAAAAAAAAAA	533
Dn	421 CCATCCCTTCCCGGCGCCCTCTCAAAGTAAAGTGTTTAAGGCGCAAGAAAGAGGA	480
Dn	534 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 570	
Dn	481 CAAGAGAAAGAACGCAAAAACAGACAAAAACACA 517	

RESULT 13	
B1819045	
LOCUS	
DEFINITION	B1819045            961 bp       mRNA          linear      EST 04-OCT-2001
ACCESSION	G630331B6F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174540 5' ,
VERSION	mRNA sequence.
KEYWORDS	B1819045
SOURCE	B1819045.1 GI:15930595
ORGANISM	EST.
	Homo sapiens (human)
	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	NIH-MGC http://mgc.nci.nih.gov/..
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
	Contact: Robert Straubeberg Ph.D

1. [Gene Procurement: Life Technologies, Inc.](#)  
 2. [cDNA Library Preparation: Life Technologies, Inc.](#)  
 3. [DNA Sequencing by: Incyte Genomics, Inc.](#)  
 4. [Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>](#)  
 5. [Plate: L14M1434 row: k column: 21](#)  
 6. [High quality sequence start: 3](#)  
 7. [High quality sequence stop: 511.](#)

## FEATURES

Location/Qualifiers

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/note="Organ: pooled brain, lung, testis; Vector: pcMV-SPORE6; Site 1: Notch; Site 2: Ecorev (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (Ecorev site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 79.4%; Score 452.6; DB 4; Length 961;  
Best Local Similarity 97.6%; Pred. No. 3.8e-76;  
Matches 491; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

QY CCCGAGCCCCCGGCGCATGAAGCTGCGC-GCCCTCTGGGGCTCTGGGTGGCCCTGCT 121  
DB 5 CCCCAGAGCCCCCGGCGCATGAAGCTGCGCCTCTCTGGGGCTCTGGGTGGCCCTGCT 64

QY 122 GCAGCTCGGTGCTCTTTCTTAGTGGGCTCGGCGCAAGCTGTGGCCAGCTGTGCTG 181  
DB 65 GCAGCTCGGTGCTCTTTCTTAGTGGGCTCGGCGCAAGCTGTGGCCAGCTGTGCTG 124

QY 182 CGCTGAGTGGGGCGGCGAGCGCGGGCGCGGACCTGTGGCAACCCCTCTGGCACTCTCA 241  
DB 125 CGCTGAGTGGGGCGGCGAGCGCGGGCGCGGACCTGTGGCAACCCCTCTGGCACTCTCA 184

QY 242 ACCCGTGAAGCTCTCTGCTGAGCAAGCTGGGCACTCCCGTGAACCACTCATAGAGGCT 301  
DB 185 ACCCGTGAAGCTCTCTGCTGAGCAAGCTGGGCACTCCCGTGAACCACTCATAGAGGCT 244

QY 302 CCCGAGAGTGTGTGCTGAGCTGGGTCCCGAGCGGTGGGGCGGTGAAGGCGCTGAAG 361  
DB 245 CCCGAGAGTGTGTGCTGAGCTGGGTCCCGAGCGGTGGGGCGGTGAAGGCGCTGAAG 304

QY 362 CCTGTGCTGGGGCGCTGACAGTGTGGTGGTGAAGCGGACCTTACACTTGAAGG 421  
DB 305 CCTGTGCTGGGGCGCTGACAGTGTGGTGGTGAAGCGGACCTTACACTTGAAGG 364

QY 422 ACAAGAAGCTGCGCAAGCGGAGGAGTGAAGCCCGCGCGGGGAGGACCGTCAATCC 481  
DB 365 ACAAGAAGCTGCGCAAGCGGAGGAGTGAAGCCCGCGCGGGGAGGACCGTCAATCC 423

QY 482 CTTTCCCC-GGCGCTCTCATTAACGTGTGTTAAGACCAAAAAAAAAAAAAAAAAAAAA 540  
DB 424 CTTTCCCCGGGGCGCTCTCATTAACGTGTGTTAAGACCAAAAAAAAAAAAAAAAAAAAA 483

QY 541 AAAAAAAAAAAAAAAAAAAAAA 563  
DB 484 ATATTAACAAAAAAAAAAAAA 506

## RESULT 14

BI824102 885 bp mRNA linear EST 04-OCT-2001  
LOCUS 603039244F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5180195 5',  
DEFINITION mRNA sequence.

## ACCESSION

BI824102

## VERSION

BI824102.1 GI:15935652

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens (human)

## REFERENCE

1 (bases 1 to 885)  
NIH-MGC <http://imgc.nhl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLM1449 row: 5 column: 12  
High quality sequence stop: 469.

## FEATURES

source

Location/Qualifiers

1. .885  
/organism="Homo sapiens"  
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/note="Organ: pooled brain, lung, testis; Vector: pcMV-SPORE6; Site 1: Notch; Site 2: Ecorev (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (Ecorev site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 79.1%; Score 450.6; DB 4; Length 885;  
Best Local Similarity 94.9%; Pred. No. 9.2e-76;  
Matches 487; Conservative 0; Mismatches 24; Indels 2; Gaps 2;

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DB 1 CGCGCGCCCCGAGCCCCCGGCGCATGAAGCTGCGCCTCTCTGGGGCTTGTGGGCCC 60

QY 116 TGTCTGAGCTCGGTGCTCTTTCTTAGTGGGCTCGGCGCAAGCTGTGGGCGGAGCTG 175  
DB 61 TGTCTGAGCTCGGTGCTCTTTCTTAGTGGGCTCGGCGCAAGCTGTGGGCGGAGCTG 120

QY 176 TCGCTGC-GCTGAGTTC-GGCGCGGAGGCGGGGCGGGAGCCCTGAGCCAAACCCCTCG 233  
DB 121 TCGCTGCAGTGTGCTGAGTGTGGCGGAGGCGGGGCGGGAGCCCTGAGCCAAACCCCTCG 180

QY 234 GACCTCAACCGCTGAAGCTCTCTGCTGAGCAAGCTGGGAGTCCCGTGAACCACTCAT 293  
DB 181 GACCTCAACCGCTGAAGCTCTCTGCTGAGCAAGCTGGGAGTCCCGTGAACCACTCAT 240

QY 294 AGAGGCTCCCAAGAGTGTGCTGAGCTGGGTCCCGAGCGGTGGGGCGGTGAAGGC 353  
DB 241 AGAGGCTCCCAAGAGTGTGCTGAGCTGGGTCCCGAGCGGTGGGGCGGTGAAGGC 300

QY 354 CTTGAAGGCGCTGCTGGGGCGCTGACAGTGTGGCTGAGCGGAGCTGAGCATCTAC 413  
DB 301 CTTGAAGGCGCTGCTGGGGCGCTGACAGTGTGGCTGAGCGGAGCTGAGCATCTAC 360

QY 414 ACCTGAGGAGAGAGCTGCTGAGCCGCGAGGAGGAGTGAAGCCCGCGCGGGAGGAGCG 473  
DB 361 ACCTGAGGAGAGAGCTGCTGAGCCGCGAGGAGGAGTGAAGCCCGCGCGGGAGGAGCG 420

QY 474 TCCATCCCTTCCCGCGCGCGCTGCAATTAAGTGTGAAGCAAAAAAAAAAAAAA 533  
DB 421 TCCATCCCTTCCCGCGCGCGCTGCAATTAAGTGTGAAGCAAAAAAAAAAAAAA 480

QY 534 AAAAAAAAAAAAAAAAAAAAAA 566



Db 481 CCACACCAAGCCATCACAACCAACACAA 513

## RESULT 15

BM977779/c

## LOCUS

BM977779 472 bp mRNA linear EST 21-FEB-2003

UI-CF-EN1-aef-n-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone

UI-CF-EN1-aef-n-17-0-UI 3', mRNA sequence.

BM977779.1 GI:19596542

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

BM977779 472 bp mRNA linear EST 21-FEB-2003  
UI-CF-EN1-aef-n-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
UI-CF-EN1-aef-n-17-0-UI 3', mRNA sequence.  
BM977779.1 GI:19596542  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eultheria; Primates; Catarrhini; Homidae; Homo.  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.researchgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=yes.

## FEATURES

## SOURCE

Location/Qualifiers  
1..472  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-EN1-aef-n-17-0-UI"  
/tissue\_type="Primary Lung Cystic Fibrosis Epithelial  
Cells"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EN1"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-EN1 is a normalized cDNA library containing the  
following tissue(s): Primary Lung Cystic Fibrosis  
Epithelial Cells. The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into pT73-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CTGCTCAGGT.  
TAG\_TISSUE=Human Lung Epithelial Cell lines untreated LPS  
6hr to LPS 24h  
TAG\_LIB=UI-CF-EN1  
TAG\_SEQ=CTGCTCAGGT"

## ORIGIN

Query Match 78.6%; Score 448; DB 5; Length 472;  
Best Local Similarity 97.8%; Pred. No. 2.9e-75;  
Matches 454; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 73 GCGCCATGAAAGCTGCGCCCTTCCTGAGGCTGCGGAGCCCTGCTGAGCTCCGCT 132  
Db 464 GCGCCATGAAAGCTGCGCCCTTCCTGAGGCTGCGGAGCCCTGCTGAGCTCCGCT 405  
QY 133 GCTGCTTTTAAAGGAGCTGCGGCAAGCCCTGAGGCTGCGGAGCTGCGGAGCTG 192  
Db 404 GCTGCTTTTAAAGGAGCTGCGGCAAGCCCTGAGGCTGCGGAGCTGCGGAGCTG 345  
QY 193 GCGCGGAGGCTGCGGAGCCCTGAGGCTGCGGAGCCCTGAGGCTGCGGAGCTG 252  
Db 344 GCGCGGAGGCTGCGGAGCCCTGAGGCTGCGGAGCCCTGAGGCTGCGGAGCTG 285  
QY 253 CTCCTGCTGAGGAGCTGCGGAGCCCTGAGGCTGCGGAGCCCTGAGGCTGCGGAG 312  
Db 284 CTCCTGCTGAGGAGCTGCGGAGCCCTGAGGCTGCGGAGCCCTGAGGCTGCGGAG 225  
QY 313 GTGCTGAGCTGAGGCTGCGGAGCCCTGAGGCTGCGGAGCCCTGAGGCTGCGGAG 372  
Db 224 GTGCTGAGCTGAGGCTGCGGAGCCCTGAGGCTGCGGAGCCCTGAGGCTGCGGAG 165  
QY 373 GCGCTGAGCTGAGGCTGCGGAGCCCTGAGGCTGCGGAGCCCTGAGGCTGCGGAG 432  
Db 164 GCGCTGAGCTGAGGCTGCGGAGCCCTGAGGCTGCGGAGCCCTGAGGCTGCGGAG 105  
QY 433 CCCACCCGAGGAGCTGAAACCCCGCGGAGGAGACCTGATCCCTCCCGCGG 492  
Db 104 CCCACCCGAGGAGCTGAAACCCCGCGGAGGAGACCTGATCCCTCCCGCGG 45  
QY 493 CCTCTCATTAACGTGTTAAGCAAAAAAAAAAAAAAAAAAAAAA 536  
Db 44 CCTCTCATTAACGTGTTAAGCAAAAAAAAAAAAAAAAAAAAAA 1

Search completed: March 8, 2005, 07:03:37  
Job time : 3282 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: March 5, 2005, 21:13:08 ; Search time 39 Seconds  
(without alignments)  
256.578 Million cell updates/sec

Title: US-09-989-731-408

Perfect score: 502

Sequence: 1 MKLALGLGCVMLSCSSAAA.....QAVGAVKALKALGLTVFG 104

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 1500 summaries

PIR 79: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	81	16.1	496	2	T09931	probable phosphodi
2	79.5	15.8	1381	2	S60004	hypothetical prote
3	77.5	15.4	601	2	T35054	probable transport
4	77	15.3	335	2	T36304	probable anhranil
5	76	15.1	355	2	AD2973	hypothetical prote
6	76	15.1	355	2	G98309	probable ABC trans
7	76	15.1	699	2	H87275	thio-disulfide int
8	76	15.1	732	2	T47269	copper-transportin
9	75.5	15.0	544	2	H72647	hypothetical prote
10	73.5	14.6	331	2	G84358	transport protein
11	73	14.5	502	2	F83553	gamma-glutamyltran
12	73	14.5	584	2	B87315	hypothetical prote
13	73	14.5	1279	2	T13613	amaastigote-specifi
14	72	14.3	236	2	A56010	succinyl-CoA synth
15	72	14.3	397	2	F97675	succinyl-CoA synth
16	72	14.3	397	2	AE2900	hypothetical prote
17	72	14.3	528	2	D70968	L-serine dehydrata
18	71.5	14.2	462	2	B87634	ATP-dependent CIP
19	71.5	14.2	874	2	AC3070	endopeptidase clp
20	71.5	14.2	887	2	F98216	probable MFS trans
21	71	14.1	440	2	G83368	heat shock protein
22	70.5	14.0	668	2	G85160	probable endopepti
23	70.5	14.0	831	2	D71409	hypothetical prote
24	70	13.9	431	2	C86178	zinc finger protei
25	70	13.9	452	2	T46147	probable multidrug
26	70	13.9	477	2	D82179	hypothetical prote
27	69.5	13.8	244	2	S75653	hypothetical prote
28	69.5	13.8	396	2	G75454	probable PPE prote
29	69.5	13.8	423	2	C70582	

30	69.5	13.8	455	2	AD0782	probable L-serine
31	69	13.7	170	2	AF3312	hypothetical prote
32	69	13.7	627	2	D75393	serine proteinase,
33	69	13.7	953	2	T36551	probable ATP-depen
34	69	13.6	3295	2	AE0074	probable adhesin x
35	68.5	13.6	277	2	F84336	hypothetical prote
36	68.5	13.6	335	2	AB0575	ferric enterobacti
37	68.5	13.6	1724	2	T18343	P-glycoprotein - S
38	68	13.5	334	2	S16296	ferric enterobacti
39	68	13.5	334	2	A85558	ferric enterobacti
40	68	13.5	334	2	E90707	ferric enterobacti
41	67.5	13.4	560	2	F70719	hypothetical prote
42	67.5	13.4	387	2	C75312	branched-chain ami
43	67.5	13.4	1179	2	H82706	hypothetical prote
44	67.5	13.4	1206	2	B87247	probable conserved
45	67.5	13.4	2698	2	B96571	similar to transla
46	67	13.3	218	2	F82220	glyoxylase II faml
47	67	13.3	228	2	D75048	aspartate racemase
48	67	13.3	290	2	S72996	probable glycoprot
49	67	13.3	351	2	S72817	probable glycoprot
50	67	13.3	419	2	AB3519	leucine-specific b
51	67	13.3	636	2	F72736	hypothetical prote
52	67	13.3	724	2	H87423	cation-transportin
53	67	13.3	760	2	AB2225	hypothetical prote
54	67	13.3	840	2	B87467	conserved hypochet
55	66.5	13.2	106	2	F86565	CT483 hypothetical
56	66.5	13.2	106	2	C72057	conserved hypochet
57	66.5	13.2	146	2	F72709	hypothetical prote
58	66.5	13.2	180	2	TU0149	zein protein - mal
59	66.5	13.2	243	2	T36637	hypothetical prote
60	66.5	13.2	341	2	I55623	chromoboxane A2 rec
61	66.5	13.2	465	2	G02738	PREAC-4 - human
62	66.5	13.2	667	2	T23010	hypothetical prote
63	66.5	13.2	873	2	B53225	ecdysone-induced p
64	66.5	13.2	1510	2	T13634	probable minor tal
65	66	13.1	118	2	S45680	lipid transfer pro
66	66	13.1	310	2	AB0312	LYSR-family transp
67	66	13.1	330	2	B82063	chiamin ABC transp
68	66	13.1	337	2	B84133	hypothetical prote
69	66	13.1	638	2	S22490	acetoacetate synth
70	66	13.1	70	2	B70963	hypothetical prote
71	66	13.1	1467	2	A75564	conserved hypochet
72	65.5	13.0	264	2	D87504	hypothetical prote
73	65.5	13.0	289	2	S70547	sepb protein - Sal
74	65.5	13.0	343	2	F86412	p28N4.25 protein
75	65.5	13.0	361	2	H87700	citrate synthase l
76	65.5	13.0	491	2	C70868	hypothetical prote
77	65.5	13.0	593	2	A10850	pathogenicty isla
78	65.5	13.0	593	2	S70216	slpB protein - Sal
79	65.5	13.0	665	2	G97819	hypothetical prote
80	65.5	13.0	848	2	G87220	heat shock protein
81	65.5	13.0	861	2	D82814	ATP-dependent CIP
82	65	12.9	267	2	F87665	hypothetical prote
83	65	12.9	275	2	B72484	hypothetical prote
84	65	12.9	276	2	T05778	hypothetical prote
85	65	12.9	312	2	H83245	hypothetical prote
86	65	12.9	367	2	AG3649	iron(III)-binding
87	65	12.9	385	2	H70503	probable PPE prote
88	65	12.9	461	2	A31237	alpha-2C-adreneryl
89	65	12.9	693	1	JH0265	DNA recombinase (E
90	65	12.9	845	2	T17291	hypothetical prote
91	65	12.9	4377	2	A55575	ankyrin 3, long sp
92	64.5	12.8	184	1	A41331	membrane-bound cys
93	64.5	12.8	320	2	F64384	hypothetical prote
94	64.5	12.8	346	2	C87397	iron compound ABC
95	64.5	12.8	385	2	C83174	hypothetical prote
96	64.5	12.8	411	2	F84135	multidrug-efflux c
97	64.5	12.8	480	2	T35214	hypothetical prote
98	64.5	12.8	482	2	TC7332	endoglycosylceram
99	64.5	12.8	529	2	C82487	conserved hypochet
100	64.5	12.8	784	2	A26601	elastin precursor
101	64.5	12.8	905	2	G83314	NADH dehydrogenase
102	64.5	12.8	952	2	A99823	probable tail leng

103	64.5	12.8	1022	1	139643	RTX-toxin I - Acti
104	64.5	12.8	1026	2	C30854	probable tail leng
105	64.5	12.8	1026	2	F85692	probable tail comp
106	64.5	12.8	1080	2	H90908	probable tail leng
107	64.5	12.8	1608	2	A28182	hemolysin A - Serr
108	64.5	12.8	1767	2	T00458	hypothetical prote
109	64.5	12.8	2274	2	T30258	adenomatous polypo
110	64	12.7	185	2	B75586	urease accessory p
111	64	12.7	327	2	TC7337	chiazole biosynthe
112	64	12.7	426	2	A41831	hypothetical prote
113	64	12.7	464	2	H82011	probable outer mem
114	64	12.7	469	2	T35526	probable integral
115	64	12.7	491	2	F81655	conserved hypotet
116	64	12.7	520	2	AD2616	chromosomal replic
117	64	12.7	529	2	D97398	dnna protein (L254
118	64	12.7	569	2	F75381	probable two-compo
119	64	12.7	637	2	C87322	methyl-accepting c
120	64	12.7	655	2	B64752	probable dihydroxy
121	64	12.7	693	2	G91194	DNA helicase RecG
122	64	12.7	693	2	C87575	sensor histidine k
123	64	12.7	704	2	H86041	hypothetical prote
124	64	12.7	2479	2	F87386	conserved hypotet
125	63.5	12.6	82	1	CCPS55	cytochrome c551 [v
126	63.5	12.6	82	1	CCPS55	50S ribosomal prot
127	63.5	12.6	130	2	A87146	probable methylate
128	63.5	12.6	175	2	G72692	probable dehydroge
129	63.5	12.6	263	2	G70583	ribose transport s
130	63.5	12.6	284	2	AE3547	probable anthranil
131	63.5	12.6	345	2	H72488	D-lactate dehydrog
132	63.5	12.6	353	2	E84393	probable transport
133	63.5	12.6	394	2	B85916	probable transport
134	63.5	12.6	398	2	G91071	proton/sodium-glut
135	63.5	12.6	407	2	B70415	probable chorismat
136	63.5	12.6	411	2	D86973	metal ion efflux m
137	63.5	12.6	432	2	C87586	hypothetical prote
138	63.5	12.6	458	2	A70714	L-serine dehydrata
139	63.5	12.6	519	2	D82974	mercury(II) reduct
140	63.5	12.6	548	1	T06752	flagella-associate
141	63.5	12.6	548	1	F37014	conserved hypotet
142	63.5	12.6	677	2	F83954	nitrous oxide redu
143	63.5	12.6	779	2	T44659	conserved hypotet
144	63.5	12.6	1026	2	G90876	probable tail leng
145	63.5	12.6	1086	2	F59438	large structural p
146	63.5	12.6	1048	1	XPBR39	pyruvate:ferredoxi
147	63.5	12.6	1157	2	T43259	hypothetical prote
148	63	12.5	177	2	B83906	transpore protein
149	63	12.5	239	2	A83620	arabinogalactan-1
150	63	12.5	264	2	S52955	hypothetical prote
151	63	12.5	266	2	C70788	phosphate ABC tran
152	63	12.5	307	2	G86839	iron(III) diglitrat
153	63	12.5	343	2	AC2129	probable PPE prote
154	63	12.5	358	2	H70857	conserved hypotet
155	63	12.5	380	2	T35953	hypothetical prote
156	63	12.5	387	2	F84392	probable PPE prote
157	63	12.5	391	2	D70922	3-oxoacyl-l-lacyl-ca
158	63	12.5	414	2	A89866	probable PPE prote
159	63	12.5	434	2	B70857	hypothetical prote
160	63	12.5	613	2	S27770	hypothetical prote
161	63	12.5	620	2	H82761	sulfur deprivation
162	63	12.5	684	2	T67771	probable integral
163	63	12.5	931	2	AF3276	ATP-dependent c1p
164	63	12.5	932	2	S47597	multi protein homol
165	63	12.5	1157	2	T43258	pyruvate:ferredoxi
166	63	12.5	1677	2	T18344	P-glycoprotein E -
167	62.5	12.5	115	2	F97467	hypothetical prote
168	62.5	12.5	265	2	A48121	retrovirus-related
169	62.5	12.5	288	2	G75613	chiamin biosynthes
170	62.5	12.5	314	2	E87427	conserved phosphor
171	62.5	12.5	361	2	H70785	probable phosphori
172	62.5	12.5	388	2	A97672	N-acetylglucosamin
173	62.5	12.5	388	2	AG2896	hypothetical prote
174	62.5	12.5	401	2	F83179	hypothetical prote
175	62.5	12.5	426	2	C96804	hypothetical prote
176	62.5	12.5	445	2	F81378	probable phospho-s
177	62.5	12.5	511	2	G87609	L-aspartate oxidas
178	62.5	12.5	513	2	T12997	hypothetical prote
179	62.5	12.5	573	2	G75463	O-acetylhomoserine
180	62.5	12.5	601	2	H69274	probable long-chain
181	62.5	12.5	618	2	G83494	hypothetical prote
182	62.5	12.5	685	2	AH3414	soluble lytic mure
183	62.5	12.5	760	1	C2MS	classical-compleme
184	62	12.4	98	2	E83763	PTS system, cellub
185	62	12.4	117	2	T12079	non-specific lipid
186	62	12.4	137	2	A72731	hypothetical prote
187	62	12.4	200	2	T05055	hypothetical prote
188	62	12.4	222	2	T37019	probable integral
189	62	12.4	222	2	C84380	hypothetical prote
190	62	12.4	287	2	B72568	hypothetical prote
191	62	12.4	295	2	T36201	probable transcrip
192	62	12.4	338	2	AE3334	metal chelate tran
193	62	12.4	363	2	T34931	hypothetical prote
194	62	12.4	382	2	A70705	probable PE protei
195	62	12.4	382	2	T14336	MD23 protein, iso
196	62	12.4	388	2	UC5516	naringenin-chalcon
197	62	12.4	389	2	G87332	hypothetical prote
198	62	12.4	393	2	AE3503	probable iron-cont
199	62	12.4	407	2	A44374	3-carboxy-cis,cis-
200	62	12.4	426	2	A96000	probable C4-dicarb
201	62	12.4	474	2	AB0002	probable membrane
202	62	12.4	505	2	F84344	hypothetical prote
203	62	12.4	535	2	AF0103	probable sulfatase
204	62	12.4	541	2	F95343	probable copper ex
205	62	12.4	549	2	T14606	probable sugar tra
206	62	12.4	574	2	H83117	probable ATP-bindl
207	62	12.4	594	2	G83878	L-lactate permease
208	62	12.4	620	2	UH0593	Schwann cell myell
209	62	12.4	641	2	AG2164	hypothetical prote
210	62	12.4	643	2	C87412	ABC transporter, H
211	62	12.4	645	2	G90819	hypothetical prote
212	62	12.4	665	2	A12733	NADH-ubiquinone ox
213	62	12.4	665	2	C97515	soluble lytic tran
214	62	12.4	682	2	AE2702	probable soluble l
215	62	12.4	694	2	F97484	ecdysone-induced p
216	62	12.4	775	2	A32494	puif 748 protein -
217	62	12.4	829	2	A34692	N-chimerin homolog
218	62	12.4	883	2	S04722	glycine cleavage s
219	62	12.4	903	2	T00705	glycine cleavage s
220	62	12.4	954	2	AE2756	probable ATP-bindl
221	62	12.4	984	2	B97537	hypothetical prote
222	62	12.4	998	2	T35745	hypothetical prote
223	62	12.4	1025	2	AC0930	probable bacteriop
224	62	12.4	1025	2	AB0836	hypothetical prote
225	62	12.4	1030	2	F96762	hypothetical prote
226	61.5	12.3	124	2	I40348	ribosomal protein
227	61.5	12.3	124	2	I40350	ribosomal protein
228	61.5	12.3	124	2	AF3345	LSU ribosomal prot
229	61.5	12.3	133	2	A70986	hypothetical prote
230	61.5	12.3	145	2	C75590	hypothetical prote
231	61.5	12.3	211	2	T35071	probable membrane
232	61.5	12.3	217	2	AB2665	ribo nuclease H11
233	61.5	12.3	221	2	T02923	probable oxalate o
234	61.5	12.3	229	2	A97447	ribo nuclease H11
235	61.5	12.3	237	2	T35711	hypothetical prote
236	61.5	12.3	253	2	D69098	phosphate transpor
237	61.5	12.3	304	2	A87258	D-alanine-D-alanin
238	61.5	12.3	306	2	F64185	hypothetical prote
239	61.5	12.3	313	2	B84289	hypothetical prote
240	61.5	12.3	333	2	B84195	hypothetical prote
241	61.5	12.3	338	2	C83785	hypothetical prote
242	61.5	12.3	351	2	B75631	iron ABC transport
243	61.5	12.3	355	2	S17704	anthranilate phosph
244	61.5	12.3	361	2	G72636	hypothetical prote
245	61.5	12.3	368	2	T40115	uv excision repair
246	61.5	12.3	386	2	C87549	hypothetical prote
247	61.5	12.3	394	2	AD0842	probable transmemb
248	61.5	12.3	400	2	H91182	probable resistanc

249	61.5	12.3	400	2	D86029	probable resistant
250	61.5	12.3	402	2	S47768	hypothetical 43K p
251	61.5	12.3	405	2	G90194	hypothetical prote
252	61.5	12.3	434	1	MMBER3	UL43 protein - hum
253	61.5	12.3	441	2	B70773	probable thra prot
254	61.5	12.3	445	2	AB2022	hypothetical prote
255	61.5	12.3	503	2	S43017	puromycin resistan
256	61.5	12.3	587	2	S61038	D-lactate dehydrog
257	61.5	12.3	739	2	A55134	glycine-tRNA ligase
258	61.5	12.3	820	2	D83337	probable TonB-depe
259	61.5	12.3	1068	2	T48756	mitochondrial nico
260	61.5	12.3	1492	2	T14652	protein J - Yersin
261	61.5	12.3	1545	2	T14966	phage lambda-relat
262	61.5	12.3	2103	2	G86925	probable polyketid
263	61	12.2	117	2	AB2495	conserved hypotet
264	61	12.2	172	2	AB3528	hypothetical prote
265	61	12.2	185	2	S20593	alcohol dehydrogen
266	61	12.2	207	2	A69069	precortin-6y methy
267	61	12.2	215	2	T44791	probable 2-dehydro
268	61	12.2	247	2	AF2182	hypothetical prote
269	61	12.2	259	1	A69162	gufa protein homol
270	61	12.2	257	2	T36675	probable integral
271	61	12.2	320	2	B37767	stress-inducible p
272	61	12.2	323	2	H81154	ADP-hepseose syntha
273	61	12.2	343	2	H70517	probable lppd prot
274	61	12.2	355	2	AF2746	UDP glucosamine N-
275	61	12.2	355	2	E97527	lpxd protein (U516
276	61	12.2	355	2	C87684	conserved hypotet
277	61	12.2	350	2	T16782	hypothetical prote
278	61	12.2	395	2	H75457	hypothetical prote
279	61	12.2	406	2	F83830	nucleoside transpo
280	61	12.2	419	2	C95091	conserved hypotet
281	61	12.2	419	2	G97958	conserved hypotet
282	61	12.2	420	2	H75395	ABC transporter, p
283	61	12.2	422	2	A96015	probable hydroxypry
284	61	12.2	433	2	C69600	magnesium citrate
285	61	12.2	480	2	E75433	hypothetical prote
286	61	12.2	487	2	B72755	probable antitoxi
287	61	12.2	525	2	E87076	probable secreted
288	61	12.2	562	2	T43726	K+-transporting AT
289	61	12.2	582	2	C82961	conserved hypotet
290	61	12.2	589	2	F75398	transporter, sodiu
291	61	12.2	625	2	A26456	nicotinic acetylch
292	61	12.2	802	2	B43735	bcsB protein - Ace
293	61	12.2	920	2	C70668	probable mmp17 pro
294	61	12.2	1010	1	PX2P2P	H+-exporting ATPas
295	61	12.2	1470	1	S45323	genome polypeptid
296	60.5	12.1	99	1	R6MXL2	ribosomal protein
297	60.5	12.1	138	2	A32998	chorion protein S1
298	60.5	12.1	144	2	AE3423	hypothetical prote
299	60.5	12.1	192	2	AB3587	hypothetical prote
300	60.5	12.1	203	2	T36327	2-amino-4-hydroxy-
301	60.5	12.1	204	2	AE3302	multiple antitoxi
302	60.5	12.1	209	2	T05164	hypothetical prote
303	60.5	12.1	219	2	T18541	moB protein precu
304	60.5	12.1	223	1	S72693	detribiotin synth
305	60.5	12.1	223	2	AB2339	hypothetical prote
306	60.5	12.1	226	2	D87061	hypothetical prote
307	60.5	12.1	233	2	AB0273	detribiotin synth
308	60.5	12.1	244	2	T29079	probable membrane
309	60.5	12.1	259	2	B95335	hypothetical prote
310	60.5	12.1	260	2	AB0698	protein (imported
311	60.5	12.1	260	2	AB0698	probable pathogeni
312	60.5	12.1	267	2	B86766	hypothetical prote
313	60.5	12.1	307	2	B39098	allergen Poa p IX
314	60.5	12.1	312	2	AH0797	NADH dehydrogenase
315	60.5	12.1	316	1	A39407	1-phosphofructokin
316	60.5	12.1	341	2	JH0606	chromoxane A2 rec
317	60.5	12.1	349	2	AB4350	hypothetical prote
318	60.5	12.1	367	2	AG0555	2-aminoethylphosph
319	60.5	12.1	367	2	T46947	2-aminoethylphosph
320	60.5	12.1	378	2	B75547	iron-sulfur cofact
321	60.5	12.1	383	2	T08705	hypothetical prote
322	60.5	12.1	385	2	T35885	agas protein - Str
323	60.5	12.1	322	2	H70658	probable aroF prot
324	60.5	12.1	323	2	D83351	hypothetical prote
325	60.5	12.1	324	2	AF0276	probable membrane
326	60.5	12.1	325	2	T35729	hypothetical prote
327	60.5	12.1	326	2	T46923	hypothetical prote
328	60.5	12.1	327	2	A41718	polypyrimidine tra
329	60.5	12.1	328	2	A95861	hypothetical prote
330	60.5	12.1	329	2	A40595	methyImalonyl-CoA
331	60.5	12.1	330	2	A72428	methy1-accepting c
332	60.5	12.1	331	2	E73379	methy1-accepting c
333	60.5	12.1	332	2	G72316	methy1-accepting c
334	60.5	12.1	333	2	T19501	hypothetical prote
335	60.5	12.1	334	2	T19500	hypothetical prote
336	60.5	12.1	335	2	A28392	penicillin amidase
337	60.5	12.1	336	2	E86815	ClpB protein (impo
338	60.5	12.1	337	2	T17188	Clp3C protein - ra
339	60.5	12.1	338	2	T17200	Clp3C protein - ra
340	60.5	12.1	339	2	T25604	hypothetical prote
341	60	12.0	340	2	S49537	ribosomal protein
342	60	12.0	341	2	S41123	ribosomal protein
343	60	12.0	342	2	A70615	probable ribosomal
344	60	12.0	343	2	S35784	mucin - rat (fragm
345	60	12.0	344	2	A42840	ribosomal protein
346	60	12.0	345	2	AC2124	hypothetical prote
347	60	12.0	346	2	AE2164	hypothetical prote
348	60	12.0	347	2	B61615	fibroin heavy chai
349	60	12.0	348	2	D71326	conserved hypotet
350	60	12.0	349	2	S45662	histone H1 - comat
351	60	12.0	350	2	AE2953	transcription regu
352	60	12.0	351	2	E86061	D-ribose high-affi
353	60	12.0	352	2	AD0952	high affinity ribo
354	60	12.0	353	2	G65178	high affinity ribo
355	60	12.0	354	2	D91215	high affinity ribo
356	60	12.0	355	2	F83300	probable enoyl-CoA
357	60	12.0	356	2	T50915	hypothetical prote
358	60	12.0	357	2	T40013	thiazole biosynthe
359	60	12.0	358	2	H98329	transcription regu
360	60	12.0	359	2	E64702	cytochrome-c perox
361	60	12.0	360	2	S45128	regulatory protei
362	60	12.0	361	2	T04779	hypothetical prote
363	60	12.0	362	2	S49786	3-isopropylmalate
364	60	12.0	363	2	G82328	aminotransferase,
365	60	12.0	364	2	A42343	alcohol dehydrogen
366	60	12.0	365	2	AE3382	nifs protein [impo
367	60	12.0	366	2	A49308	nitrite reductase
368	60	12.0	367	2	A13381	selenocysteine lya
369	60	12.0	368	2	T36597	protein F53A3.6 [l
370	60	12.0	369	2	D88395	nitrogenase molybd
371	60	12.0	370	2	A26940	outer membrane pro
372	60	12.0	371	2	A81239	mannose-1-phosphat
373	60	12.0	372	2	AC3622	isocitrate dehydro
374	60	12.0	373	2	A97744	isocitrate dehydro
375	60	12.0	374	2	E71681	phosphotransferase
376	60	12.0	375	2	G65051	UDP-N-acetylmuramo
377	60	12.0	376	2	B87023	mannose-6-phosphat
378	60	12.0	377	2	S30187	conserved hypotet
379	60	12.0	378	2	E83551	variant surface gl
380	60	12.0	379	2	C35480	variant surface gl
381	60	12.0	380	2	A45175	phosphotransferase
382	60	12.0	381	2	G64918	PTS system, maltos
383	60	12.0	382	2	F85768	PTS system, maltos
384	60	12.0	383	2	A99920	methy1-accepting c
385	60	12.0	384	2	ORECM2	methy1-accepting c
386	60	12.0	385	2	C90953	methy1-accepting c
387	60	12.0	386	2	G85801	sensor histidine k
388	60	12.0	387	2	AB7458	sodium/dicarboxyla
389	60	12.0	388	2	146528	3-methylcrotonyl-C
390	60	12.0	389	2	AF2984	3-methylcrotonyl-C
391	60	12.0	390	2	A98399	subtilisin-like pr
392	60	12.0	391	2	S52769	subtilisin-like pr
393	60	12.0	392	2	C95202	primosomal protein
394	60	12.0	393	2	C98069	primosomal replica
395	60	12.0	394	2	T05602	hypothetical prote

395	60	12.0	825	2	S26706	transcription fact
396	60	12.0	927	2	A48085	transcription fact
397	60	12.0	1011	2	T50344	poly(A) + RNA trans
398	60	12.0	1012	2	T50300	poly(A) + RNA trans
399	60	12.0	1060	2	S33641	homeotic protein z
400	60	12.0	1122	2	T14180	exit protein - Myc
401	60	12.0	1123	1	NMBEH7	U37 protein - hum
402	60	12.0	1439	2	T02087	gag/pol polyprotei
403	60	12.0	1517	2	T13329	hypothetical prote
404	60	12.0	1533	2	A46221	abdominal segment
405	60	12.0	3938	2	T42761	Bassoon protein -
406	60	12.0	4613	2	T17409	polyketide synthas
407	59.5	11.9	136	2	H70938	hypothetical prote
408	59.5	11.9	139	2	S76129	hypothetical prote
409	59.5	11.9	142	2	H87265	conserved hypotet
410	59.5	11.9	169	2	C75595	hypothetical prote
411	59.5	11.9	230	2	AH0692	hypothetical prote
412	59.5	11.9	247	2	H70432	conserved hypotet
413	59.5	11.9	293	2	G87093	ABC transporter -
414	59.5	11.9	295	2	AB2464	probable transfera
415	59.5	11.9	305	2	F75573	tRNA delta-2-isope
416	59.5	11.9	327	2	C91118	conserved hypotet
417	59.5	11.9	327	2	C91118	hypothetical prote
418	59.5	11.9	327	2	B85963	hypothetical prote
419	59.5	11.9	328	2	G87391	ABC transporter, A
420	59.5	11.9	341	2	JC4051	Jun-D protein - ra
421	59.5	11.9	352	2	C47293	serine-pyruvate am
422	59.5	11.9	357	2	T01494	NADPH HC toxin red
423	59.5	11.9	357	2	T03970	NADPH HC-toxin red
424	59.5	11.9	363	2	G84385	dipeptide ABC tran
425	59.5	11.9	367	1	DESCDA	aspartate-semialde
426	59.5	11.9	367	1	F91163	aspartate-semialde
427	59.5	11.9	367	2	G86009	aspartate-semialde
428	59.5	11.9	368	2	AB0095	aspartate-semialde
429	59.5	11.9	372	2	AC2952	aspartate-semialde
430	59.5	11.9	372	2	B98331	aspartate-semialde
431	59.5	11.9	383	2	G72777	probable transamin
432	59.5	11.9	389	2	B86017	probable S2P metat
433	59.5	11.9	389	2	B91171	probable 3-oxoacyl
434	59.5	11.9	396	2	T35254	probable 3-oxoacyl
435	59.5	11.9	399	2	D95279	conserved hypotet
436	59.5	11.9	425	2	T36585	probable alcohol
437	59.5	11.9	425	2	T36585	probable alcohol
438	59.5	11.9	444	1	B92130	amino acid permeas
439	59.5	11.9	444	1	B92130	amino acid permeas
440	59.5	11.9	448	2	A26190	probable membrane
441	59.5	11.9	448	2	AH1952	sensor histidine k
442	59.5	11.9	469	2	H97064	histidine-CRMA 11g
443	59.5	11.9	491	2	C46230	glucanase permease
444	59.5	11.9	491	2	C46230	glucanase permease
445	59.5	11.9	499	2	A38891	two-component sens
446	59.5	11.9	520	2	G95945	probable sugar-pro
447	59.5	11.9	520	2	A95423	probable histidine
448	59.5	11.9	536	2	S15552	probable histidine
449	59.5	11.9	536	2	B46230	probable histidine
450	59.5	11.9	538	1	VGNZMM	RNA-binding protei
451	59.5	11.9	538	1	VGNZMM	RNA-binding protei
452	59.5	11.9	538	1	VGNZMM	RNA-binding protei
453	59.5	11.9	538	1	VGNZMM	RNA-binding protei
454	59.5	11.9	538	1	VGNZMM	RNA-binding protei
455	59.5	11.9	538	1	VGNZMM	RNA-binding protei
456	59.5	11.9	538	1	VGNZMM	RNA-binding protei
457	59.5	11.9	538	1	VGNZMM	RNA-binding protei
458	59.5	11.9	538	1	VGNZMM	RNA-binding protei
459	59.5	11.9	538	1	VGNZMM	RNA-binding protei
460	59.5	11.9	538	1	VGNZMM	RNA-binding protei
461	59.5	11.9	538	1	VGNZMM	RNA-binding protei
462	59.5	11.9	538	1	VGNZMM	RNA-binding protei
463	59.5	11.9	538	1	VGNZMM	RNA-binding protei
464	59.5	11.9	538	1	VGNZMM	RNA-binding protei
465	59.5	11.9	538	1	VGNZMM	RNA-binding protei
466	59.5	11.9	538	1	VGNZMM	RNA-binding protei
467	59.5	11.9	538	1	VGNZMM	RNA-binding protei

541	59	11.8	1019	2	AB2136	polyketide synthas	614	58.5	11.7	1438	2	T17402	dihydroaeruginosic
542	59	11.8	1086	1	DEBOXM	NAD(P) transhydrog	615	58.5	11.7	1607	2	T02837	long chain fatty a
543	59	11.8	1136	2	AB1581	different protein	616	58.5	11.7	1607	2	T02837	ALR protein - huma
544	59	11.8	3591	1	S21010	filamentous hemaggl	617	58.5	11.7	4957	2	T03455	ALR protein - huma
545	58.5	11.7	104	1	CCP85B	cytochrome c51 pr	618	58.5	11.6	5252	2	T03454	hypothetical prote
546	58.5	11.7	130	2	SC1143	ribosomal protein	619	58	11.6	184	2	E87619	hypothetical prote
547	58.5	11.7	132	1	E70434	conserved hypothet	620	58	11.6	191	2	E87253	major secreted imm
548	58.5	11.7	137	2	S42026	acyl carrier prote	621	58	11.6	193	2	A48320	probable mpt70 pro
549	58.5	11.7	181	2	AF1931	hypothetical prote	622	58	11.6	215	2	A95879	probable dihydroxy
550	58.5	11.7	166	2	D83354	hypothetical prote	623	58	11.6	222	2	G72459	hypothetical prote
551	58.5	11.7	233	2	T35186	ribonuclease H1 -	624	58	11.6	222	2	AD2899	chito1,disulfide in
552	58.5	11.7	256	2	S07371	histone H1 - fruit	625	58	11.6	222	2	E98284	in chito1,disulfide in
553	58.5	11.7	256	2	E83287	hypothetical prote	626	58	11.6	223	2	H58523	conserved hypothet
554	58.5	11.7	261	2	B81934	probable tryptopha	627	58	11.6	236	2	E83144	conserved hypothet
555	58.5	11.7	261	2	D81171	tryptophan synthas	628	58	11.6	251	2	AG3116	hypothetical prote
556	58.5	11.7	272	2	D87436	2-keto-4-pentenoat	629	58	11.6	255	2	F98170	hypothetical prote
557	58.5	11.7	296	2	A48496	transcription regu	630	58	11.6	279	1	C42646	dihydropteroate sy
558	58.5	11.7	302	2	F69000	cobalamin biosynth	631	58	11.6	279	1	SYECOG	dihydropteroate sy
559	58.5	11.7	312	2	G65000	transcription regu	632	58	11.6	279	2	S07654	dihydropteroate sy
560	58.5	11.7	312	2	E91025	lyser-type transcri	633	58	11.6	279	2	T45123	dihydropteroate sy
561	58.5	11.7	325	2	F85669	lyser-type transcri	634	58	11.6	280	2	C86889	zinc ABC transport
562	58.5	11.7	325	2	D98282	ribose ABC transpo	635	58	11.6	283	2	S10828	dihydropteroate sy
563	58.5	11.7	325	2	AE2991	ABC transporter, m	636	58	11.6	294	2	A70942	hypothetical prote
564	58.5	11.7	333	1	C69812	ferriochrome ABC tr	637	58	11.6	297	2	AE2805	permease (imported
565	58.5	11.7	338	2	AC0711	asparaginase (EC 3	638	58	11.6	312	2	E87354	integral membrane
566	58.5	11.7	340	2	AF2896	hypothetical prote	639	58	11.6	318	2	A40944	1-phosphofructokin
567	58.5	11.7	340	2	H97671	hypothetical prote	640	58	11.6	321	2	E97584	hypothetical prote
568	58.5	11.7	343	2	C69212	conserved hypothet	641	58	11.6	323	2	S20099	transforming prote
569	58.5	11.7	352	2	AC2760	sodium bile acid s	642	58	11.6	338	2	T46855	anthranilate phosp
570	58.5	11.7	352	2	A97541	hypothetical prote	643	58	11.6	339	2	E83496	hypothetical prote
571	58.5	11.7	353	2	C72479	hypothetical prote	644	58	11.6	339	2	C95119	iron-compound ABC
572	58.5	11.7	384	2	B82973	probable peptidic	645	58	11.6	339	2	G97988	hypothetical prote
573	58.5	11.7	389	2	H82825	transport protein	646	58	11.6	340	2	A35630	regulatory protein
574	58.5	11.7	400	2	E83675	hypothetical prote	647	58	11.6	342	2	AF3357	anthranilate phosp
575	58.5	11.7	412	2	A83129	tyrosyl-tRNA synth	648	58	11.6	345	2	A70664	hypothetical prote
576	58.5	11.7	412	2	S02072	phosphopyruvate hy	649	58	11.6	349	2	B90285	alcohol dehydrogen
577	58.5	11.7	435	2	AD2223	dihydroxocotase (im	650	58	11.6	370	2	F95363	probable serine-py
578	58.5	11.7	451	2	H75559	conserved hypothet	651	58	11.6	379	1	S71570	alcohol dehydrogen
579	58.5	11.7	454	2	H65054	hypothetical prote	652	58	11.6	383	2	H71323	probable spore coa
580	58.5	11.7	469	2	B83368	hypothetical prote	653	58	11.6	386	2	AH3467	glycine betaine/1-
581	58.5	11.7	475	2	D84593	hypothetical prote	654	58	11.6	390	2	T35206	glutamate synthase-1
582	58.5	11.7	476	2	H82431	L-serine dehydrata	655	58	11.6	397	2	AF2870	HLVD family secret
583	58.5	11.7	492	2	AB4507	probable sucrose-p	656	58	11.6	403	2	T04821	hypothetical prote
584	58.5	11.7	492	2	AD3047	copper tolerance p	657	58	11.6	403	2	H97646	probable membrane
585	58.5	11.7	492	2	H98238	hypothetical prote	658	58	11.6	408	2	T45721	hypothetical prote
586	58.5	11.7	499	2	F70418	conserved hypothet	659	58	11.6	410	2	PN0008	phosphoglycerate K
587	58.5	11.7	511	2	A69369	glutamate synthase	660	58	11.6	419	2	G70602	hypothetical prote
588	58.5	11.7	512	2	AF3628	nitrate reductase	661	58	11.6	421	2	E87277	S4 domain protein
589	58.5	11.7	516	2	F70521	hypothetical prote	662	58	11.6	422	2	B82966	probable phosphat
590	58.5	11.7	532	2	E87343	ABC transporter, A	663	58	11.6	449	2	F91259	hypothetical prote
591	58.5	11.7	532	2	D95287	conserved hypothet	664	58	11.6	449	2	B86100	hypothetical prote
592	58.5	11.7	551	2	F83015	hypothetical prote	665	58	11.6	449	2	G66214	hypothetical 45.7
593	58.5	11.7	556	2	E70814	probable pdc prote	666	58	11.6	460	2	T35539	probable alpha hel
594	58.5	11.7	570	2	G75282	probable glutathio	667	58	11.6	467	2	H82152	PTS system, fructo
595	58.5	11.7	592	2	S46273	tryptophan transpo	668	58	11.6	473	2	C86841	hypothetical prote
596	58.5	11.7	620	2	AP0554	1-deoxyxylulose-5-	669	58	11.6	480	2	E72471	probable DNA-damag
597	58.5	11.7	631	2	B42603	beta-glucoside-spe	670	58	11.6	481	2	T10036	hypothetical prote
598	58.5	11.7	634	2	C83530	potassium uptake p	671	58	11.6	488	2	T31296	glycolate oxidase
599	58.5	11.7	641	2	T44585	acyl-CoA oxidase h	672	58	11.6	491	2	H83979	lysine decarboxyla
600	58.5	11.7	682	2	H87409	3-phytase, fusioin,	673	58	11.6	492	2	B90373	sugar transport re
601	58.5	11.7	682	2	H83024	hypothetical prote	674	58	11.6	521	1	DNVC77	NADH2 dehydrogenas
602	58.5	11.7	706	2	H81943	probable polyribon	675	58	11.6	534	2	A12172	pantothenate synth
603	58.5	11.7	758	2	JC2521	endothelin convert	676	58	11.6	543	2	A11011	probable membrane
604	58.5	11.7	770	2	JC4136	endothelin convert	677	58	11.6	543	2	C65209	hypothetical 59.5
605	58.5	11.7	787	2	H71453	hypothetical prote	678	58	11.6	543	2	B91246	probable alpha hel
606	58.5	11.7	848	2	AF0020	nitrite reductase	679	58	11.6	543	2	H86093	probable alpha hel
607	58.5	11.7	856	2	C71956	probable endopepti	680	58	11.6	544	2	B75541	probable multidrug
608	58.5	11.7	983	2	A87063	conserved large me	681	58	11.6	546	2	C69450	anthranilate synth
609	58.5	11.7	983	2	A84503	probable TNP1-like	682	58	11.6	557	2	T41588	probable amino-aci
610	58.5	11.7	1008	2	S72698	transport protein	683	58	11.6	558	2	G85545	probable transport
611	58.5	11.7	1108	2	A48508	cyclic-nucleotide	684	58	11.6	558	2	C90695	probable transport
612	58.5	11.7	1240	1	DJBR21	DNA-directed DNA p	685	58	11.6	558	2	E64778	probable membrane
613	58.5	11.7	1256	2	T03096	CNO protein - rat	686	58	11.6	579	2	D84137	methyl-accepting c

687	58	11.6	590	2	T42202	probable acyl-CoA
688	58	11.6	590	2	T42206	probable acyl-CoA
689	58	11.6	601	2	E84160	glutamine-fructose
690	58	11.6	638	2	S22491	acetolactate synth
691	58	11.6	633	2	A45456	NADH2 dehydrogenas
692	58	11.6	693	2	AE0005	ATP-dependent DNA
693	58	11.6	712	2	AD2721	H+ translocating p
694	58	11.6	714	2	H97502	h+ translocating p
695	58	11.6	725	2	D75294	hypothetical prote
696	58	11.6	754	2	S47268	endothelin-conver
697	58	11.6	904	2	G90563	lipoprotein [impor
698	58	11.6	985	2	T29910	hypothetical prote
699	58	11.6	1019	2	T00117	dve protein - fru
700	58	11.6	1322	2	D82685	phosphoribosylform
701	58	11.6	1374	2	T30809	plasmaogen relate
702	58	11.6	1531	2	T42218	s1t-1 protein hom
703	58	11.6	1731	2	AB3045	lice nucleation pro
704	58	11.6	1731	2	B98241	hypothetical prote
705	58	11.6	1744	1	C4HU	complement C4a pre
706	57.5	11.5	111	2	S43115	acidic ribosomal p
707	57.5	11.5	137	2	H70811	hypothetical glyco
708	57.5	11.5	166	2	D69695	ribosomal protein
709	57.5	11.5	214	2	S42244	NADH2 dehydrogenas
710	57.5	11.5	224	1	S74541	negative regulator
711	57.5	11.5	255	1	CPSMMU	muramoylpentapepti
712	57.5	11.5	271	2	T36040	hypothetical prote
713	57.5	11.5	278	2	C75275	hypothetical prote
714	57.5	11.5	287	2	T49329	hypothetical prote
715	57.5	11.5	297	2	S74671	hypothetical prote
716	57.5	11.5	317	2	H75297	conserved hypotnet
717	57.5	11.5	323	2	H81951	probable DP-heptos
718	57.5	11.5	323	2	G83461	hypothetical prote
719	57.5	11.5	330	2	H75608	probable acyl-CoA
720	57.5	11.5	332	2	AE3267	peptidyl-prolyl ci
721	57.5	11.5	332	2	F75473	conserved hypotnet
722	57.5	11.5	336	2	C64329	anthranilate synth
723	57.5	11.5	340	2	S54821	chrb protein - Etw
724	57.5	11.5	363	2	C83128	2,3-butanediol deh
725	57.5	11.5	368	2	G71961	hypothetical prote
726	57.5	11.5	376	2	JC7759	alcohol dehydrata
727	57.5	11.5	383	2	T02642	probable ripening-
728	57.5	11.5	387	2	S16568	ADP-ATP carrier pr
729	57.5	11.5	391	2	A70663	probable PPG prote
730	57.5	11.5	396	2	B75290	hypothetical prote
731	57.5	11.5	417	2	B83487	probable oxidoredu
732	57.5	11.5	428	2	A75423	multitidng resistn
733	57.5	11.5	445	2	T37161	probable integral
734	57.5	11.5	451	2	G69392	multitidng resistn
735	57.5	11.5	455	2	A65062	multitidng resistn
736	57.5	11.5	455	2	C85931	L-serine ammonia-1
737	57.5	11.5	455	2	A98086	L-serine dehydrata
738	57.5	11.5	460	2	G82847	hypothetical prote
739	57.5	11.5	460	2	T33110	hypothetical prote
740	57.5	11.5	461	2	S74414	Na+/H+-exchanging
741	57.5	11.5	461	2	F86468	protein F12K21.24
742	57.5	11.5	483	2	T48328	importin alpha-1lk
743	57.5	11.5	504	2	T05543	hypothetical prote
744	57.5	11.5	507	2	B83264	hypothetical prote
745	57.5	11.5	513	2	C95089	ABC transporter, A
746	57.5	11.5	513	2	P97956	ABC transporter, A
747	57.5	11.5	514	2	A64427	phosphoglycerate d
748	57.5	11.5	538	1	B60004	cell fusion glycop
749	57.5	11.5	538	1	G82792	conserved hypotnet
750	57.5	11.5	539	2	B71373	probable oxaloacet
751	57.5	11.5	600	2	A87020	probable long-chain
752	57.5	11.5	617	2	T01227	glutathione-regula
753	57.5	11.5	623	2	G81346	heat shock protein
754	57.5	11.5	673	2	AD2667	chemotaxis methyl-
755	57.5	11.5	678	2	D87607	hypothetical prote
756	57.5	11.5	715	2	A97449	methy1-accepting c
757	57.5	11.5	720	2	D81097	cation transport A
758	57.5	11.5	721	2	T41530	hypothetical prote
759	57.5	11.5	727	2	B84847	probable CCGH-type
760	57.5	11.5	728	2	H59435	phosphoinositide-3
761	57.5	11.5	756	2	S74929	adenylate cyclase
762	57.5	11.5	761	2	S73328	probable lipoprote
763	57.5	11.5	794	2	S69204	pheromone response
764	57.5	11.5	840	1	T03461	methyl-accepting c
765	57.5	11.5	888	2	I58378	tyrosine kinase -
766	57.5	11.5	940	2	A87502	hypothetical prote
767	57.5	11.5	1018	2	T13525	hypothetical prote
768	57.5	11.5	1324	2	S51622	cut3 protein - Its
769	57.5	11.5	2475	2	T00047	gellan lyase (EC 4
770	57	11.4	85	2	A82258	phosphocarrier pro
771	57	11.4	125	2	D72658	hypothetical prote
772	57	11.4	145	2	B82573	hypothetical prote
773	57	11.4	148	2	AD0483	hypothetical prote
774	57	11.4	150	2	E72677	universal stress p
775	57	11.4	158	2	A12718	hypothetical prote
776	57	11.4	158	2	E97500	conserved hypotnet
777	57	11.4	172	2	T03380	hypothetical prote
778	57	11.4	207	2	T07854	oleosin 18K - rice
779	57	11.4	216	2	T45430	germin-like protei
780	57	11.4	260	2	C55230	hypothetical prote
781	57	11.4	265	2	T40757	conserved hypotnet
782	57	11.4	276	2	E55072	conserved hypotnet
783	57	11.4	301	2	G96013	conserved hypotnet
784	57	11.4	318	2	AG1441	conserved hypotnet
785	57	11.4	321	2	A99258	phosphoglycerate d
786	57	11.4	321	2	A93026	L-arabinose transp
787	57	11.4	325	2	A13635	hypothetical prote
788	57	11.4	335	2	B87151	chitinase biosynthe
789	57	11.4	336	2	H72618	lytB homolog (impo
790	57	11.4	337	2	S29814	hypothetical prote
791	57	11.4	350	2	F75259	glyceraldehide-3-p
792	57	11.4	356	2	T01498	glutamy1-tRNA redu
793	57	11.4	356	2	T01435	NADPH HC toxin red
794	57	11.4	358	2	T36415	NADPH HC toxin red
795	57	11.4	358	2	T01435	probable iron-side
796	57	11.4	365	2	F87315	SIS domain protein
797	57	11.4	366	2	T47001	hypothetical prote
798	57	11.4	366	2	A10238	calcium/proton ant
799	57	11.4	366	2	S66272	alcohol dehydrogen
800	57	11.4	375	1	AD1035	probable major tai
801	57	11.4	392	1	S18593	hypothetical prote
802	57	11.4	399	2	E72453	probable transmemb
803	57	11.4	404	2	T36602	probable penicilli
804	57	11.4	405	2	A70845	conserved hypotnet
805	57	11.4	407	2	G81010	glutamate N-acetyl
806	57	11.4	428	2	S73647	dihydrolipoamide S
807	57	11.4	428	2	S14426	molhydropexin co-f
808	57	11.4	430	2	T44851	hypothetical prote
809	57	11.4	431	2	G70561	O-acetylhomoserine
810	57	11.4	437	2	T45481	probable PG protei
811	57	11.4	437	2	H70918	hypothetical prote
812	57	11.4	445	2	S75859	probable oxidoredu
813	57	11.4	455	2	E91098	hypothetical prote
814	57	11.4	455	2	A85944	hypothetical prote
815	57	11.4	460	2	A75615	conserved hypotnet
816	57	11.4	464	2	F83639	hypothetical prote
817	57	11.4	464	2	T36256	hypothetical prote
818	57	11.4	469	2	B84372	conserved hypotnet
819	57	11.4	471	2	F82223	DNA damage-inducib
820	57	11.4	485	2	C91075	sodium/dicarboxyla
821	57	11.4	485	2	F82223	hypothetical prote
822	57	11.4	486	2	B85920	hypothetical prote
823	57	11.4	486	2	T06907	probable ABC trans
824	57	11.4	487	2	A47729	1-aminocyclopropan
825	57	11.4	502	2	H70520	hypothetical glycol
826	57	11.4	524	2	S28663	cytochrome-c oxida
827	57	11.4	527	1	C70558	probable membrane
828	57	11.4	532	2	E75617	probable ABC trans
829	57	11.4	549	2	D64537	sensor histidine k
830	57	11.4	550	1	D69172	L-lactate permease
831	57	11.4	567	2	C75340	DNA-dependent DNA
832	57	11.4	569	2	G95418	probable L-lactate
	57	11.4	571	2	B86150	probable KdpA pota
						hypothetical prote



833	57	11.4	575	2	AH2367	Two-component syst	906	56.5	11.3	414	2	T51707	hypothetical prote
834	57	11.4	577	2	S72227	finger protein sob	907	56.5	11.3	427	2	A11906	hypothetical prote
835	57	11.4	578	2	D97856	hypothetical prote	908	56.5	11.3	428	2	H97481	probable transmem
836	57	11.4	596	2	G69038	dnax-type molecula	909	56.5	11.3	430	2	F90976	hypothetical prote
837	57	11.4	608	2	T35183	probable ABC-type	910	56.5	11.3	437	2	A38534	branched-chain am1
838	57	11.4	617	2	G72466	probable translati	911	56.5	11.3	438	2	B64915	probable membrane
839	57	11.4	635	2	G86744	hypothetical prote	912	56.5	11.3	438	2	G85764	probable chloride
840	57	11.4	650	2	E71496	probable sigma reg	913	56.5	11.3	438	2	B90916	glutamate chloride
841	57	11.4	693	2	AE0969	ATP-dependent DNA	914	56.5	11.3	449	2	A64053	glutamate dehydrog
842	57	11.4	724	2	AS3371	glutamate-ammonia	915	56.5	11.3	450	2	E72615	probable hlye ABPI
843	57	11.4	729	2	AF0458	enoyl-CoA hydratase	916	56.5	11.3	452	2	E72387	hypothetical prote
844	57	11.4	736	2	H75460	conserved hypochet	917	56.5	11.3	452	2	AF0896	L-serine ammonia-1
845	57	11.4	745	2	G83011	hypothetical prote	918	56.5	11.3	462	2	B83123	probable endoprote
846	57	11.4	758	2	AS4667	endoheilin convert	919	56.5	11.3	478	2	C72658	hypothetical prote
847	57	11.4	819	2	F75196	pyruvate, water di	920	56.5	11.3	491	2	T45236	probable membrane
848	57	11.4	844	2	B84773	probable mitochond	921	56.5	11.3	492	2	AD2993	succinoglycan bios
849	57	11.4	856	2	H64552	endopeptidase C1P	922	56.5	11.3	493	2	F98290	exot protein limpo
850	57	11.4	865	2	D97018	ATPase with chapex	923	56.5	11.3	503	2	H70509	hypothetical prote
851	57	11.4	1021	2	T42566	tegument protein 2	924	56.5	11.3	508	2	AH2688	Na+/H+ antiporter
852	57	11.4	1054	2	T18304	acid trehalase hom	925	56.5	11.3	512	2	AF3402	exopolysphatase
853	57	11.4	1057	2	B87545	AcetB/AcetD/AcrF fam	926	56.5	11.3	518	2	D97310	ATPase component o
854	57	11.4	1067	2	D75625	probable extracell1	927	56.5	11.3	520	2	B87621	hypothetical prote
855	57	11.4	1127	2	D70671	pyruvate extracell1	928	56.5	11.3	525	2	C97470	probable NADH dehy
856	57	11.4	1583	2	T00727	myosin heavy chain	929	56.5	11.3	532	2	B87496	protein-export mem
857	57	11.4	1752	2	A45407	collagen alpha 3(I	930	56.5	11.3	547	2	S26858	isocitrate lyase (
858	57	11.4	2432	2	T12687	MR protein homolo	931	56.5	11.3	547	2	B64963	membrane protein Y
859	57	11.4	3839	2	T49789	related to TOM1 pr	932	56.5	11.3	556	2	C84031	ATP-dependent prot
860	56.5	11.3	130	2	D82620	histone-like prote	933	56.5	11.3	559	2	AD3017	hypothetical prote
861	56.5	11.3	170	2	B75548	transcription regu	934	56.5	11.3	599	2	D98267	ABC transporter AT
862	56.5	11.3	174	2	A35383	superoxide dismuta	935	56.5	11.3	604	2	C90619	NADH dehydrogenase
863	56.5	11.3	207	2	S34234	germin-like protein - P	936	56.5	11.3	609	2	D75633	conserved hypochet
864	56.5	11.3	208	2	F96750	germin-like protel	937	56.5	11.3	627	2	JC4021	nicotinic acetylch
865	56.5	11.3	212	2	A64045	3-hydroxybutyryl-C	938	56.5	11.3	648	2	T04837	probable serine/th
866	56.5	11.3	227	2	SS6941	molycopdopexin bios	939	56.5	11.3	649	2	AF2866	probable serine/th
867	56.5	11.3	229	2	B83281	heat shock protein	940	56.5	11.3	670	2	C97643	methy1-accepting c
868	56.5	11.3	237	1	G87541	histidine transpor	941	56.5	11.3	678	2	D98267	stimul1 to mcpc go
869	56.5	11.3	245	2	G87541	hypothetical prote	942	56.5	11.3	686	1	WZBE43	gene 43 protein -
870	56.5	11.3	249	2	A70786	conserved hypochet	943	56.5	11.3	688	2	AE0272	probable carbon at
871	56.5	11.3	258	2	E84037	probable Ccb5 - My	944	56.5	11.3	709	2	AD2843	methy1-accepting c
872	56.5	11.3	269	2	AF3494	3-hydroxybutyryl-C	945	56.5	11.3	717	2	E97520	methy1-accepting c
873	56.5	11.3	272	1	A36082	insulin-like growt	946	56.5	11.3	733	2	B38749	3-phosphatidylinos
874	56.5	11.3	277	2	S35304	homeotic protein G	947	56.5	11.3	739	1	A34873	transcription fact
875	56.5	11.3	286	2	S62370	hypothetical prote	948	56.5	11.3	752	2	F84192	DNA helicase/prima
876	56.5	11.3	289	2	T25682	probable carboxype	949	56.5	11.3	773	2	G86856	phosphoenolpyruvat
877	56.5	11.3	293	2	AB2295	hypothetical prote	950	56.5	11.3	832	2	B70507	hypothetical prote
878	56.5	11.3	296	2	B83417	succinyl-CoA synth	951	56.5	11.3	902	2	H87323	hypothetical prote
879	56.5	11.3	305	2	S32237	hypothetical prote	952	56.5	11.3	1242	2	T45976	myosin heavy chain
880	56.5	11.3	307	2	B87388	astrohaem synchase	953	56.5	11.3	1436	2	T30172	transmembrane prot
881	56.5	11.3	308	2	B82253	acetyl-CoA carboxy	954	56.5	11.3	1436	2	B70520	probable PPE prote
882	56.5	11.3	308	2	E72627	hypothetical prote	955	56.5	11.3	1536	2	S39510	glutamate synthase
883	56.5	11.3	311	2	T09656	orYR protein homol	956	56.5	11.3	1636	2	S60403	probable membrane
884	56.5	11.3	315	2	T35566	probable integral	957	56.5	11.3	2541	2	S11661	calin - mouse
885	56.5	11.3	316	2	S61237	capsid protein - b	958	56.5	11.3	5762	2	A41819	proline-rich pepc1
886	56.5	11.3	326	2	D84412	glucose kinase [im	959	56.5	11.2	129	2	B71350	probable ribosomal
887	56.5	11.3	337	2	T46958	anthranilate phosp	960	56.5	11.2	130	2	A26316	interferon-induced
888	56.5	11.3	340	2	A12932	hypothetical prote	961	56.5	11.2	157	2	B87117	conserved hypochet
889	56.5	11.3	344	2	B97687	engat ABC transpor	962	56.5	11.2	186	2	D75005	probable CDP-alcoh
890	56.5	11.3	363	2	AH2796	hypothetical prote	963	56.5	11.2	195	2	T02788	probable ribosomal
891	56.5	11.3	363	2	H97575	probable permease	964	56.5	11.2	197	2	H81184	Na(+)-translocatin
892	56.5	11.3	365	2	C83629	probable permease	965	56.5	11.2	199	1	A38285	interleukin-11 pre
893	56.5	11.3	365	2	A43720	parathion hydrolas	966	56.5	11.2	208	1	F69462	hypothetical prote
894	56.5	11.3	375	1	A49107	alcohol dehydrogen	967	56.5	11.2	216	2	S38655	tetr protein - Pse
895	56.5	11.3	379	2	D85823	hypothetical prote	968	56.5	11.2	216	2	JQ1478	regulatory protein
896	56.5	11.3	389	2	C90215	molycopdopexin bios	969	56.5	11.2	220	2	T44702	hypothetical prote
897	56.5	11.3	395	2	G83768	galactokinase [imp	970	56.5	11.2	223	2	AG3288	2-hydroxy-6-oxo-2,
898	56.5	11.3	395	2	T44985	methy1matonyl-CoA	971	56.5	11.2	226	2	C98211	epoxidease [importe
899	56.5	11.3	399	2	AB0091	probable flagellin	972	56.5	11.2	238	2	AE0006	cRNA nucleotidyltr
900	56.5	11.3	401	2	AC0091	probable flagellin	973	56.5	11.2	245	2	S76632	hypothetical prote
901	56.5	11.3	404	2	A10080	probable flagellin	974	56.5	11.2	256	2	G83232	probable permease
902	56.5	11.3	409	2	AH2659	MFS permease [impo	975	56.5	11.2	257	2	S16865	gene F41 protein -
903	56.5	11.3	411	2	S47436	flagellin antigen	976	56.5	11.2	260	2	AF3389	cobalamin (5'-phos
904	56.5	11.3	413	2	S55890	plasma protein rec	977	56.5	11.2	267	2	A30988	ly1-1 protein - hu
905	56.5	11.3	413	2	F70560	probable PPE prote	978	56.5	11.2	270	2	C86838	hypothetical prote

979	56	11.2	270	2	T02955	probable cytochrom
980	56	11.2	272	2	D70312	hypothetical prote
981	56	11.2	299	2	E75254	conserved hypotet
982	56	11.2	304	2	B75595	conserved hypotet
983	56	11.2	310	2	D87704	integral membrane
984	56	11.2	325	2	T00686	similar to late em
985	56	11.2	327	2	S30405	hypothetical prote
986	56	11.2	341	2	B71564	probable cationic
987	56	11.2	343	2	F82400	probable hemin ABC
988	56	11.2	347	1	DEP0MW	malate dehydrogena
989	56	11.2	347	1	DEP0MW	hypothetical prote
990	56	11.2	350	2	T12260	caffeoyl-coa O-met
991	56	11.2	350	2	AB1865	hypothetical prote
992	56	11.2	351	2	T50594	probable oxidoredu
993	56	11.2	352	2	G82990	arginate regulator
994	56	11.2	354	2	AC0389	phosphate binding
995	56	11.2	366	2	AC0389	probable calcium/p
996	56	11.2	367	2	AT0647	urophytyingene d
997	56	11.2	369	2	F84291	iron (III) ARC tra
998	56	11.2	370	2	D86957	probable inosine-5
999	56	11.2	373	2	S48451	probable membrane
1000	56	11.2	375	1	S72812	IMP dehydrogenase-
1001	56	11.2	382	2	A72503	hypothetical prote
1002	56	11.2	384	2	AG0149	probable membrane
1003	56	11.2	386	2	H87180	conserved hypotet
1004	56	11.2	392	2	H83198	probable transp
1005	56	11.2	398	2	AC2911	MPS permease [lipo
1006	56	11.2	406	2	C75537	conserved hypotet
1007	56	11.2	406	2	F70019	nifs protein homol
1008	56	11.2	407	2	T34912	3-oxoacyl-lacyl-ca
1009	56	11.2	415	2	D87020	probable membrane
1010	56	11.2	415	2	D87020	hypothetical prote
1011	56	11.2	424	2	T20032	conserved hypotet
1012	56	11.2	425	2	A96014	methy1-accepting c
1013	56	11.2	433	2	H84120	conserved hypotet
1014	56	11.2	435	2	A46231	he1ix-loop-helix p
1015	56	11.2	441	2	G82253	hypothetical prote
1016	56	11.2	441	2	E72579	hypothetical prote
1017	56	11.2	443	2	T17220	probable PTS syste
1018	56	11.2	451	2	AF0441	hemolysin homolog
1019	56	11.2	457	2	A10955	UDP-N-acetylglucos
1020	56	11.2	461	2	B69827	hypothetical prote
1021	56	11.2	462	2	G87534	hypothetical prote
1022	56	11.2	468	2	F82012	two-component sens
1023	56	11.2	472	2	A70951	angiotensin precur
1024	56	11.2	473	2	G83932	RND divalent metal
1025	56	11.2	477	1	A29978	transmembrane prot
1026	56	11.2	486	2	F83330	cytosol aminopepti
1027	56	11.2	493	2	A87459	hypothetical prote
1028	56	11.2	511	2	T51544	hypothetical prote
1029	56	11.2	513	2	AC3061	hypothetical prote
1030	56	11.2	513	2	D98225	hypothetical prote
1031	56	11.2	517	2	H87022	permease protein o
1032	56	11.2	518	2	AB1855	probable transp
1033	56	11.2	533	2	T35722	oxidoreductase, GM
1034	56	11.2	540	2	G87407	l-lactate permease
1035	56	11.2	549	2	C71969	conserved hypotet
1036	56	11.2	556	2	B82379	gamma-glutamyltran
1037	56	11.2	561	2	A41125	serine proteinase,
1038	56	11.2	561	2	A75474	NADH dehydrogenase
1039	56	11.2	605	2	C90613	NAH2 dehydrogenas
1040	56	11.2	605	2	T11529	dark-type molecula
1041	56	11.2	613	2	T43738	class I heat-shock
1042	56	11.2	613	2	AB1258	cell cycle histidi
1043	56	11.2	613	2	AB1621	hypothetical prote
1044	56	11.2	633	2	B87383	ComC/Rec2 family
1045	56	11.2	691	2	T02361	probable fusidic a
1046	56	11.2	720	2	G87485	hypothetical prote
1047	56	11.2	725	2	T35778	hypothetical prote
1048	56	11.2	735	2	AB2729	hypothetical prote
1049	56	11.2	753	2	C97510	hypothetical prote
1050	56	11.2	767	2	G96661	hypothetical prote
1051	56	11.2	767	2	G96661	hypothetical prote
1052	56	11.2	775	2	AC3400	inorganic diphosph
1053	56	11.2	786	2	E87565	conserved hypotet
1054	56	11.2	790	2	D83011	conserved hypotet
1055	56	11.2	827	2	T20492	hypothetical prote
1056	56	11.2	854	2	D83077	ClpB protein PA454
1057	56	11.2	876	2	E96674	hypothetical prote
1058	56	11.2	947	2	G86420	probable receptor-
1059	56	11.2	977	2	C96745	hypothetical prote
1060	56	11.2	1020	1	W2BBB5	gene 23 protein -
1061	56	11.2	1047	1	T41343	probable translati
1062	56	11.2	1086	2	G02257	Mad(p) transhydrog
1063	56	11.2	1151	2	T18535	high molecular mas
1064	56	11.2	1254	1	VHMVVE	structural polypiro
1065	56	11.2	1289	2	T00387	KIAA0622 protein -
1066	56	11.2	1327	2	D70759	probable otub prot
1067	56	11.2	1398	2	T13741	hypothetical prote
1068	56	11.2	1589	2	T13606	hypothetical prote
1069	56	11.2	1626	2	D72120	excinuclease ABC,
1070	56	11.2	1839	2	S77626	mannuronan C-5-epi
1071	55.5	11.1	100	2	H70316	ATP synthase F0 su
1072	55.5	11.1	138	1	SYAD93	hexon-associated p
1073	55.5	11.1	138	1	SYAD93	hexon-associated p
1074	55.5	11.1	144	2	FXAD97	enoyl-CoA hydratase
1075	55.5	11.1	161	2	S33624	allophycocyanin be
1076	55.5	11.1	161	2	B44462	allophycocyanin be
1077	55.5	11.1	166	2	S78003	cuticle structural
1078	55.5	11.1	180	1	YOECF7	P17 fibribial prote
1079	55.5	11.1	198	2	AE2534	hypothetical prote
1080	55.5	11.1	199	2	B84259	hypothetical prote
1081	55.5	11.1	200	2	H30203	glutamine amidotra
1082	55.5	11.1	208	2	T43385	60S ribosomal prot
1083	55.5	11.1	211	2	S18463	lysosyme (EC 3.2.1
1084	55.5	11.1	211	2	D69413	conserved hypotet
1085	55.5	11.1	228	2	T08110	germin-like protei
1086	55.5	11.1	231	2	B64920	probable membrane
1087	55.5	11.1	231	2	A85770	hypothetical prote
1088	55.5	11.1	236	2	E90921	hypothetical prote
1089	55.5	11.1	236	2	T36188	hypothetical prote
1090	55.5	11.1	236	2	E70800	probable transp
1091	55.5	11.1	239	2	A42768	homeotic protein g
1092	55.5	11.1	256	1	T17337	hypothetical prote
1093	55.5	11.1	266	2	B82749	4-hydroxybenzoyl-C
1094	55.5	11.1	275	2	E82737	thiamin biosynthes
1095	55.5	11.1	277	2	C70017	probable sugar kin
1096	55.5	11.1	277	2	S73282	hypothetical prote
1097	55.5	11.1	290	2	AD0367	hypothetical prote
1098	55.5	11.1	291	2	AE2416	lysR-type transcri
1099	55.5	11.1	292	2	T34997	leucyl aminopeptid
1100	55.5	11.1	295	2	C83344	conserved hypotet
1101	55.5	11.1	300	2	A75599	ribokinase - Delno
1102	55.5	11.1	301	2	B64164	hypothetical prote
1103	55.5	11.1	304	2	D69744	conserved hypotet
1104	55.5	11.1	305	2	D64963	nitrogen assimilati
1105	55.5	11.1	305	2	F85823	nitrogen assimilati
1106	55.5	11.1	305	2	H90976	nitrogen assimilati
1107	55.5	11.1	306	2	AG0518	D-alanine,D-alanin
1108	55.5	11.1	309	2	E72784	probable dihydroor
1109	55.5	11.1	309	2	B75565	hypothetical prote
1110	55.5	11.1	311	2	D87164	probable LysR-fami
1111	55.5	11.1	320	2	AG3543	acetylglutamate ki
1112	55.5	11.1	333	2	A33098	allergen Poa p IX
1113	55.5	11.1	336	2	AP1378	B. subtilis ferric
1114	55.5	11.1	337	2	AG1747	B. subtilis ferric
1115	55.5	11.1	341	1	TVMSJD	conserved hypotet
1116	55.5	11.1	342	2	T51703	transforming prote
1117	55.5	11.1	346	1	B64976	nicotinate-nucleot
1118	55.5	11.1	346	1	B64976	galactitol-1-phosp
1119	55.5	11.1	346	2	F90990	galactitol-1-phosp
1120	55.5	11.1	346	2	H85835	immunogenic protei
1121	55.5	11.1	346	2	A84017	probable regulator
1122	55.5	11.1	350	2	E71373	fructose-bisphosph
1123	55.5	11.1	358	2	T43289	fructose-bisphosph
1124	55.5	11.1	358	2	T39798	fructose-bisphosph

1125	55.5	11.1	361	2	T27504	hypothetical prote
1126	55.5	11.1	362	2	T14393	probable oleoyl-la
1127	55.5	11.1	365	2	F95857	probable sugar ABC
1128	55.5	11.1	374	2	D83328	probable aminotran
1129	55.5	11.1	376	1	A26468	alcohol dehydrogen
1130	55.5	11.1	380	2	AB1709	N-acetylglucosamin
1131	55.5	11.1	384	2	D69471	iron-sulfur bindin
1132	55.5	11.1	388	2	S34672	alkaline serine pr
1133	55.5	11.1	389	2	E72537	probable cysteine
1134	55.5	11.1	395	2	AE1801	D-3-phosphoglycera
1135	55.5	11.1	395	2	AG1427	D-3-phosphoglycera
1136	55.5	11.1	400	2	T03460	probable leucine/i
1137	55.5	11.1	403	1	C69213	protein-export mem
1138	55.5	11.1	408	2	AC2800	aminotransferase l
1139	55.5	11.1	411	2	B75506	hypothetical prote
1140	55.5	11.1	416	2	E97579	hypothetical prote
1141	55.5	11.1	418	2	C89772	hypothetical prote
1142	55.5	11.1	419	1	DEECNB	glycerol-3-phospha
1143	55.5	11.1	425	2	AC3391	tetracenomycin c p
1144	55.5	11.1	433	2	F75566	probable benzate
1145	55.5	11.1	439	2	G82184	glycerol-3-phospha
1146	55.5	11.1	449	2	E87639	hypothetical prote
1147	55.5	11.1	461	2	S01840	nitrogenase (EC 1.
1148	55.5	11.1	463	2	T36810	probable integral
1149	55.5	11.1	476	2	D87386	sodium-dicarboxyla
1150	55.5	11.1	485	2	AH0756	probable inner mem
1151	55.5	11.1	486	2	AB1356	amino acid ABC tra
1152	55.5	11.1	486	2	AC1726	amino acid ABC tra
1153	55.5	11.1	488	2	AB1194	C4-dicarboxylate t
1154	55.5	11.1	488	2	B81831	probable integral
1155	55.5	11.1	493	2	F96696	protein FIN21.12 l
1156	55.5	11.1	498	2	F98149	hypothetical prote
1157	55.5	11.1	500	2	B81929	probable phosphate
1158	55.5	11.1	504	2	G87532	tyctophan halogen
1159	55.5	11.1	504	2	T32488	hypothetical prote
1160	55.5	11.1	507	2	S64507	probable membrane
1161	55.5	11.1	513	2	D70836	probable PEP prote
1162	55.5	11.1	518	2	D69813	ABC transporter (A
1163	55.5	11.1	522	2	T26276	hypothetical prote
1164	55.5	11.1	528	2	AC3236	hypothetical prote
1165	55.5	11.1	529	2	A69025	translational elonga
1166	55.5	11.1	530	2	G95386	probable Dioxigena
1167	55.5	11.1	531	2	T12056	xpsr protein - Xan
1168	55.5	11.1	533	2	D83468	probable decarboxy
1169	55.5	11.1	533	2	AB3138	hypothetical prote
1170	55.5	11.1	538	2	H83466	probable ATP-bindi
1171	55.5	11.1	551	2	E64537	L-lactate permease
1172	55.5	11.1	551	2	D71969	1-lactate permease
1173	55.5	11.1	559	2	F83283	precortin-3 methyl
1174	55.5	11.1	560	2	S53382	protein YKR029c ho
1175	55.5	11.1	569	2	SS7812	leucyl aminopeptid
1176	55.5	11.1	570	2	A83118	probable ATP-bindi
1177	55.5	11.1	582	2	H82393	probable L-lactate
1178	55.5	11.1	595	2	B97415	hypothetical prote
1179	55.5	11.1	595	2	AF2632	conserved hypotet
1180	55.5	11.1	660	2	H87590	cytochrome c-type
1181	55.5	11.1	675	2	S25005	diak-type molecula
1182	55.5	11.1	689	2	T08988	cadmium-transporti
1183	55.5	11.1	711	2	A85352	cadmium-transporti
1184	55.5	11.1	711	2	T12525	hypothetical prote
1185	55.5	11.1	725	2	F81845	probable cation-tr
1186	55.5	11.1	754	2	T46614	chemotaxis protein
1187	55.5	11.1	754	2	A53679	endothelin convert
1188	55.5	11.1	771	2	F70757	probable cation tr
1189	55.5	11.1	780	2	T00366	hypothetical prote
1190	55.5	11.1	792	2	C71250	probable cation-tr
1191	55.5	11.1	795	2	H70934	5-methyltetrahydro
1192	55.5	11.1	814	2	S65083	probable efflux pr
1193	55.5	11.1	815	2	T35970	fructose phosphotr
1194	55.5	11.1	827	1	S10639	probable transposa
1195	55.5	11.1	892	2	J00424	glycoprotein B pre
1196	55.5	11.1	903	1	VGBEB1	glycoprotein B pre
1197	55.5	11.1	904	1	VGBEW7	glycoprotein B pre



1417	54.5	10.9	353	2	F83190	probable UDP-3-O-(
1418	54.5	10.9	354	2	S70595	NADH2 dehydrogenas
1419	54.5	10.9	356	2	S71179	cinammyl-alcohol d
1420	54.5	10.9	358	2	C72526	hypothetical prote
1421	54.5	10.9	360	2	T08581	cinammyl-alcohol d
1422	54.5	10.9	362	2	T38621	probable isopropyl
1423	54.5	10.9	364	2	T02364	hypothetical prote
1424	54.5	10.9	368	2	C69590	choistamate synthas
1425	54.5	10.9	368	2	AD3493	leucine-3, isoleuci
1426	54.5	10.9	376	1	KDBHP	thymidine kinase (
1427	54.5	10.9	378	2	AE0484	probable glycerate
1428	54.5	10.9	384	2	H75476	probable branched-
1429	54.5	10.9	387	2	F82998	probable iron-cont
1430	54.5	10.9	387	2	S14876	ADP,ATP carrier pr
1431	54.5	10.9	387	2	S07259	coat protein - tom
1432	54.5	10.9	390	2	T04096	glucose-6-phosphat
1433	54.5	10.9	390	2	T49705	related to transcr
1434	54.5	10.9	397	2	T39579	nccb protein - Alc
1435	54.5	10.9	398	2	E86923	conserved hypochet
1436	54.5	10.9	401	2	D82429	acetyl-CoA acetyl
1437	54.5	10.9	404	2	T50335	mating pheromone r
1438	54.5	10.9	413	2	T06325	malate dehydrogena
1439	54.5	10.9	422	2	AD0484	GntP family permea
1440	54.5	10.9	422	2	AB1853	hypothetical prote
1441	54.5	10.9	430	2	C72721	probable alkylidihy
1442	54.5	10.9	431	2	F96764	hypothetical prote
1443	54.5	10.9	433	2	T19632	hypothetical prote
1444	54.5	10.9	439	2	B81997	L-serine ammonia-1
1445	54.5	10.9	439	2	S51378	probable membrane
1446	54.5	10.9	441	2	T31482	hypothetical prote
1447	54.5	10.9	443	2	G83350	hypothetical prote
1448	54.5	10.9	458	2	B83341	L-serine dehydrata
1449	54.5	10.9	459	2	G69075	nitrogenase molybd
1450	54.5	10.9	461	2	C81225	L-serine dehydrata
1451	54.5	10.9	462	2	D87630	conserved hypochet
1452	54.5	10.9	464	2	C75474	conserved hypochet
1453	54.5	10.9	465	2	T35712	integral membrane
1454	54.5	10.9	465	2	AD2016	hypothetical prote
1455	54.5	10.9	469	2	AE3353	L-serine ammonia-1
1456	54.5	10.9	471	2	AE4739	indole-3-acetate b
1457	54.5	10.9	471	2	G69809	aminocacid carrier
1458	54.5	10.9	473	1	S18586	inactive mercury (I
1459	54.5	10.9	476	2	T29054	probable transmemb
1460	54.5	10.9	486	2	G95865	probable ribulose-
1461	54.5	10.9	488	2	AH2792	L-serine dehydrata
1462	54.5	10.9	488	2	G97571	1-serine dehydrata
1463	54.5	10.9	491	2	T27128	hypothetical prote
1464	54.5	10.9	491	2	B87452	ankyrin-related pr
1465	54.5	10.9	493	2	B72704	hypothetical prote
1466	54.5	10.9	500	2	T35666	probable transcrip
1467	54.5	10.9	504	2	S73163	H+-transporting tw
1468	54.5	10.9	508	2	B30310	glucose transport
1469	54.5	10.9	510	2	A70580	probable UDP-N-ace
1470	54.5	10.9	511	2	S43686	monomine transpor
1471	54.5	10.9	524	2	T09937	cytokinin oxidase
1472	54.5	10.9	527	2	A13494	chromosomal replic
1473	54.5	10.9	533	2	G75348	conserved hypochet
1474	54.5	10.9	535	2	AE9537	cytochrome oxidase
1475	54.5	10.9	537	2	F84248	iron transporter-1
1476	54.5	10.9	545	2	C95910	probable membrane
1477	54.5	10.9	549	2	T36879	probable CRP synth
1478	54.5	10.9	555	2	B87670	GDDP family prote
1479	54.5	10.9	556	2	S36639	polypyrimidine tra
1480	54.5	10.9	560	2	AG2640	flagellar M-ring p
1481	54.5	10.9	566	2	T34842	probable transfera
1482	54.5	10.9	566	2	H97422	flagellar m-ring p
1483	54.5	10.9	567	2	T52585	probable nitrate t
1484	54.5	10.9	574	2	T14162	HABC transport pro
1485	54.5	10.9	592	2	D95383	hypothetical prote
1486	54.5	10.9	596	2	A28088	oxalacetate decar
1487	54.5	10.9	597	2	E70928	hypothetical prote
1488	54.5	10.9	607	2	H90054	conserved hypochet
1489	54.5	10.9	621	2	A82153	PTS system, fructo

1490	54.5	10.9	623	2	T35377	probable membrane
1491	54.5	10.9	625	2	H98148	hypothetical prote
1492	54.5	10.9	628	1	S22396	pyruvate synthase
1493	54.5	10.9	634	2	G90779	hypothetical prote
1494	54.5	10.9	637	2	UH0674	L-proline transpor
1495	54.5	10.9	638	2	C64156	hypothetical prote
1496	54.5	10.9	639	2	D82809	exodeoxyribonuclea
1497	54.5	10.9	640	2	F84268	hypothetical prote
1498	54.5	10.9	645	2	AD5641	hypothetical prote
1499	54.5	10.9	651	2	AD3139	methyl-accepting c
1500	54.5	10.9	652	2	S50210	surface layer prot

## ALIGNMENTS

```
RESULT 1
T09931
probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4.J
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09931
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16897
A:Accession: T09931
A:Molecule type: DNA
A:Residues: 1496 <BEV>
A:Cross-references: UNIPROT:Q9S0B3; EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
A:Experimental source: cultivar Columbia; BAC clone T16L4
C:Genes:
A:Gene: ATSP:T16L4.190
A:Map position: 4
A:Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4
C:Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase

Query Match 16.1%; Score 81; DB 2; Length 496;
Best Local Similarity 41.3%; Pred. No. 5.3;
Matches 26; Conservative 14; Mismatches 17; Indels 6; Gaps 3;

QY 6 LIGLCVALSCSSAAAFVGSAPVQAPVALESAAENGA--GTLANPLGTLN-PLKLLLS 62
DB 57 LVTVCIALSAASAFAPLFSSQ--KPVSLIANISKSPARDRSVAPRLKIDRPVLLIS 113

QY 63 SLG 65
DB 114 SDG 116

RESULT 2
S60004
hypothetical protein - common roundworm retrotransposon R4 (fragment)
C:Species: Ascaris lumbricoideae (common roundworm)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C/Accession: S60004
R:Burke, W.D.; Mueller, F.; Eickbush, T.H.
Nucleic Acids Res. 23, 4628-4634, 1995
A:Title: R4, a non-LTR retrotransposon specific to the large subunit rRNA genes of nematoc
A:Reference number: S60004; MVID:96103592; PMID:8524653
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 11381 <BUR>
A:Cross-references: EMBL:U29445; NID:G903660; PIDD:AAA97394.1; PIDD:G903661
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C:Genes:
A:Genome: retrotransposon

Query Match 15.8%; Score 79.5; DB 2; Length 1381;
Best Local Similarity 27.8%; Pred. No. 21;
Matches 25; Conservative 15; Mismatches 23; Indels 27; Gaps 3;

QY 11 VALSCSSAAAFVGSAPVQAPVALESAAENAGAGT-----LANPLG----- 52
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Db 27 IAMPCTNSFPERGTPEHPHPISGTDSSESLSKMGTHRSPLNDDEVINGPKHESDPVH 86  
Qy 53 -----TLNPLKLLSLGIPVNHLEGSQ 76  
Db 87 VVRAPRTLHPRL---ELPIGVNLTGASQ 113

## RESULT 3

T35054  
probable transport system permease protein - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C/Accession: T35054  
R/Seeger, K.U.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
Submitted to the EMBL Data Library, August 1998  
A/Reference number: Z21566  
A/Accession: T35054  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-601 <SEB>  
A/Cross-references: UNIPROT:O86691; EMBL:AL031371; PIDN:CA20556.1; GSPDB:GN00070; SCOE  
C/Genetics:  
A/Map position: linear chromosome  
A/Gene: SCOE8B:SC4G2.19

Query Match 15.4%; Score 77.5; DB 2; Length 601;  
Best Local Similarity 30.7%; Pred. No. 14;

Matches 42; Conservative 10; Mismatches 48; Indels 37; Gaps 4;

Qy 3 LAALIGLVALSCSSAAFLVGSAA--KVA-----QPVAALESAAAGAG-----45

Db 426 LVALLVTAVAGSGATPTLAVGAVAMAPLAHTSLLRQERATLITATKGLGAGPVHL 485

Qy 46 -----TLNPLGTINPLKLLSLGIPVNHLEGSQKCVAAELG 85

Db 486 RHELLPAVVPVPLRHALLRLPGVALALASLGLGAGPPSPFEGLLAENQPIAERAPW 545

Qy 86 AVGAVKALKALLGALTIV 102

Db 546 AVLAAPAVALMLGLALAV 562

RESULT 4

T36304

probable anthranilate phosphoribotransferase - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: T36304

R/Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, March 1999

A/Reference number: Z21604

A/Accession: T36304

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-335 <SAU>

A/Cross-references: UNIPROT:Q9Z4W9; EMBL:AL035654; PIDN:CA338583.1; GSPDB:GN00070; SCOE

C/Genetics:  
A/Gene: trpD2; SCOE8B:SC8.05C  
A/Map position: linear chromosome  
A/Gene: trpD2; SCOE8B:SC8.05C

Query Match 15.3%; Score 77; DB 2; Length 335;  
Best Local Similarity 34.5%; Pred. No. 8.3;  
Matches 30; Conservative 9; Mismatches 36; Indels 12; Gaps 4;

Qy 7 LGLCVALLSCSSAAFLVGSAA-----KPAVAPVAALESAA-----EGAGTANPLGTLNP 56

Db 117 LCVRIIDLGEAEAAACLDRTGRTFLPAVFNH--AFRTTAGRRRELGATVFNLLGPIGICNP 174

Qy 57 LKLLSLGIPVNHLEGSQKCVAAELG 83

Db 175 SGARLRTLGVPSELVEPMTVEVLERLG 201

## RESULT 5

AD2973

hypothetical protein Atu3389 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C/Accession: AD2973

R/Mood, D.W.; Serubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Moo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A/Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; WUID:21608550; PMID:11743193

A/Accession: AD2973

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-355 <KUR>

A/Cross-references: UNIPROT:O8UA14; GB:AE008689; PIDN:AAL44202.1; PID:g17741761; GSPDB:GN

C/Genetics:  
A/Map position: linear chromosome  
A/Gene: Atu3389

Query Match 15.1%; Score 76; DB 2; Length 355;  
Best Local Similarity 23.3%; Pred. No. 11;

Matches 28; Conservative 22; Mismatches 42; Indels 28; Gaps 3;

Qy 2 KLAALIGLVALSCSSAAFLVGSAAKPAVAPVAALESAAAGAGTANPLGTLNP 61

Db 24 RLIIIVGLFLALCFPMADMLGPARVTLSEVLA-----TIDPAVAGVQLRV 73

Qy 62 SSLGIPVNHLEGSQKCVAA-----ELGPQAVGAVKALKALLGALTIV 103

Db 74 WDIRMPIALMAVTVGASLSVAGAQMTILSNPLASPTTLGISAAASFGALALVGVAVIF 133

RESULT 6

G98309

probable ABC transporter permease protein WU087 AGR\_L\_2865 [imported] - Agrobacterium t

C/Species: Agrobacterium tumefaciens

C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004

C/Accession: G98309

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappae, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume

A/Reference number: A97359; WUID:21608551; PMID:11743194

A/Accession: G98309

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-355 <KUR>

A/Cross-references: UNIPROT:Q8UA14; GB:AE007870; PIDN:AAK90001.1; PID:g15159970; GSPDB:GN

C/Genetics:  
A/Gene: AGR\_L\_2865  
A/Map position: linear chromosome

Query Match 15.1%; Score 76; DB 2; Length 355;  
Best Local Similarity 23.3%; Pred. No. 11;  
Matches 28; Conservative 22; Mismatches 42; Indels 28; Gaps 3;

Qy 2 KLAALIGLVALSCSSAAFLVGSAAKPAVAPVAALESAAAGAGTANPLGTLNP 61

Db 24 RLIIIVGLFLALCFPMADMLGPARVTLSEVLA-----TIDPAVAGVQLRV 73

Qy 62 SSLGIPVNHLEGSQKCVAA-----ELGPQAVGAVKALKALLGALTIV 103

Db 74 WDIRMPIALMAVTVGASLSVAGAQMTILSNPLASPTTLGISAAASFGALALVGVAVIF 133

RESULT 7

H87275  
 chio-disulfide interchange protein, probable [imported] - *Caulobacter crescentus*  
 C/Species: *Caulobacter crescentus*  
 C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
 C/Accession: H87275  
 R./Nierman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 B.; Laub, M.C.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4135-4141, 2001  
 A/Title: Complete Genome Sequence of *Caulobacter crescentus*.  
 A/Reference number: H87249; MUID:21173698; PMID:11259667  
 A/Accession: H87275  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Releasers: 1-699 <STO>  
 A/Cross-references: UNIPROT:Q9ABL0; GB:AE005673; NID:gl3421344; PIDN:AAK22204.1; GSPDB:G  
 C/Genetics:  
 C/Gene: CC0217

	Query Match	15.1%	Score 76;	DB 2;	Length 699;
	Best Local Similarity	30.5%	Pred. No. 22;		
	Matches	32;	Conservative 18;	Mismatches 37;	Indels 18; Gaps 5;
Qy	3 LAALLGCVALLSCSSAAAFIVGSAKPVNAQPVAALESAABAGCTLANPLGTIANPDKL-L-LL :::     :				61
Dd	545 VSMILGLVAVGALALAAAASLSAKP--PYAAAEASTPSGGITAE--AWSEPKVAL 				598
Qy	62 SSLGIPIVNHLEIGS-----QKVAELGEPOAIVGAVKLKALL  : :~::~             :				97
Dd	599 QABRPFI-LVDFTPAAMCVTTCVNNEKVALLSPKAERFAEKANAVL  : :~::~             :				641

```

RESULT 8
T47269
copper-transporting ATPase (EC 3.6.1.-) P-type copA [validated] - Helicobacter felis
C:Species: Helicobacter felis
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47269
R:Bayle, D.; Mangler, S.; Weitzenecker, T.; Steinhilber, W.; Volz, J.; Przybylski, M.; S
U: Bacteriol. 180, 317-329, 1998
A:Title: Properties of the P-type ATPases encoded by the copA operons of Helicobacter p
A:Reference number: 224437; MUID:98101471; PMID:9440521
A:Accession: T47269
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-732 <BAV>
A:Cross-references: UNIPROT:O32619; EMBL:AJ001932; NID:92660538; PIDN:CA05104.1; PID:92
A:Experimental source: strain ATCC 49179
C:Genetics:
A:Gene: copA
C:Function:
A:Description: binds copper specifically [validated, MUID:98101471]
A:Note: involved in copper resistance
C:Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding d
C:Keywords: copper binding; hydrolase
F:8-37/Domain: heavy-metal-associated homology <HMA>
F:532-674/Domain: ATPase nucleotide-binding domain homology <ATN>

```

	Query Match	15.1%	Score 76;	DB 2;	Length 732;
	Best Local Similarity	26.3%;	Pred. No. 23;		
	Matches	35;	Conservative 17;	Mismatches 39;	Indels 42; Gaps 6;
QY	6	LIGLCVALLSCSSAAFLVIGSAKPVAGPVAAI	---	ESAAEAGAG	-----45
Db	447	LITTCASIEAOSSEHVIYAKGIYAAHAKKEGIALQEVQEVQAKGFGIKGVGDDQITKAGNLE			506
QY	46	--TLANPLGTINPKLLLS---	LGIPV-	NHLIEGSQKCAELGPQAVGA	-----89
Db	507	FFNLPPNPGTLEGIQVFGVETQTLLGVVVLADSLKEGSKAISEL-		KALGVKTTLLSGD	564
QY	90	---VKALKALLG			98
Db	565	NLENVVALATQLG			577

**RESULT 9**

H72647  
hypothetical protein APE0614 - Aeropyrum pernix (strain K1)  
C|Species: Aeropyrum pernix  
C|Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #ext\_change 09-Jul-2004  
A|Accession: H72647  
R|Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakeyama, H.; Jin-no, K.; Takahara, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kanaoka, R.  
DNA Res. 6, 83-101, 1999  
A|Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1  
A|Reference number: A72450; MUID:9310339; PMID:10382566  
A|Accession: H72647  
A|Status: preliminary  
A|Molecule type: DNA  
A|Residues: 1-544 <KAW>  
A|Cross-references: UNIPROT:O9YEG2; DDBJ:A000060; NID:G5104188; P|DN:BAA79584.1; P|D:d1  
A|Experimental source: strain K1  
C|Genetics:  
A|Gene: APE0614

```

Query Match Similarity      15.0%; Score 75.5; DB 2; Length 544;
Best Local Similarity      26.4%; Pred. No. 19;
Matches 33; Conservative 19; Mismatches 36; Indels 37; Gaps 5;

QY      5  ALLGCVALLSCSSA-----AALVGSAGKPVAPQEVAA-----TESAAEGAGTLANP 50
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      18  ALVAVAAVAVAAVAALLSVSGRTAGLIGAGGAASQSIILAAASNPLMEAWTEAGA----- 71

QY      51  LGTLNPLKLLLSLGI PVNHLI-----EGSQKVAELGPQAVGAVYALK-----ALLGA 99
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      72  -----LKVRFYSPGAPFVSVVVLKPGEGVAARVELPEPAVEGVADMEGYDSCPVILGV 125

QY      100 LTVFG 104
      |||
DB      126 FTVGG 130

```

RESULT 10  
CQ4358  
transport protein [imported] - Halobacterium sp. NRC-1  
CjSpecies: Halobacterium sp. NRC-1  
CjDate: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #ext\_change 09-Jul-2004  
CjAccession: CQ4358  
R.Ng, M.V.; Kennedy, S.P.; Mahaias, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
; Lelthausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li  
A>Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483; PMID:11016550  
A:Accession: CQ4358  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-331 <STO>  
A:Cross-references: UNIPROT:Q9HNT9; GB:AE004437; NID:g10581500; PDB:AA020231.1; GSPDB:G  
CjGenetics:  
A:Gene: phnE

	Query Match	Similarity	14.6%	Score 73.5	DB 2	Length 331
	Best local	Similarity	27.9%	Pred. No. 17		
	Matches	Conservative	17	Mismatches	35	Gaps 5
QY	3	LAALIGLCVSLSCSNAATLVGSAKFPAQPVNVALESAAEGAGTIANPGLTNPYKLLLS	62			
DB	83	LTSLEGVVPFVGVQYYSFLAHENP-SIPLAAVETLTGIAFQTV--LGA--PLALTFG	136			
QY	63	SLG-----IPVNLIEGSOQCVABLGPOAVGAKALKALLGL	100			
DB	137	VGSEKRVVTFPLNPLFRG-----VMSIRSIIPALVWAL	169			



## RESULT 11

Probable aldehyde dehydrogenase PA0747 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
 C/Species: *Pseudomonas aeruginosa*  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 C/Accession: F83553  
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Linn, Nature 406, 959-964, 2000  
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
 A/Reference number: A82950; MUID:20437337; PMID:10984043  
 A/Accession: F83553  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-502 <STO>  
 A/Cross-references: UNIPROT:Q91512; GB:AE004509; GB:AE004091; NID:G9946622; PIDN:AA00413  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Gene: PA0747  
 C/Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 14.5%; Score 73; DB 2; Length 502;  
 Best Local Similarity 29.1%; Pred. No. 30;  
 Matches 32; Conservative 13; Mismatches 41; Indels 24; Gaps 5;

QY 4 AALLGLCVALLSCSSA-----AFLVGSAR-----PVAQPVAALES-----AAGAGTL 47  
 DB 264 AOVGLNVGASCGAAGORCAISAAVFGAAREMPELAERMAVLRPHQDPDAVGPL 323  
 QY 48 ANPLGTLPKLLSLGIPVNHLEGSQKVAE-----LGPQAVAV 90  
 DB 324 ISFOARQVRLRLAEGKAGACGLDGSQ-CVGEISYVGNWLGPTLFRAY 372

## RESULT 12

Gamma-glutamyltransferase [imported] - *Caulobacter crescentus*  
 C/Species: *Caulobacter crescentus*  
 C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
 C/Accession: B87315  
 R/Nietman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.N.; J. Ermolaeva, M.; White, O.; Salzbey, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A/Title: Complete Genome Sequence of *Caulobacter crescentus*.  
 A/Reference number: A87249; MUID:21173698; PMID:11259647  
 A/Accession: B87315  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-584 <STO>  
 A/Cross-references: UNIPROT:Q9AAR5; GB:AE005673; NID:G13421716; PIDN:AAK22518.1; GSPDB:G  
 C/Genetics:  
 A/Gene: CC0531  
 C/Superfamily: gamma-glutamyltransferase

Query Match 14.5%; Score 73; DB 2; Length 584;  
 Best Local Similarity 28.6%; Pred. No. 35;  
 Matches 28; Conservative 10; Mismatches 38; Indels 22; Gaps 2;

QY 2 KLAALLGLCVALLSCSSAAAFVGSAPVAPV-ALLESAAEAGGTLANPLGTLPKL 59  
 DB 7 RLASLLASALLQSLAPVAALAESIPLMPPRRMASTAKGMVAANPLAVEAGIRV 66  
 QY 60 LLSLSIGIPVNHLEGSQKVAELGPQAVGAVKALKAL 97  
 DB 67 LRD-----GSAVDAVAIVDAVL 84

## RESULT 13

hypothetical protein 8D8.2 - fruit fly (*Drosophila melanogaster*)  
 C/Species: *Drosophila melanogaster*

C/Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
 C/Accession: T13613  
 R/Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C. submitted to the EMBL Data Library, April 1999  
 A/Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.  
 A/Reference number: Z17695  
 A/Accession: T13613  
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
 A/Residues: 1-1279 <PAP>  
 A/Cross-references: UNIPROT:O46099; EMBL:AL022018; NID:e1273253; PID:e1426350; PIDN:CAAT  
 C/Genetics:  
 A/Cross-references: FlyBase:FBgn0024367  
 A/Introns: 65/2  
 A/Note: EG:8D8.2

Query Match 14.5%; Score 73; DB 2; Length 1279;  
 Best Local Similarity 31.6%; Pred. No. 77;  
 Matches 31; Conservative 12; Mismatches 29; Indels 26; Gaps 4;

QY 25 SAKVAPVAALES-----AAGAGTLANPLGTLPKLLSLGIPV 69  
 DB 213 SANPAAAEAAKFSHYAKNAQFLRKPSPGGGSLSS---TVKPVADILSLGIVSG 269  
 QY 70 HLIEGSQK-----CVAELGPQ-AVGAVKALKALGA 99  
 DB 270 GKSDAHRKRYALDDVYPAESAPQPSVAVADLRGLHGA 307

## RESULT 14

amastigote-specific protein A2 precursor - *Leishmania donovani* infantum  
 C/Species: *Leishmania donovani* infantum  
 C/Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 09-Jul-2004  
 C/Accession: A56010  
 R/Charast, H.; Matlahbewski, G. Mol. Cell. Biol. 14, 2975-2984, 1994  
 A/Title: Developmental gene expression in *Leishmania donovani*: differential cloning and  
 A/Reference number: A56010; MUID:94217695; PMID:7545921  
 A/Accession: A56010  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-236 <CHA>  
 A/Cross-references: UNIPROT:Q26351; GB:S69693; NID:G546453; PID:G546454  
 C/Superfamily: proline-rich protein  
 C/Keywords: tandem repeat

Query Match 14.3%; Score 72; DB 2; Length 236;  
 Best Local Similarity 29.8%; Pred. No. 17;  
 Matches 31; Conservative 15; Mismatches 42; Indels 16; Gaps 4;

QY 1 MKLAALLGLCVALLSCSSAAAFVGSAPV-VAQPVAALESAAEAGGTLANPLGTLPKL 58  
 DB 1 MKIRSVRLPVLLVVAALVLAISASAEPRKAAVVGPL-SVGQSVGPLSVGPQAVGPLS 59  
 QY 59 LLSLSIGIPVNHLEGSQKVAELGPQAVGAVKALKALKAL 102  
 DB 60 VGQSVG-PLS-----VGQAVGPLSVGPQSVGPLSV 90

## RESULT 15

suicinyl-CoA synthetase beta chain (AF326913) [imported] - *Agrobacterium tumefaciens* (str  
 C/Species: *Agrobacterium tumefaciens*  
 C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 16-Aug-2004  
 C/Accession: F97675  
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirolo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001  
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*.  
 A/Reference number: A97359; MUID:21608551; PMID:11743194  
 A/Accession: F97675  
 A/Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-397 <KUR>  
A:Cross-references: UNIPROT:Q8UC60; GB:AE007869; PIDN:AK88359.1; PID:G15157842; GSPDB:G  
C:Genetics:  
A:Gene: AGR\_C\_4780  
A:Map position: circular chromosome  
C:Superfamily: Succinyl-CoA synthetase, beta subunit

Query Match 14.3%; Score 72; DB 2; Length 397;  
Best Local Similarity 36.2%; Pred. No. 29;  
Matches 29; Conservative 8; Mismatches 31; Indels 12; Gaps 4;

OY 18 AAFLVGSAPVAPVALE-SAAEAGGTIANPLGTINPLKLLSSIGIPVNHLEGSQ 76  
Db 8 AKALLKGYGAPVPAEGVAALKVEEAEAAKQLPGLYV---VKSQIHAGS-----RKG 57

OY 77 KCVAEIGPQAVGAVKALKAL 96  
Db 58 K-FKEIGPDAKGGVRLAKSI 76

Search completed: March 5, 2005, 21:23:52  
Job time : 58 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2005, 21:19:33 ; Search time 176 Seconds  
(without alignments)  
302.592 Million cell updates/sec

Title: US-09-989-731-408  
Perfect score: 502  
Sequence: 1 MKLAALIGLVALSCSSAAA.....QAVGAVKALKALGALTVEG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	100.0	104	1 UGR2_HUMAN	Q96gr1 homo sapien
2	261	52.0	104	2 Q71MT8	Q71me8 ratu musculi
3	250	49.8	104	1 UGR2_MOUSE	Q920s7 mus musculi
4	232	46.2	93	2 Q7M7A1	Q7m7a1 ratu musculi
5	225	44.8	94	2 Q8C0C6	Q8c0c6 mus musculi
6	160	31.9	93	1 UGR1_HUMAN	Q96p11 homo sapien
7	148.5	29.6	93	2 Q71MM7	Q71mm7 ratu musculi
8	135	26.9	139	1 UGR1_MOUSE	Q920h1 mus musculi
9	88	17.5	255	2 Q82LA6	Q82la6 streptomycete
10	83.5	16.6	281	2 Q8FST3	Q8fst3 corynebacte
11	83	16.5	1327	1 TNK1_HUMAN	Q95271 homo sapien
12	82.5	16.4	247	2 Q9K3G4	Q9k3g4 streptomycete
13	82.5	16.4	694	2 Q98CR1	Q98cr1 rhizobium 1
14	82	16.3	117	2 Q6H4X3	Q6h4x3 oryza sativ
15	82	16.3	540	2 Q62CFO	Q62cf0 burkholderi
16	82	16.3	540	2 Q63K09	Q63km9 burkholderi
17	81	16.1	2	2 Q6AFG5	Q6afg5 leifsonia x
18	81	16.1	496	2 Q9SU83	Q9suh3 arabidopsis
19	80	15.9	148	2 Q8XW23	Q8xw23 ralstonia s
20	79	15.7	136	2 Q82R50	Q82r50 streptomycete
21	79	15.7	176	2 Q61E83	Q61e83 sus bactrofa
22	78	15.5	344	2 Q7P4X9	Q7p4x9 fusobacteri
23	77.5	15.4	229	2 Q7VYA1	Q7vya1 bordetella
24	77.5	15.4	229	2 Q7WA34	Q7wa34 bordetella
25	77.5	15.4	229	2 Q7WJ66	Q7wj66 bordetella
26	77.5	15.4	601	2 Q86691	Q86691 streptomycete
27	77	15.3	189	2 Q64UD8	Q64ud8 bacteroides
28	77	15.3	335	1 TRD2_STRECO	Q64u9 streptomycete
29	77	15.3	453	1 Q8THL0	Q8thl0 methanosaarc
30	77	15.3	719	2 Q63RH3	Q63rh3 burkholderi
31	76	15.1	355	2 Q8UA14	Q8ua14 agrobacteri
32	76	15.1	529	2 Q62IX9	Q62ix9 burkholderi
33	76	15.1	546	2 Q63SM0	Q63sm0 burkholderi
34	76	15.1	609	2 Q9ABL0	Q9abl0 caulobacter
35	76	15.1	732	1 COPA_HELPF	Q926t9 helicobacte
36	76	15.1	889	1 CLPB_BIFLO	Q8g4x4 bifidobacte
37	75.5	15.0	492	2 Q9F2I6	Q9f2i6 streptomycete
38	75.5	15.0	496	2 Q8G3S2	Q8g3s2 bifidobacte
39	75.5	15.0	544	2 Q9VEG2	Q9veg2 aeropyrum p
40	75.5	15.0	667	2 Q8XW8	Q8xw8 ralstonia s
41	75	14.9	299	2 Q89XU3	Q89xu3 bradyrhizob
42	75	14.9	355	2 Q8RFX3	Q8rfx3 corynebacte
43	75	14.9	362	1 MED1_HUMAN	Q9h1e6 homo sapien
44	75	14.9	362	1 MED1_MOUSE	Q9erh8 mus musculi
45	75	14.9	370	2 Q89H46	Q89h46 bradyrhizob
46	75	14.9	463	2 Q8C3I3	Q8c3i3 mus musculi
47	75	14.9	574	2 Q6FQW0	Q6fqw0 candida gla
48	74.5	14.8	331	2 Q6N849	Q6n849 rhodospseud
49	74.5	14.8	398	2 Q69UA9	Q69ua9 oryza sativ
50	74	14.7	283	2 Q75D55	Q75d55 ashbya gos
51	74	14.7	547	2 Q6M849	Q6m849 corynebacte
52	74	14.7	631	2 Q9LOK1	Q9lok1 streptomycete
53	74	14.7	779	1 SNL1_MOUSE	Q8o670 mus musculi
54	73.5	14.6	119	2 Q86D11	Q86d11 leishmania
55	73.5	14.6	242	2 Q757F5	Q757f5 ashbya gos
56	73.5	14.6	331	2 Q9HN19	Q9hn19 halobacteri
57	73.5	14.6	358	2 Q8N028	Q8n028 corynebacte
58	73.5	14.6	389	2 Q8EJ01	Q8ej01 shewanella
59	73.5	14.6	422	2 Q6AN39	Q6an39 desulfocale
60	73.5	14.6	626	1 DXS_WIGBR	Q6d357 wigglewort
61	73.5	14.6	776	1 SNL1_RAP	Q9r1u5 ratu musculi
62	73.5	14.6	882	1 SYA_THER2	P61707 thermus the
63	73.5	14.6	882	1 SYA_THER1	P74941 thermus the
64	73.5	14.6	1468	2 Q9GBH5	Q9gub5 galliera me
65	73	14.5	317	2 Q9BD48	Q9bd48 rhizobium 1
66	73	14.5	429	2 Q82SM1	Q82sm1 streptomycete
67	73	14.5	502	2 Q9I5I2	Q9i5i2 pseudomonas
68	73	14.5	526	2 Q6NHX3	Q6nhx3 corynebacte
69	73	14.5	542	2 Q8GYA1	Q8gya1 arabidopsis
70	73	14.5	584	2 Q9AAR5	Q9aar5 caulobacter
71	73	14.5	620	1 DXS_BORBR	Q7v137 bordetella
72	73	14.5	620	1 DXS_BORPA	Q7w740 bordetella
73	73	14.5	630	1 DXS_BORPE	Q7v687 bordetella
74	73	14.5	802	2 Q6F5A9	Q6f5a9 xanthomonas
75	73	14.5	802	2 Q6C3R3	Q6c3r3 xanthomonas
76	73	14.5	1279	2 Q46099	Q46099 diatrophila
77	73	14.5	1552	2 Q67SX8	Q67sx8 bymbiobacte
78	73	14.4	240	2 Q84CV5	Q84cv5 uncultured
79	72.5	14.4	373	2 Q7WYC1	Q7wyc1 toxoplasma
80	72.5	14.4	384	2 Q88KE1	Q88ke1 pseudomonas
81	72.5	14.4	421	2 Q93J77	Q93j77 thermus the
82	72.5	14.4	421	2 Q72KV7	Q72kv7 thermus the
83	72.5	14.4	482	2 Q9BHF9	Q9bhf9 leishmania
84	72.5	14.4	616	2 Q7W2M5	Q7w2m5 bordetella
85	72.5	14.4	3165	2 Q939Z1	Q939z1 amycolatops
86	72	14.3	236	2 Q26351	Q26351 leishmania
87	72	14.3	397	1 SUCC_AGRTS	Q8uc60 agrobacteri
88	72	14.3	433	2 Q98NR3	Q98nr3 rhizobium 1
89	72	14.3	438	2 Q744A8	Q744a8 mycobacteri
90	72	14.3	518	2 Q7D6T0	Q7d6t0 mycobacteri
91	72	14.3	528	2 P71969	P71969 mycobacteri
92	72	14.3	528	2 Q7TW52	Q7tw52 mycobacteri
93	72	14.3	531	2 Q9RJ14	Q9rj14 streptomycete
94	72	14.3	589	2 Q6CJZ1	Q6cjz1 kluyveromycete
95	71.5	14.2	88	2 Q6A4X0	Q6a4x0 kluyveromycete
96	71.5	14.2	343	2 Q88WU3	Q88wu3 lactobacilli
97	71.5	14.2	460	2 Q749Y1	Q749y1 geobacter g
98	71.5	14.2	462	2 Q9A3U4	Q9a3u4 caulobacter
99	71.5	14.2	474	2 Q89FZ0	Q89fz0 bradyrhizob
100	71.5	14.2	520	2 Q94E69	Q94e69 oryza sativ
101	71.5	14.2	590	2 Q6LT07	Q6lt07 photobacter
102	71.5	14.2	694	2 Q8KBL2	Q8kbl2 rhizobium
103	71.5	14.2	874	1 CLPB_AGRTS	Q7cu32 agrobacteri
104	71	14.1	275	2 Q82U00	Q82u00 nitrosomonas

105	71	14.1	315	2	Q89P63	Q89p63 bradyrhizob	178	69	13.7	865	1	CLPB_STRCO	Q8c1y9 streptomyc
106	71	14.1	322	2	Q8S1R4	Q8s1r4 oryza sativ	179	69	13.7	3295	2	Q74Rt8	Q74t18 yersinia pe
107	71	14.1	337	2	Q89Tf3	Q89tcf bradyrhizob	180	69	13.7	3295	2	Q8ZtA8	Q8z1a8 yersinia pe
108	71	14.1	341	2	Q9AMX3	Q9amx3 bradyrhizob	181	69	13.7	3378	2	Q65S06	Q65sg6 yersinia pe
109	71	14.1	409	2	Q8S5W5	Q8s5w5 oryza sativ	182	68.5	13.6	202	2	Q921J1	Q921j1 rhizobium m
110	71	14.1	422	2	Q8ZUN5	Q8zun5 nitrosomona	183	68.5	13.6	208	2	Q7W2P8	Q7w2p8 bordetella
111	71	14.1	428	1	FXB2_MOUSE	Q4f733 mus musculu	184	68.5	13.6	230	2	Q84Cw2	Q84cw2 uncultured
112	71	14.1	440	1	Q911Q3	Q911q3 pseudomonas	185	68.5	13.6	248	2	Q84Cw2	Q84cw2 uncultured
113	71	14.1	448	2	Q826U4	Q826u4 streptomyc	186	68.5	13.6	277	2	Q84Cw2	Q84cw2 uncultured
114	71	14.1	480	1	DNA_RHIME	Q35890 rhizobium m	187	68.5	13.6	281	2	Q8DJM7	Q8djm7 halobacteri
115	71	14.1	721	2	Q7JY99	Q7jy99 mycobacteri	188	68.5	13.6	302	2	Q8BRP3	Q8brp3 pseudomonas
116	71	14.1	826	2	Q74ER8	Q74er8 geobacteri	189	68.5	13.6	311	2	Q82CH3	Q82ch3 pseudomonas
117	71	14.1	947	2	Q8FJF8	Q8ffj8 escherichia	190	68.5	13.6	335	2	Q8ARF5	Q8arf5 synchococc
118	71	14.1	1541	2	Q63LQ3	Q63lq3 mycobacteri	191	68.5	13.6	335	2	Q8ARF5	Q8arf5 synchococc
119	70.5	14.0	183	2	Q73TAY	Q73tay burkholderi	192	68.5	13.6	350	2	Q6N615	Q6ncg29 salmoneila
120	70.5	14.0	260	2	Q93EM4	Q93em4 mycobacteri	193	68.5	13.6	370	2	Q7WXA9	Q7wxa9 rhodospseud
121	70.5	14.0	326	2	Q9DPB4	Q9dpb4 desulfovibr	194	68.5	13.6	377	1	PROB_BIFLO	Q8kng9 actinobact
122	70.5	14.0	353	2	Q8XQV5	Q8xqv5 ralestonia s	195	68.5	13.6	391	2	Q6F6R4	Q6f6r4 rhizobium m
123	70.5	14.0	484	2	Q64H13	Q64hy3 mus musculu	196	68.5	13.6	402	2	Q8KNG9	Q8kng9 rhodospseud
124	70.5	14.0	668	2	Q23323	Q23323 arabidopsis	197	68.5	13.6	404	2	Q741J9	Q741j9 mycobacteri
125	70.5	14.0	691	2	Q8FTB0	Q8ftb0 corynebacte	198	68.5	13.6	415	2	Q6AAB3	Q6aae3 propionibac
126	70.5	14.0	754	2	Q6ESB4	Q6esb4 oryza sativ	199	68.5	13.6	434	2	Q7JY12	Q7jy12 streptomyc
127	70.5	14.0	830	2	Q6ESB5	Q6esb5 oryza sativ	200	68.5	13.6	499	2	Q82M67	Q82m67 streptomyc
128	70.5	14.0	937	2	Q6N973	Q6n973 rhodospseud	201	68.5	13.6	507	2	Q829B3	Q829b3 streptomyc
129	70	13.9	122	2	Q63PE5	Q63pe5 burkholderi	202	68.5	13.6	541	2	Q985J3	Q985j3 staphylococ
130	70	13.9	135	2	Q33526	Q33526 rhizobium l	203	68.5	13.6	556	2	Q6GK21	Q6gk21 rhodospseud
131	70	13.9	324	2	Q98B15	Q98b15 pseudomonas	204	68.5	13.6	774	2	P95636	Q9u0c4 rhodospseud
132	70	13.9	366	2	Q88911	Q88911 brucella su	205	68.5	13.6	1267	2	Q9U0C4	Q9u0c5 leishmania
133	70	13.9	403	2	Q8FWQ3	Q8fwq3 erwinia car	206	68.5	13.6	1724	2	Q25425	Q25425 leishmania
134	70	13.9	407	1	SUFS_BRWCT	Q6625 erwinia car	207	68.5	13.6	1724	2	Q9SNM1	Q9snm1 brassica na
135	70	13.9	425	2	Q6CTJ9	Q6ctj9 yarrowia li	208	68.5	13.6	1724	2	Q6NUG5	Q6nug5 corynebacte
136	70	13.9	431	2	Q23028	Q23028 arabidopsis	209	68.5	13.6	184	2	Q6NUG5	Q6nug5 corynebacte
137	70	13.9	452	2	Q82N00	Q82n00 streptomyc	210	68.5	13.6	221	2	Q6ESZ8	Q6esz8 oryza sativ
138	70	13.9	466	2	Q82N00	Q82n00 streptomyc	211	68.5	13.6	221	2	Q621E9	Q621e9 burkholderi
139	70	13.9	477	2	Q9KHN5	Q9khn5 halobacteri	212	68.5	13.6	221	2	Q921R1	Q921r1 rhizobium m
140	70	13.9	491	2	Q89VK1	Q89vk1 bradyrhizob	213	68.5	13.6	308	2	Q6A568	Q6a568 bradyrhizob
141	70	13.9	632	2	Q67R15	Q67r15 mycobacteri	214	68.5	13.6	331	2	Q76B84	Q76b84 escherichia
142	70	13.9	689	2	Q98ED7	Q98ed7 rhizobium l	215	68.5	13.6	334	2	Q8XBV5	Q8xbv5 escherichia
143	70	13.9	88	2	Q8ED13	Q8ed13 leishmania	216	68.5	13.6	334	2	Q8XBV5	Q8xbv5 escherichia
144	69.5	13.8	102	2	Q8ED12	Q8ed12 leishmania	217	68.5	13.6	334	2	Q8XBV5	Q8xbv5 escherichia
145	69.5	13.8	244	2	P74128	P74128 synchocyst	218	68.5	13.6	338	2	Q8FK21	Q8fk21 escherichia
146	69.5	13.8	305	2	Q8BM41	Q8bm41 m mus muscu	219	68.5	13.6	338	2	Q83SB7	Q83sb7 shigella fl
147	69.5	13.8	362	2	Q88Q82	Q88q82 pseudomonas	220	68.5	13.6	360	2	Q91UX1	Q91ux1 plasmid pip
148	69.5	13.8	387	2	Q88L86	Q88l86 pseudomonas	221	68.5	13.6	377	2	Q9FRT6	Q9f8t6 streptomyc
149	69.5	13.8	396	2	Q9RVR2	Q9rvr2 deinococcus	222	68.5	13.6	407	2	Q67BA4	Q67ba4 streptomyc
150	69.5	13.8	409	2	Q8Y2W6	Q8y2w6 ralestonia s	223	68.5	13.6	456	2	Q91LCW0	Q91lcw0 streptomyc
151	69.5	13.8	423	2	Q79FW1	Q79fw1 mycobacteri	224	68.5	13.6	560	2	Q86320	Q86320 mycobacteri
152	69.5	13.8	423	2	Q7U114	Q7u114 mycobacteri	225	68.5	13.6	569	1	SILF_MOUSE	Silf mouse
153	69.5	13.8	426	2	Q7D938	Q7d938 streptomyc	226	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
154	69.5	13.8	427	2	Q9FB37	Q9fb37 streptomyc	227	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
155	69.5	13.8	435	2	Q82599	Q82599 salmoneila	228	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
156	69.5	13.8	435	2	Q82599	Q82599 salmoneila	229	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
157	69.5	13.8	435	2	Q82599	Q82599 salmoneila	230	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
158	69.5	13.8	435	2	Q82599	Q82599 salmoneila	231	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
159	69.5	13.8	435	2	Q82599	Q82599 salmoneila	232	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
160	69.5	13.8	435	2	Q82599	Q82599 salmoneila	233	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
161	69.5	13.8	435	2	Q82599	Q82599 salmoneila	234	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
162	69.5	13.8	435	2	Q82599	Q82599 salmoneila	235	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
163	69.5	13.8	435	2	Q82599	Q82599 salmoneila	236	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
164	69.5	13.8	435	2	Q82599	Q82599 salmoneila	237	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
165	69.5	13.8	435	2	Q82599	Q82599 salmoneila	238	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
166	69.5	13.8	435	2	Q82599	Q82599 salmoneila	239	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
167	69.5	13.8	435	2	Q82599	Q82599 salmoneila	240	68.5	13.6	589	2	Q7W6F4	Q7w6f4 streptomyc
168	69.5	13.7	141	2	Q7NHT5	Q7nhu5 ralestonia s	241	67.5	13.4	292	2	Q7SE33	Q7se33 ashya goss
169	69.5	13.7	170	2	Q8YIG0	Q8yig0 geobacteri	242	67.5	13.4	312	2	Q9MGO1	Q9mgo1 bordetella
170	69.5	13.7	285	2	Q6CR99	Q6cr99 kluyveromyc	243	67.5	13.4	342	2	Q889K2	Q889k2 pseudomonas
171	69.5	13.7	353	2	Q72GNS	Q72gns thermus the	244	67.5	13.4	343	2	Q7U1P6	Q7u1p6 bordetella
172	69.5	13.7	359	2	Q7UV47	Q7uv47 rhodopirell	245	67.5	13.4	349	2	Q9EY91	Q9ey91 clostridium
173	69.5	13.7	388	2	Q7WP66	Q7wp66 bordetella	246	67.5	13.4	367	2	Q8H658	Q8h658 oryza sativ
174	69.5	13.7	512	2	Q89E27	Q89e27 ralestonia s	247	67.5	13.4	387	2	Q7NPH3	Q7nph3 glaoebacter
175	69.5	13.7	541	2	Q8XQV8	Q8xqv8 ralestonia s	248	67.5	13.4	387	2	Q9RSK2	Q9rsk2 deinococcus
176	69.5	13.7	581	2	Q9YVD3	Q9yv33 diosopphila	249	67.5	13.4	408	2	Q72C12	Q72c12 desulfovibr
177	69.5	13.7	627	2	Q9RUD0	Q9rud0 deinococcus	250	67.5	13.4	408	2	Q72C12	Q72c12 desulfovibr

251	67.5	13.4	470	2	Q6AB56	Q6ab6 propionibac	324	66.5	13.2	446	2	Q6D7N9	Q6d7n9 erwinia car
252	67.5	13.4	491	2	Q93J96	Q93j96 streptomyce	325	66.5	13.2	448	2	Q8TKX9	Q8tkx9 methanocarc
253	67.5	13.4	520	2	Q9ABF7	Q9abf7 bacteroides	326	66.5	13.2	465	1	FXD1_HUMAN	O16676 homo sapien
254	67.5	13.4	571	2	Q75R19	Q75r19 ashyia goss	327	66.5	13.2	491	2	Q9PG00	O9fg00 arabidopsis
255	67.5	13.4	583	2	Q82B40	Q82b40 streptomyce	328	66.5	13.2	502	2	Q66OR8	O66or8 borrelia ga
256	67.5	13.4	588	2	Q7NH19	Q7nh19 gloeobacter	329	66.5	13.2	502	2	Q82K76	O82k76 streptomyce
257	67.5	13.4	603	2	Q8FP00	Q8fp00 corynebacte	330	66.5	13.2	545	2	Q7X7G3	O7xc73 oryza sativ
258	67.5	13.4	782	2	Q6YUW7	Q6ywu7 oryza sativ	331	66.5	13.2	587	2	Q65Z17	O65z17 chlamydomon
259	67.5	13.4	784	2	Q50199	Q50199 mycobacteri	332	66.5	13.2	667	2	Q93839	O93839 caenorhabdt
260	67.5	13.4	942	2	Q8CAH0	Q8cah0 mus musculu	333	66.5	13.2	752	2	Q8FWM1	O8fwm1 corynebacte
261	67.5	13.4	1179	2	Q87E19	Q87e19 xylella fas	334	66.5	13.2	838	2	Q6ACL7	O6acl7 leishonia x
262	67.5	13.4	1179	2	Q9PD26	Q9pd26 xylella fas	335	66.5	13.2	873	1	E74H_DROVI	O7m3n6 drosophi
263	67.5	13.4	1206	2	Q9CCX9	Q9ccx9 mycobacteri	336	66.5	13.2	1114	2	Q8A7H2	O8a7h2 bacteroides
264	67.5	13.4	1245	2	Q9RL54	Q9rl54 streptomyce	337	66.5	13.2	1510	2	Q80179	O80179 streptococc
265	67.5	13.4	1389	2	Q6MG27	Q6mg27 mycobacteri	338	66.5	13.2	1787	2	Q9MAX9	O9max9 chlamydomon
266	67.5	13.4	1452	2	Q6NG26	Q6ng26 mycobacteri	339	66.5	13.2	2006	2	Q8XCE7	O8xc7 raleronia s
267	67.5	13.4	1840	2	Q6PD15	Q6pd15 mus musculu	340	66.5	13.2	2737	2	Q8XPU7	O8xpu7 raleronia s
268	67.5	13.4	2035	1	F38A_HUMAN	Q92508 homo sapien	341	66.5	13.2	2948	2	Q86WG6	O86wg6 homo sapien
269	67.5	13.4	2698	2	Q9XIR5	Q9xir5 arabidopsis	342	66.5	13.2	3288	2	Q7T5D9	O7t5d9 cercopithec
270	67.5	13.4	14130	2	Q6MZ72	Q6mz72 mycobacteri	343	66.5	13.2	3326	2	Q7T591	O7t591 cercopithec
271	67.5	13.4	16990	2	Q6MZA4	Q6mza4 mycobacteri	344	66	13.1	103	2	Q9KJ37	O9k37 leprolmyngb
272	67	13.3	109	2	Q9VY10	Q9vy10 dirosophila	345	66	13.1	118	1	NLTD_BRAOL	O43304 braesica ol
273	67	13.3	147	2	Q9AF35	Q9af35 uncultured	346	66	13.1	121	1	MP70_MYCKA	O49614 mycobacteri
274	67	13.3	147	2	Q8PPE1	Q8pei1 xanthomonas	347	66	13.1	239	1	CLRC_IDEDB	P60000 ideonella d
275	67	13.3	218	2	Q9KSI6	Q9ksi6 vibrio chol	348	66	13.1	266	2	Q83Y03	O83y03 uncultured
276	67	13.3	228	2	Q9UYX1	Q9uyx1 pyrococcus	349	66	13.1	293	2	Q7NLV1	O7nlv1 gloeobacter
277	67	13.3	233	2	Q89V28	Q89v28 bradyrhizob	350	66	13.1	306	2	Q73SE1	O73se1 mycobacteri
278	67	13.3	297	2	Q6N709	Q6n709 rhodopseudo	351	66	13.1	310	2	Q668Z9	O668z9 yerastinia ps
279	67	13.3	346	2	Q8KR73	Q8kr73 photorhabdu	352	66	13.1	310	2	Q82DK6	O82dk6 yerastinia pe
280	67	13.3	351	1	GCP_MYCLE	P37969 mycobacteri	353	66	13.1	314	2	Q74R26	O74r26 yerastinia pe
281	67	13.3	369	2	Q92RF4	Q92rf4 rhizobium m	354	66	13.1	329	2	Q7NJ15	O7nj15 gloeobacter
282	67	13.3	369	2	Q651P3	Q651p3 oryza sativ	355	66	13.1	330	2	Q9KP40	O9kp40 vibrio chol
283	67	13.3	419	2	Q8YBM4	Q8ybm4 bruceella me	356	66	13.1	331	2	Q8RGF4	O8rgf4 fusobacteri
284	67	13.3	444	1	FUNC_PBSM	Q85V0 pseudomonas	357	66	13.1	335	2	Q8FTH0	O8fth0 corynebacte
285	67	13.3	472	2	Q8PHB8	Q8phb8 xanthomonas	358	66	13.1	337	2	Q9K633	O9k633 bacillus ha
286	67	13.3	487	2	Q9EY49	Q9ey49 pseudomonas	359	66	13.1	373	2	Q63NQ9	O63nq9 streptomyce
287	67	13.3	636	2	Q9EY10	Q9ey10 aeropyrum p	360	66	13.1	396	2	Q82QW0	O82qw0 streptomyce
288	67	13.3	724	2	Q9ABE7	Q9abe7 caulobacter	361	66	13.1	400	2	Q8U488	O8u488 pyrococcus
289	67	13.3	746	2	Q7OR12	Q7orf12 anophelae g	362	66	13.1	409	2	Q9EG571	O9eg571 rhizobium 1
290	67	13.3	760	2	Q8FRU0	Q8fru0 anabena sp	363	66	13.1	442	2	Q6D0L4	O6d0l4 erwinia car
291	67	13.3	772	2	Q7Q6Z6	Q7q6z6 anophelae g	364	66	13.1	448	1	PLSX_PROMM	O7v417 prochloroco
292	67	13.3	840	2	Q9A7G5	Q9a7g5 caulobacter	365	66	13.1	456	2	Q7MTG2	O7mtg2 streptomyce
293	67	13.3	848	2	Q7W1M4	Q7w1m4 bordetella	366	66	13.1	521	2	Q7SCZ8	O7scz8 neurospora
294	67	13.3	854	1	CLPB_PSRPK	Q88G71 pseudomonas	367	66	13.1	527	1	PTB_MOUSE	P17225 mus musculu
295	67	13.3	856	2	Q65RMO	Q65rmo manhelinia	368	66	13.1	529	2	Q6AAL8	O6aal8 propionibac
296	67	13.3	1041	2	Q8CK05	Q8ck05 streptomyce	369	66	13.1	538	2	Q61SK7	O61sk7 oryza sativ
297	67	13.3	1249	2	Q9BK63	Q9bk63 homo sapien	370	66	13.1	540	1	LEU1_PROMM	O7tuv5 prochloroco
298	67	13.3	1747	2	Q9NBQ1	Q9nbq1 trypanosoma	371	66	13.1	581	2	Q6V7G5	O6vtg5 vibrio para
299	67	13.3	2541	2	Q8AM10	Q8am10 gallus gall	372	66	13.1	581	2	Q986R2	O986r2 rhizobium 1
300	67	13.3	13536	2	Q83VS0	Q83vs0 pseudomonas	373	66	13.1	585	1	NUP1_RAT	P70581 ratus norv
301	66.5	13.2	106	2	Q9Z7V3	Q9z7v3 chlamydia p	374	66	13.1	603	2	Q7Q8L4	O7q8l4 anophelae g
302	66.5	13.2	112	2	Q6IED3	Q6ied3 bos taurus	375	66	13.1	613	2	Q82BL8	O82bl8 streptomyce
303	66.5	13.2	144	2	Q70KA2	Q70ka2 gordonia we	376	66	13.1	638	2	Q41768	O41768 zea mays (m
304	66.5	13.2	146	2	Q9YD19	Q9ydl9 aeropyrum p	377	66	13.1	665	2	Q9F5F6	O9f5f6 glycobacteri
305	66.5	13.2	172	2	Q7U521	Q7u521 synechococc	378	66	13.1	686	2	Q82V51	O82v51 nltrosomona
306	66.5	13.2	178	2	Q946W0	Q946w0 zea mays (m	379	66	13.1	697	2	Q745I8	O745i8 mycobacteri
307	66.5	13.2	180	2	Q41888	Q41888 zea mays (m	380	66	13.1	710	2	Q7WEC6	O7wec6 bordetella
308	66.5	13.2	195	2	Q7XRX4	Q7xrx4 oryza sativ	381	66	13.1	817	2	Q964V6	O964v6 dictyostell
309	66.5	13.2	243	2	Q88062	Q88062 streptomyce	382	66	13.1	823	2	Q980B9	O980b9 mycobacteri
310	66.5	13.2	245	2	Q89GZ5	Q89gz5 bradyrhizob	383	66	13.1	857	1	CLPB_STRAL	Q9z664 streptomyce
311	66.5	13.2	291	2	Q84FP5	Q84fp5 apitullina p	384	66	13.1	879	1	CLPB_BRAVA	O89u12 bradyrhizob
312	66.5	13.2	304	2	Q8KX52	Q8kx52 uncultured	385	66	13.1	934	2	Q6C2T4	O6c2t4 yarrowia 11
313	66.5	13.2	307	2	Q74HB8	Q74hb8 lactobacill	386	66	13.1	999	2	Q7P102	O7p102 chremobacte
314	66.5	13.2	322	2	Q88918	Q88918 pseudomonas	387	66	13.1	1043	2	Q851S7	O851s7 photorhabdu
315	66.5	13.2	326	2	Q7W4P0	Q7w4p0 bordetella	388	66	13.1	1366	2	Q8K7N9	O8k7n9 streptococc
316	66.5	13.2	336	2	Q7W6P6	Q7w6p6 bordetella	389	66	13.1	1372	2	Q878N3	O878n3 streptococc
317	66.5	13.2	333	2	Q8PI08	Q8pi08 xanthomonas	390	66	13.1	1400	2	Q7DA75	O7d7a5 mycobacteri
318	66.5	13.2	341	1	TA2R_RAT	P34978 ratus norv	391	66	13.1	1400	2	P96419	P96419 mycobacteri
319	66.5	13.2	368	2	Q8GFF1	Q8gff1 streptomyce	392	66	13.1	1400	2	Q7U2H8	O7u2h8 mycobacteri
320	66.5	13.2	377	2	Q6E208	Q6e208 edwardsiell	393	66	13.1	1467	2	Q9K175	O9k175 delnoccocus
321	66.5	13.2	377	2	Q82N80	Q82n80 streptomyce	394	66	13.1	1664	2	Q7KR59	O7kr59 drosophi
322	66.5	13.2	389	2	Q986N1	Q986n1 rhizobium 1	395	66	13.1	1674	2	Q9V9V5	O9v9v5 drosophi
323	66.5	13.2	437	2	Q9AMU5	Q9amu5 bradyrhizob	396	65.5	13.0	122	2	Q81249	O81249 salmonella

397	65.5	13.0	183	2	08PA47	08p4a7	xanthomonas	470	65	12.9	312	2	09H227	09h227	pseudomonas
398	65.5	13.0	212	2	06SV37	06sv37	manheimia	471	65	12.9	331	2	07WK72	07wk72	bordetella
399	65.5	13.0	226	2	093MT8	093mt8	uncultured	472	65	12.9	344	1	TRD2	RALSO	08x60 ralstonia s
400	65.5	13.0	257	1	EUTC_RHOER	09t82	rhodococcus	473	65	12.9	350	2	06W1M0	06w1m0	rhizobium s
401	65.5	13.0	254	2	09A6M8	09a6m8	caulobacter	474	65	12.9	358	1	CHB2_PSESM	08b8v8 pseudomonas	
402	65.5	13.0	266	2	093UR8	09a28	desulfocvibr	475	65	12.9	367	2	08YAV1	08yav1	brucella me
403	65.5	13.0	289	2	056024	056024	salmonella	476	65	12.9	377	2	08FXG2	08fxg2	brucella gu
404	65.5	13.0	321	2	0839P4	0839p4	enterococcus	477	65	12.9	388	2	07ZE12	07ze12	desulfocvibr
405	65.5	13.0	326	2	08R532	08r532	mus musculus	478	65	12.9	370	2	07W449	07w449	bordetella
406	65.5	13.0	335	2	08R532	08r532	bradyrhizob	479	65	12.9	370	2	07W449	07w449	bordetella
407	65.5	13.0	336	1	COBR_RHIL0	08r532	mus musculus	480	65	12.9	370	2	07W449	07w449	bordetella
408	65.5	13.0	343	2	09LP34	09lp34	arabidopsis	481	65	12.9	385	2	07MD43	07md43	bordetella
409	65.5	13.0	344	2	08GVF7	08gvf7	oryza sativ	482	65	12.9	385	2	07W449	07w449	bordetella
410	65.5	13.0	361	2	092S90	092s90	caulobacter	483	65	12.9	385	2	07W449	07w449	bordetella
411	65.5	13.0	361	2	092S90	092s90	caulobacter	484	65	12.9	391	2	07W449	07w449	bordetella
412	65.5	13.0	383	2	06ZPS4	06zps4	burkholderi	485	65	12.9	393	2	08XK45	08xk45	mycobacteri
413	65.5	13.0	383	2	06ZPS4	06zps4	burkholderi	486	65	12.9	393	2	08XK45	08xk45	mycobacteri
414	65.5	13.0	393	2	098L25	098l25	rhizobium 1	487	65	12.9	399	1	YMG6_SYNEL	07y322	mycobacteri
415	65.5	13.0	402	2	07Z702	07z702	homo sapien	488	65	12.9	410	2	073Y22	073y22	mycobacteri
416	65.5	13.0	436	2	099PE1	099pe1	mus musculus	489	65	12.9	416	2	073Y22	073y22	mycobacteri
417	65.5	13.0	455	2	094DES	094des	oryza sativ	490	65	12.9	426	2	09RLJ0	09rlj0	pseudomonas
418	65.5	13.0	457	2	094DES	094des	oryza sativ	491	65	12.9	427	2	08N835	08n835	rhodopseudo
419	65.5	13.0	470	2	073VU4	073vu4	mycobacteri	492	65	12.9	429	2	08RAJ9	08raj9	thiomaner
420	65.5	13.0	491	2	Y084_MYCTU	05z209	mycobacteri	493	65	12.9	442	2	09LS41	09ls41	arabidopsis
421	65.5	13.0	491	2	07YVH3	07yvh3	mycobacteri	494	65	12.9	462	1	A2NC_HUMAN	07z2c38	desulfocvibr
422	65.5	13.0	535	2	07WMT4	07wmt4	pseudomonas	495	65	12.9	462	2	072C38	072c38	desulfocvibr
423	65.5	13.0	539	2	087WC7	087wc7	pseudomonas	496	65	12.9	482	2	06YEP4	06yep4	cyprinodon
424	65.5	13.0	556	2	08CK61	08ck61	erwinia car	497	65	12.9	525	2	08Y4G0	08y4g0	rhizobium 1
425	65.5	13.0	564	2	08CK61	08ck61	streptomyce	498	65	12.9	544	2	06T442	06t442	leishmania
426	65.5	13.0	593	2	079BT1	079bt1	salmonella	499	65	12.9	603	2	06VTO1	06vto1	vibrio para
427	65.5	13.0	593	2	056019	056019	salmonella	500	65	12.9	617	2	06UYK6	06uyk6	burkholderi
428	65.5	13.0	593	2	056134	056134	salmonella	501	65	12.9	617	2	06UYK6	06uyk6	burkholderi
429	65.5	13.0	616	2	07VSP8	07vsp8	bordetella	502	65	12.9	631	2	08HAU7	08ha17	burkholderi
430	65.5	13.0	616	2	07WDM1	07wdm1	bordetella	503	65	12.9	631	2	08HAU7	08ha17	burkholderi
431	65.5	13.0	618	2	093JH7	093jh7	streptomyce	504	65	12.9	680	2	06E027	06e027	bradyrhizob
432	65.5	13.0	631	2	092K91	092k91	rhizobium m	505	65	12.9	680	2	06E027	06e027	bradyrhizob
433	65.5	13.0	635	2	06LQG9	06lqg9	photobacter	506	65	12.9	693	1	RECG_ECOLI	09kx14	mycoplasma
434	65.5	13.0	658	2	06R8C5	06r8c5	sedalia glo	507	65	12.9	693	1	RECG_ECOLI	09kx14	mycoplasma
435	65.5	13.0	665	2	07P987	07p987	ricketelia	508	65	12.9	704	2	0821A1	0821a1	shigella fl
436	65.5	13.0	665	2	092PH3	092ph3	ricketelia	509	65	12.9	704	2	08FC81	08fc81	eschcherichia
437	65.5	13.0	682	2	09NKA3	09nka3	homo sapien	510	65	12.9	706	2	07X4W5	07x4w5	rhodospirill
438	65.5	13.0	713	2	084NK5	084nk5	oryza sativ	511	65	12.9	771	2	06Z9Y1	06z9y1	burkholderi
439	65.5	13.0	803	2	093H55	093h55	bradyrhizob	512	65	12.9	771	2	06Z9Y1	06z9y1	burkholderi
440	65.5	13.0	808	2	07VW44	07vw44	bordetella	513	65	12.9	786	2	08S053	08s053	burkholderi
441	65.5	13.0	808	2	07VW44	07vw44	bordetella	514	65	12.9	845	2	09UPP0	09upp0	oryza sativ
442	65.5	13.0	846	1	CLPB_MYCLE	06vq29	pseudomonas	515	65	12.9	857	2	06A678	06a678	homo sapien
443	65.5	13.0	848	1	CLPB_MYCLE	09pc26	mycobacteri	516	65	12.9	910	2	060324	060324	propionibac
444	65.5	13.0	861	1	CLPB_XYUFA	09pc26	mycobacteri	517	65	12.9	949	2	08W709	08w709	homo sapien
445	65.5	13.0	861	1	CLPB_XYUFA	09pc26	mycobacteri	518	65	12.9	1024	2	077CD5	077cd5	homo sapien
446	65.5	13.0	863	2	06JND3	06jnd3	rattus norv	519	65	12.9	1024	2	077CD5	077cd5	homo sapien
447	65.5	13.0	879	1	CLPB_RHOPA	06jnd3	rattus norv	520	65	12.9	1024	2	077CD5	077cd5	homo sapien
448	65.5	13.0	898	1	0823I9	0823i9	chlamydomon	521	65	12.9	1374	2	06Y3H7	06y3h7	chlamydomon
449	65.5	13.0	1246	2	09Y632	09y632	homo sapien	522	65	12.9	1892	2	084HM3	084hm3	nocardia ae
450	65.5	13.0	1685	2	09UM8	09um8	homo sapien	523	65	12.9	2092	2	07SA55	07sa55	neutrospora
451	65.5	13.0	2303	2	09S596	09s596	homo sapien	524	65	12.9	2632	2	070511	070511	rattus norv
452	65.5	13.0	2691	2	08XPU1	08xpu1	ralstonia s	525	65	12.9	2849	2	08W6K4	08w6k4	simonrhizobi
453	65.5	13.0	4928	2	09ALM3	09alm3	saccharopol	526	65	12.9	4106	2	08W6K4	08w6k4	simonrhizobi
454	65.5	12.9	88	2	067L12	067l12	syndiotact	527	65	12.9	4377	1	ANK3_HUMAN	0846x2	homo sapien
455	65.5	12.9	126	2	063N39	063n39	syndiotact	528	65	12.9	5216	2	09VXZ5	09vxz5	homo sapien
456	65.5	12.9	147	2	07X9S9	07x9s9	burkholderi	529	65	12.9	5233	2	09NB71	09nb71	homo sapien
457	65.5	12.9	148	2	09AR34	09ar34	arabidopsis	530	65	12.9	89	2	041378	041378	homo sapien
458	65.5	12.9	219	2	08P8U4	08p8u4	uncultured	531	65	12.9	184	1	CYCK_BRAVA	041378	benecio odo
459	65.5	12.9	219	2	08P8U4	08p8u4	uncultured	532	65	12.9	189	2	08A8L9	08a8l9	bradyrhizob
460	65.5	12.9	236	2	08PKU5	08pku5	xanthomonas	533	65	12.9	214	2	08A8L9	08a8l9	bacteroides
461	65.5	12.9	236	2	08PKU5	08pku5	xanthomonas	534	65	12.9	245	2	08A8L9	08a8l9	streptomyce
462	65.5	12.9	261	2	0745R3	0745r3	mycobacteri	535	65	12.9	257	2	07W1Y9	07w1y9	bordeletia
463	65.5	12.9	266	2	08N2X7	08n2x7	desulfococ	536	65	12.9	294	2	08XZK7	08xz7	oryza sativ
464	65.5	12.9	267	2	08N2X7	08n2x7	desulfococ	537	65	12.9	320	1	Y678_METUA	08x2a7	pyrobaculum
465	65.5	12.9	267	2	09A346	09a346	corynebacte	538	65	12.9	321	2	08CNG5	08cng5	mechanococ
466	65.5	12.9	275	2	0918X0	0918x0	aeropyrum p	539	65	12.9	328	2	08CNG5	08cng5	staphylococ
467	65.5	12.9	276	2	065599	065599	arabidopsis	540	65	12.9	331	2	08FYEO	08fyeo	gallus galli
468	65.5	12.9	281	2	09XCV3	09xcv3	flavobacter	541	65	12.9	337	2	08FYEO	08fyeo	brucella su
469	65.5	12.9	300	2	072KL1	072kl1	thermus the	542	65	12.9	346	2	09A903	09a903	caulobacter



543	64.5	12.8	363	2	Q89H39	Q89h39 bradyrhizob	616	64	12.7	327	1	TH14 ASPOR	Q9nuz9 aspergillus
544	64.5	12.8	366	2	Q8FM30	Q8fm30 corynebacte	617	64	12.7	339	2	Q8R3J0	Q8r3j0 mus musculu
545	64.5	12.8	375	2	Q7WwM0	Q7wwo bordetella	618	64	12.7	345	2	Q8SPB8	Q8spb8 glycine max
546	64.5	12.8	375	2	Q7WKL7	Q7wkl7 bordetella	619	64	12.7	392	2	Q44305	Q44305 acinetobact
547	64.5	12.8	375	2	Q9KZL8	Q9kzl8 streptomyce	620	64	12.7	400	2	Q82H99	Q82h99 streptomyce
548	64.5	12.8	378	2	Q749L4	Q749l4 geobacter s	621	64	12.7	409	2	Q8P9R8	Q8p9r8 xanthomonas
549	64.5	12.8	378	2	Q6NZ21	Q6nzz1 brachydanio	622	64	12.7	422	1	Q741X1	Q741x1 mycobacteri
550	64.5	12.8	379	2	Q72DP0	Q72dp0 desulfovibr	623	64	12.7	426	2	Y200 ANASP	Q8z08 anabena sp
551	64.5	12.8	384	2	Q6K9Y0	Q6ky90 oryza sativ	624	64	12.7	426	2	Q7U9D6	Q7u9d6 synechococ
552	64.5	12.8	385	2	Q9HKM2	Q9hkm2 pseudomonas	625	64	12.7	437	2	Q7TXF8	Q7txf8 mycobacteri
553	64.5	12.8	390	2	Q6N1X1	Q6n1x1 rhodopseudo	626	64	12.7	437	2	Q725H4	Q725h4 desulfovibr
554	64.5	12.8	411	2	Q9FAK7	Q9fak7 rhizobium 1	627	64	12.7	464	2	Q9JWX7	Q9jwx7 niseiselia m
555	64.5	12.8	411	2	Q9K646	Q9k646 bacillus ha	628	64	12.7	468	2	Q9FCB6	Q9fc6 streptomyce
556	64.5	12.8	412	2	Q9K3M1	Q9k3m1 streptomyce	629	64	12.7	469	2	Q9X803	Q9x803 streptomyce
557	64.5	12.8	431	2	Q8AR86	Q8ar86 oryza sativ	630	64	12.7	473	2	Q827L5	Q827l5 streptomyce
558	64.5	12.8	433	2	Q8ZRP5	Q8zrp5 salmonella	631	64	12.7	487	1	DNAA_AGR75	Q8ul11 agrobacteri
559	64.5	12.8	435	2	Q92LG6	Q92lg6 rhizobium m	632	64	12.7	490	2	Q7XH50	Q7xh50 oryza sativ
560	64.5	12.8	445	2	Q83EW4	Q83ew4 coxiella bu	633	64	12.7	491	2	Q9PJG2	Q9pjg2 chlamydia m
561	64.5	12.8	461	2	Q63KJ1	Q63kj1 burholderi	634	64	12.7	501	2	Q9IBD0	Q9ibd0 brachydanio
562	64.5	12.8	463	2	Q88CP9	Q88cp9 pseudomonas	635	64	12.7	507	2	Q7PSJ7	Q7psj7 anopheles g
563	64.5	12.8	480	2	Q86704	Q86704 streptomyce	636	64	12.7	509	2	Q872L9	Q872l9 neotspora
564	64.5	12.8	482	2	Q9FAC7	Q9fac7 rhodococcus	637	64	12.7	516	2	Q8XSS2	Q8xss2 ralestonia s
565	64.5	12.8	486	2	Q6N2W0	Q6n2w0 rhodopseudo	638	64	12.7	534	2	Q72WE4	Q72we4 brachydanio
566	64.5	12.8	512	2	Q8FWZ4	Q8fwz4 bruceella su	639	64	12.7	537	2	Q8FQM7	Q8fqm7 corynebacte
567	64.5	12.8	529	2	Q9KMV5	Q9kmv5 vibrio chol	640	64	12.7	569	2	Q9RUJ9	Q9ruj9 deinococcus
568	64.5	12.8	559	2	Q8FTL2	Q8ftl2 corynebacte	641	64	12.7	582	2	Q72DM1	Q72dm1 desulfovibr
569	64.5	12.8	567	2	Q98FT7	Q98ft7 rhizobium 1	642	64	12.7	600	2	Q8UJ21	Q8uj21 oryzae lat
570	64.5	12.8	619	2	Q67RS7	Q67rs7 symbiobacte	643	64	12.7	604	2	Q7WED8	Q7wed8 bordetella
571	64.5	12.8	629	2	Q751E0	Q75le0 ashyia goss	644	64	12.7	607	2	Q7V632	Q7v632 bordetella
572	64.5	12.8	668	2	Q6APN3	Q6apn3 desulfocale	645	64	12.7	618	2	Q6BP23	Q6bp23 oryza sativ
573	64.5	12.8	669	2	Q6A8G5	Q6a8g5 propionibac	646	64	12.7	637	2	Q9AAK8	Q9aak8 caulobacter
574	64.5	12.8	688	2	Q6MWC1	Q6mwc1 bdellovibr	647	64	12.7	655	1	YAGF_ECOLI	P7596 escherichia
575	64.5	12.8	750	1	ELS_CHICK	P07916 gallus gall	648	64	12.7	693	1	REC8_ECO57	Q8xd6 escherichia
576	64.5	12.8	752	2	Q9K4U6	Q9k4u6 streptomyce	649	64	12.7	698	2	Q9A537	Q9a537 caulobacter
577	64.5	12.8	861	1	CLPB_XYLEFT	Q87ax8 xylella fas	650	64	12.7	698	2	Q67KM1	Q67km1 symbiobacte
578	64.5	12.8	905	1	NUOG_PSEAB	Q910j6 pseudomonas	651	64	12.7	700	2	Q6YXX1	Q6yxx1 oryza sativ
579	64.5	12.8	952	2	Q8X5G8	Q8x5g8 escherichia	652	64	12.7	702	2	Q89UV7	Q89uv7 bradyrhizob
580	64.5	12.8	1022	2	Q9JMP2	Q9jmp2 actinobacil	653	64	12.7	724	2	Q6FUJ0	Q6fuj0 candida gla
581	64.5	12.8	1023	1	RT11_ACRPL	P55128 actinobacil	654	64	12.7	748	2	Q8CDI5	Q8cdi5 mus musculu
582	64.5	12.8	1023	1	RT12_ACPPL	P55129 actinobacil	655	64	12.7	790	2	Q9KM22	Q9km22 xanthomonas
583	64.5	12.8	1026	2	Q7ABP0	Q7aep0 escherichia	656	64	12.7	806	2	Q33967	Q33967 xanthomonas
584	64.5	12.8	1026	2	Q8XEJ2	Q8xej2 escherichia	657	64	12.7	813	2	Q7QKS2	Q7qks2 anopheles g
585	64.5	12.8	1030	2	Q7RZE3	Q7rze3 neurospora	658	64	12.7	926	2	Q8K287	Q8k287 mus musculu
586	64.5	12.8	1080	2	Q8XAH7	Q8xah7 escherichia	659	64	12.7	962	2	Q6KAU6	Q6kau6 mus musculu
587	64.5	12.8	1106	2	Q6XDB6	Q6xdb6 rattus norv	660	64	12.7	984	2	Q7QET1	Q7qet1 anopheles g
588	64.5	12.8	1159	1	RPOC_PORCN	Q334j1 porphyromon	661	64	12.7	1043	2	Q7MZV7	Q7mzv7 photorhabdu
589	64.5	12.8	1161	2	Q9NEH0	Q9neh0 leishmania	662	64	12.7	1171	2	Q89DP3	Q89dp3 bradyrhizob
590	64.5	12.8	1240	2	Q9F3X7	P15370 serratia ma	663	64	12.7	1218	2	Q9F824	Q9fb24 streptomyce
591	64.5	12.8	1608	1	HLVA_SERMA	P15370 serratia ma	664	64	12.7	1303	2	Q9U172	Q9u172 leishmania
592	64.5	12.8	1608	2	Q8MOW4	Q8mqw4 drosophila	665	64	12.7	1480	2	Q8VNR0	Q8vnr0 photorhabdu
593	64.5	12.8	1767	2	Q80663	Q80663 aradidopsis	666	64	12.7	1480	2	Q7N9K8	Q7n9k8 photorhabdu
594	64.5	12.8	1910	2	Q7TZA7	Q7tza7 mycobacteri	667	64	12.7	1646	2	Q7WTE3	Q7wte3 streptomyce
595	64.5	12.8	2274	2	Q9ZIK7	Q9zlk7 mus musculu	668	64	12.7	2479	2	Q9A988	Q9a988 caulobacter
596	64.5	12.8	2404	2	Q9OBG4	Q9obg4 wheat yello	669	64	12.7	6842	2	Q84G24	Q84g24 streptomyce
597	64.5	12.8	2531	2	Q9VW47	Q9vw47 drosophila	670	64	12.6	82	1	C551_PSEME	P00102 pseudomonas
598	64.5	12.8	2541	1	TLN1_HUMAN	Q8y430 homo sapien	671	63.5	12.6	130	1	F14A_HUMAN	Q8h248 homo sapien
599	64.5	12.8	2541	2	Q86YD0	Q86ydo homo sapien	672	63.5	12.6	130	1	RL7_MYCLE	P30763 mycobacteri
600	64.5	12.8	2550	2	Q9UXP3	Q9upx3 homo sapien	673	63.5	12.6	147	2	Q7P0K6	Q7p0k6 chromobacte
601	64.5	12.8	7525	2	Q9KIE0	Q9kie0 streptomyce	674	63.5	12.6	172	2	Q6SK85	Q6sk85 arthrobacte
602	64	12.7	185	2	Q9RYJ5	Q9ryj5 deinococcus	675	63.5	12.6	173	2	Q9B206	Q9b206 calman croc
603	64	12.7	210	2	Q39969	Q39969 heterosigma	676	63.5	12.6	175	2	Q9YDF4	Q9ydf4 aeropyrum p
604	64	12.7	218	2	Q73W12	Q73w12 mycobacteri	677	63.5	12.6	198	2	Q7NNM7	Q7nnm7 gloeobacter
605	64	12.7	226	2	Q88AV1	Q88av1 pseudomonas	678	63.5	12.6	218	2	Q61BD4	Q61bd4 bos laurus
606	64	12.7	246	1	HIS4_METMA	Q8pw2 methanosarc	679	63.5	12.6	218	2	Q6ZFN1	Q6zfn1 oryza sativ
607	64	12.7	247	2	Q848N3	Q848n3 uncultured	680	63.5	12.6	225	2	Q888S7	Q888s7 pseudomonas
608	64	12.7	249	2	Q84ZM7	Q84zm7 oryza sativ	681	63.5	12.6	230	1	FLGH_XANCP	Q8p99 xanthomonas
609	64	12.7	261	2	Q54990	Q54990 streptomyce	682	63.5	12.6	248	2	Q7RZW8	Q7rzw8 neurospora
610	64	12.7	284	2	Q67JH8	Q67jh8 symbiobacte	683	63.5	12.6	252	2	Q7XTN9	Q7xtn9 oryza sativ
611	64	12.7	305	2	Q89HJ8	Q89hj8 bradyrhizob	684	63.5	12.6	263	1	ZUP1_CORGL	Q8nq0 corynebacto
612	64	12.7	308	2	Q8XUD0	Q8xud0 ralestonia s	685	63.5	12.6	263	2	Q05919	Q05919 mycobacteri
613	64	12.7	313	2	Q7YZX5	Q7yzx5 trypanosoma	686	63.5	12.6	263	2	Q7U104	Q7u104 mycobacteri
614	64	12.7	321	2	Q7W1L9	Q7w1l9 bordetella	687	63.5	12.6	264	2	Q6ADW8	Q6adw8 leifsonia x
615	64	12.7	321	2	Q7WPL0	Q7wpl0 bordetella	688	63.5	12.6	269	2	Q7W6M3	Q7w6m3 wolfinella s

689	63.5	12.6	284	2	067S10	067b10 symbiobacte	762	63.5	12.6	779	2	089XJ7	089xf7 bradyrhizob
690	63.5	12.6	284	2	08YD75	08ydt5 brucella me	763	63.5	12.6	865	1	CLPB_PROMM	07vbl1 prochloroco
691	63.5	12.6	284	2	072JY1	072jy1 thermus the	764	63.5	12.6	873	2	089P22	089p22 bradyrhizob
692	63.5	12.6	297	2	067P80	067p80 symbiobacte	765	63.5	12.6	881	2	028761	028761 archaeglob
693	63.5	12.6	303	2	07VY18	07vy18 bordetella	766	63.5	12.6	895	2	08H513	08h513 oxyza sativ
694	63.5	12.6	308	2	07WIM5	07wim5 bordetella	767	63.5	12.6	917	2	06XDM1	06xdm1 pseudomonas
695	63.5	12.6	317	2	08FV57	08fv57 xanthobacte	768	63.5	12.6	943	2	08RVR3	08rvr3 pseudomonas
696	63.5	12.6	318	2	07VX39	07vx39 brucella su	769	63.5	12.6	946	2	09V193	09v193 dirosophila
697	63.5	12.6	327	2	06N129	06n129 prochloroco	770	63.5	12.6	961	2	08SBN1	08sbn1 dirosophila
698	63.5	12.6	331	2	06AFK0	06afk0 leifsonia x	771	63.5	12.6	992	2	08PKN2	08pkn2 bacterioph
699	63.5	12.6	332	2	093908	093908 streptomyce	772	63.5	12.6	1026	2	08PK64	08pk64 xanthomonas
700	63.5	12.6	333	2	070W66	070w66 yersinia en	773	63.5	12.6	1046	2	08XK29	08xk29 xanthomonas
701	63.5	12.6	336	2	09SMA7	09sma7 oxyza sativ	774	63.5	12.6	1048	1	P100_ROMVA	08p64 xanthomonas
702	63.5	12.6	340	2	092S23	092s23 rhizobium m	775	63.5	12.6	1049	2	07M6Q1	08b64 xanthomonas
703	63.5	12.6	345	1	TRPD_AERPE	09ylc2 aeropyrum p	776	63.5	12.6	1060	2	06RX16	08d299 escherichia
704	63.5	12.6	353	2	08ZU64	08zu64 pyrobaculum	777	63.5	12.6	1080	2	09P789	09d318 human cytom
705	63.5	12.6	353	2	09H08	09hmg8 halobacteri	778	63.5	12.6	1157	2	06H9T7	06h9t7 human cytom
706	63.5	12.6	363	2	06N133	06n133 rhodospseudo	779	63.5	12.6	1209	2	07S2F4	06b9r7 phage phi 4
707	63.5	12.6	367	2	06M633	06m633 corynebacte	780	63.5	12.6	1211	2	0636A8	07azt4 brachydanio
708	63.5	12.6	367	2	06N133	06n133 corynebacte	781	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
709	63.5	12.6	367	2	06N133	06n133 corynebacte	782	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
710	63.5	12.6	367	2	06N133	06n133 corynebacte	783	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
711	63.5	12.6	367	2	06N133	06n133 corynebacte	784	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
712	63.5	12.6	394	1	YGAV_ECO57	07nva0 chromobacte	785	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
713	63.5	12.6	394	1	YGAV_ECOLI	08x4v6 escherichia	786	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
714	63.5	12.6	394	1	YGAV_ECOLI	08x4v6 escherichia	787	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
715	63.5	12.6	394	1	YGAV_ECOLI	08x4v6 escherichia	788	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
716	63.5	12.6	394	1	YGAV_ECOLI	08x4v6 escherichia	789	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
717	63.5	12.6	398	1	Y435_PROMA	08efq2 escherichia	790	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
718	63.5	12.6	402	2	067349	067349 prochloroco	791	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
719	63.5	12.6	402	2	08FCF7	08fcf7 aquifex aeo	792	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
720	63.5	12.6	405	2	0886G2	0886g2 pseudomonas	793	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
721	63.5	12.6	411	2	08A4V3	08a4v3 mycobacteri	794	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
722	63.5	12.6	412	2	08A4V3	08a4v3 caulobacter	795	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
723	63.5	12.6	413	2	08A4V3	08a4v3 streptomyce	796	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
724	63.5	12.6	432	1	YF10_MYCTU	071789 mycobacteri	797	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
725	63.5	12.6	434	2	07MLB5	07mlb5 vibrio vuln	798	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
726	63.5	12.6	434	2	08D957	08d957 vibrio vuln	799	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
727	63.5	12.6	458	2	06OD67	06od67 liparitis atl	800	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
728	63.5	12.6	458	2	088P66	088p66 pseudomonas	801	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
729	63.5	12.6	460	2	088P66	088p66 pseudomonas	802	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
730	63.5	12.6	460	2	088P66	088p66 pseudomonas	803	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
731	63.5	12.6	460	2	088P66	088p66 pseudomonas	804	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
732	63.5	12.6	461	2	088P66	088p66 pseudomonas	805	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
733	63.5	12.6	461	2	088P66	088p66 pseudomonas	806	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
734	63.5	12.6	461	2	088P66	088p66 pseudomonas	807	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
735	63.5	12.6	461	2	088P66	088p66 pseudomonas	808	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
736	63.5	12.6	461	2	088P66	088p66 pseudomonas	809	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
737	63.5	12.6	461	2	088P66	088p66 pseudomonas	810	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
738	63.5	12.6	461	2	088P66	088p66 pseudomonas	811	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
739	63.5	12.6	461	2	088P66	088p66 pseudomonas	812	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
740	63.5	12.6	461	2	088P66	088p66 pseudomonas	813	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
741	63.5	12.6	461	2	088P66	088p66 pseudomonas	814	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
742	63.5	12.6	461	2	088P66	088p66 pseudomonas	815	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
743	63.5	12.6	461	2	088P66	088p66 pseudomonas	816	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
744	63.5	12.6	461	2	088P66	088p66 pseudomonas	817	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
745	63.5	12.6	461	2	088P66	088p66 pseudomonas	818	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
746	63.5	12.6	461	2	088P66	088p66 pseudomonas	819	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
747	63.5	12.6	461	2	088P66	088p66 pseudomonas	820	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
748	63.5	12.6	461	2	088P66	088p66 pseudomonas	821	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
749	63.5	12.6	461	2	088P66	088p66 pseudomonas	822	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
750	63.5	12.6	461	2	088P66	088p66 pseudomonas	823	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
751	63.5	12.6	461	2	088P66	088p66 pseudomonas	824	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
752	63.5	12.6	461	2	088P66	088p66 pseudomonas	825	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
753	63.5	12.6	461	2	088P66	088p66 pseudomonas	826	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
754	63.5	12.6	461	2	088P66	088p66 pseudomonas	827	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
755	63.5	12.6	461	2	088P66	088p66 pseudomonas	828	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
756	63.5	12.6	461	2	088P66	088p66 pseudomonas	829	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
757	63.5	12.6	461	2	088P66	088p66 pseudomonas	830	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
758	63.5	12.6	461	2	088P66	088p66 pseudomonas	831	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
759	63.5	12.6	461	2	088P66	088p66 pseudomonas	832	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
760	63.5	12.6	461	2	088P66	088p66 pseudomonas	833	63.5	12.6	1440	2	06VY42	06vy42 bacterioph
761	63.5	12.6	461	2	088P66	088p66 pseudomonas	834	63.5	12.6	1440	2	06VY42	06vy42 bacterioph

835	63	12.5	470	2	Q7X4G1	Q7x4g1 xanthomonas	908	62.5	12.5	297	2	Q7NW70	Q7nw70 chromobacter
836	63	12.5	489	2	Q9DBE7	Q9dbef m mus muscu	909	62.5	12.5	299	2	Q7VTP0	Q7vtp0 bordetella
837	63	12.5	489	2	Q9ESV8	Q9esv8 rattus norv	910	62.5	12.5	304	2	Q7MTL0	Q7mtl0 porphyromon
838	63	12.5	495	2	Q9ET50	Q9et50 rattus norv	911	62.5	12.5	307	2	Q8GTL1	Q8gtl1 synechococ
839	63	12.5	505	2	Q9SQK4	Q9sqk4 vitis vinif	912	62.5	12.5	307	2	Q82PU2	Q82pu2 streptomyce
840	63	12.5	517	1	6PGD CANAL	013287 candida alb	913	62.5	12.5	314	2	Q75PX9	Q75px9 serratia ma
841	63	12.5	532	2	Q8K4G2	Q8k4g2 mus musculu	914	62.5	12.5	314	2	Q9A8B8	Q9a8b8 caulobacter
842	63	12.5	532	2	Q40622	Q40622 human papil	915	62.5	12.5	330	2	Q67P82	Q67p82 symbiobacter
843	63	12.5	540	2	Q87AC8	Q87ac8 xylella fas	916	62.5	12.5	331	2	Q72B16	Q72b16 desulfovibr
844	63	12.5	540	2	Q66HP4	Q66hp4 rattus norv	917	62.5	12.5	348	2	Q8KBQ8	Q8kbq8 chlorobium
845	63	12.5	576	2	Q641P2	Q641p2 mus musculu	918	62.5	12.5	361	1	COBT_MYCBO	P63842 mycobacteri
846	63	12.5	578	2	Q82RM4	Q82rm4 streptomyce	919	62.5	12.5	361	1	COBT_MYCTU	P63841 mycobacteri
847	63	12.5	597	2	Q6C2X7	Q6c2x7 yarrowia li	920	62.5	12.5	368	2	Q8G3D4	Q8g3d4 bruceella su
848	63	12.5	607	2	Q87XC4	Q87xc4 pseudomonas	921	62.5	12.5	372	2	Q6FTG9	Q6ftg9 candida gla
849	63	12.5	614	2	Q65D36	Q65d36 bacillus li	922	62.5	12.5	373	2	Q6N3Y9	Q6n3y9 rhodopseudo
850	63	12.5	620	2	Q6EUS5	Q6eus5 oryza sativ	923	62.5	12.5	375	2	Q6MNU9	Q6mnu9 methanococ
851	63	12.5	620	2	Q9PEP3	Q9pep3 xylella fas	924	62.5	12.5	380	2	Q7UGD5	Q7ugd5 rhodopirell
852	63	12.5	634	2	Q9W646	Q9w646 oryza sat	925	62.5	12.5	388	2	Q8UC90	Q8uc90 agrobacteri
853	63	12.5	662	2	Q64UP4	Q64up4 bacteroides	926	62.5	12.5	393	2	Q84BB5	Q84bb5 erwina chr
854	63	12.5	662	2	Q8A8T1	Q8a8t1 bacteroides	927	62.5	12.5	399	2	Q6Z4M0	Q6z4m0 oryza sativ
855	63	12.5	684	2	Q9S282	Q9s282 streptomyce	928	62.5	12.5	401	2	Q9HXQ8	Q9hxq8 pseudomonas
856	63	12.5	694	2	Q7WIS8	Q7wis8 bordetella	929	62.5	12.5	403	2	Q64ZQ8	Q64zq8 bacteroides
857	63	12.5	700	2	Q95TW3	Q95tw3 drosophila	930	62.5	12.5	404	2	Q7WOW5	Q7wow5 bordetella
858	63	12.5	739	2	Q89VS0	Q89vs0 bradyrhizob	931	62.5	12.5	404	2	Q7WN89	Q7wn89 mus musculu
859	63	12.5	740	2	Q9N3Z2	Q9n3z2 caenorhabdt	932	62.5	12.5	408	2	Q80VU9	Q80v19 mus musculu
860	63	12.5	744	2	Q6N0U4	Q6n0u4 rhodopseudo	933	62.5	12.5	417	2	Q7NKKV3	Q7nkv3 fusoobacter
861	63	12.5	825	2	Q8P5T1	Q8p5t1 xanthomonas	934	62.5	12.5	419	2	Q8RGS7	Q8rgs7 arabisdopsis
862	63	12.5	849	2	Q98E97	Q98e97 rhizobium l	935	62.5	12.5	426	2	Q4Z5Y3	Q4z5y3 arabisdopsis
863	63	12.5	874	1	CLPB_BRUME	Q8y191 bruceella me	936	62.5	12.5	426	2	Q9CAQ6	Q9caq6 arabisdopsis
864	63	12.5	874	1	CLPB_BRUSU	Q7ce66 bruceella su	937	62.5	12.5	427	2	Q87VY5	Q87vy5 pseudomonas
865	63	12.5	880	2	Q63VFS	Q63vrs burkholderi	938	62.5	12.5	430	2	Q8VR17	Q8vr17 serratia ma
866	63	12.5	891	2	Q7T2X3	Q7t2x3 gallus gall	939	62.5	12.5	430	2	Q72K00	Q72k00 thermus the
867	63	12.5	932	1	PMS1_HUMAN	P54277 homo sapien	940	62.5	12.5	443	2	Q6ACB3	Q6acb3 leifsonia x
868	63	12.5	947	2	Q8RUT5	Q8ruts oryza sativ	941	62.5	12.5	443	2	Q6ATEB	Q6ateb campylobac
869	63	12.5	985	2	Q9WA84	Q9wa84 drosophila	942	62.5	12.5	450	2	Q7NVCV5	Q7ncv5 glieobacter
870	63	12.5	988	2	Q6AMU1	Q6aw1 drosophila	943	62.5	12.5	458	2	Q88157	Q88157 pseudomonas
871	63	12.5	988	2	Q9W0Z3	Q9w0z3 drosophila	944	62.5	12.5	462	2	Q82CD6	Q82cd6 streptomyce
872	63	12.5	1062	1	NAL2_HUMAN	Q9nx02 homo sapien	945	62.5	12.5	463	2	Q6MVCU7	Q6mcv7 paracalamyd
873	63	12.5	1145	2	Q7OHF8	Q7qth8 anopheles g	946	62.5	12.5	485	2	Q6N592	Q6n592 rhodopseudo
874	63	12.5	1153	2	Q7PSX6	Q7psx6 anopheles g	947	62.5	12.5	485	2	Q87V77	Q87v77 pseudomonas
875	63	12.5	1157	2	Q27088	Q27088 trichomonas	948	62.5	12.5	511	1	NADB_CAUCR	Q9a4c3 caulobacter
876	63	12.5	1174	2	Q89N18	Q89n18 bradyrhizob	949	62.5	12.5	511	2	Q983V2	Q983v2 rhizobium l
877	63	12.5	1299	2	Q8TXZ8	Q8txz8 methanopyru	950	62.5	12.5	513	2	Q9SRY1	Q9sry1 arabisdopsis
878	63	12.5	1472	2	Q9L214	Q9l214 streptomyce	951	62.5	12.5	517	2	Q6DSW7	Q6dsw7 erwina car
879	63	12.5	1500	2	Q7QCC9	Q7qgc9 giardia lam	952	62.5	12.5	523	2	Q9CSL3	Q9cs13 arabisdopsis
880	63	12.5	1677	2	Q00805	Q00805 leishmania	953	62.5	12.5	557	2	Q741P4	Q741p4 mycobacteri
881	63	12.5	2137	2	Q84BQ6	Q84bq6 pseudomonas	954	62.5	12.5	560	1	BFS_MOUSE	Q64355 mus musculu
882	63	12.5	5541	2	Q6W5P9	Q6w5p9 streptomyce	955	62.5	12.5	560	2	Q8BSX4	Q8bsx4 mus musculu
883	63	12.5	74	2	Q9FBL3	Q9fbl3 streptomyce	956	62.5	12.5	560	2	Q8KOF6	Q8kof6 mus musculu
884	62.5	12.5	75	2	Q6A4X1	Q6a4x1 malus domes	957	62.5	12.5	573	2	Q9RVZ7	Q9rvz7 delinococcus
885	62.5	12.5	102	2	Q6C190	Q6c190 yarrowia li	958	62.5	12.5	599	2	Q8TKZ7	Q8tkz7 homo sapien
886	62.5	12.5	112	2	Q8LC40	Q8lc40 arabidopsis	959	62.5	12.5	601	2	Q30039	Q30039 archaeoglob
887	62.5	12.5	113	2	Q6N6R7	Q6n6r7 rhodopseudo	960	62.5	12.5	612	2	Q7NY06	Q7ny06 chromobacte
888	62.5	12.5	115	2	Q8USH4	Q8ush4 agrobacteri	961	62.5	12.5	618	2	Q914B7	Q914b7 pseudomonas
889	62.5	12.5	149	2	Q889R1	Q889r1 pseudomonas	962	62.5	12.5	633	2	Q8MLA8	Q8mla8 drosophila
890	62.5	12.5	150	2	Q88P31	Q88p31 xanthomonas	963	62.5	12.5	634	2	Q6A8V3	Q6a8v3 propionibac
891	62.5	12.5	151	2	Q6W8W9	Q6w8w9 pseudomonas	964	62.5	12.5	652	2	Q8G1R3	Q8g1r3 bruceella su
892	62.5	12.5	157	2	Q72G77	Q72g77 thermus the	965	62.5	12.5	662	2	Q6CON9	Q6con9 yarrowia li
893	62.5	12.5	192	2	Q8VKM1	Q8vkm1 mycobacteri	966	62.5	12.5	680	2	Q95TU3	Q95tu3 drosophila
894	62.5	12.5	195	2	Q93NU6	Q93nu6 uncultured	967	62.5	12.5	685	2	Q8YGS9	Q8ygs9 bruceella me
895	62.5	12.5	209	2	Q93NTE	Q93nte uncultured	968	62.5	12.5	710	2	Q67P71	Q67p71 symbiobacte
896	62.5	12.5	216	2	Q72GUT	Q72gut thermus the	969	62.5	12.5	738	1	CPO_DROME	Q01617 drosophila
897	62.5	12.5	244	2	Q93NV4	Q93nv4 desulfovibr	970	62.5	12.5	760	1	CO2_MOUSE	B21180 mus musculu
898	62.5	12.5	246	2	Q7W111	Q7w111 bordetella	971	62.5	12.5	760	1	Q70350	Q70350 mus musculu
899	62.5	12.5	251	2	Q7VZ36	Q7vz36 bordetella	972	62.5	12.5	802	2	Q81UM7	Q81um7 homo sapien
900	62.5	12.5	251	2	Q7W8T5	Q7w8t5 bordetella	973	62.5	12.5	802	2	Q8N8S5	Q8n8s5 mus musculu
901	62.5	12.5	251	2	Q7WK45	Q7wk45 bordetella	974	62.5	12.5	802	2	Q8BGD7	Q8bgd7 mus musculu
902	62.5	12.5	266	1	Q8G8G0	Q8g8g0 wolinetella s	975	62.5	12.5	802	2	Q8CJH6	Q8cjh6 rattus norv
903	62.5	12.5	267	1	THIG_DEIRA	Q8ryy1 deinnococcus	976	62.5	12.5	904	2	Q75017	Q75017 ashbya gos
904	62.5	12.5	271	2	Q8T1T0	Q8t1t0 methanobarc	977	62.5	12.5	909	2	Q5Z585	Q5z585 pseudomonas
905	62.5	12.5	283	2	Q833U6	Q833u6 enterococcu	978	62.5	12.5	917	2	Q9ZNM1	Q9znm1 pseudomonas
906	62.5	12.5	284	2	Q34174	Q34174 pseudomonas	979	62.5	12.5	956	2	Q8VIG0	Q8vig0 mus musculu
907	62.5	12.5	284	2	Q7W0X7	Q7w0x7 bordetella	980	62.5	12.5	967	2	Q9BJZ5	Q9bjz5 drosophila

981	62.5	12.5	970	2	Q9VN28	Q9vn28 drosophila	1054	62	12.4	408	2	Q7VX47	Q7vx47 bordetella
982	62.5	12.5	1049	2	Q6SW99	Q6sw99 human cytom	1055	62	12.4	409	2	Q7VX46	Q7vx46 bordetella
983	62.5	12.5	1224	2	Q9VXW2	Q9vwx2 drosophila	1056	62	12.4	408	2	Q8PLR6	Q8plr6 bordetella
984	62.5	12.5	1887	2	Q8TEN7	Q8tent homo sapien	1057	62	12.4	409	2	Q8PLR5	Q8plr5 xanthomonas
985	62.5	12.5	2008	2	Q96S58	Q96s58 homo sapien	1058	62	12.4	426	2	Q92UT3	Q92ut3 xanthomonas
986	62.5	12.5	2146	2	Q8IZY2	Q8izy2 homo sapien	1059	62	12.4	431	2	Q8XYF5	Q8xyf5 ralestonia s
987	62.5	12.5	2146	2	Q9NR73	Q9nr73 homo sapien	1060	62	12.4	432	2	Q6N7N0	Q6n7n0 rhodopseudo
988	62.5	12.5	2680	2	Q7PP92	Q7pp92 anopheles g	1061	62	12.4	443	2	Q67NE8	Q67ne8 symbiobacte
989	62.5	12.5	2873	2	Q93075	Q93075 gb virus c/	1062	62	12.4	464	1	MURF-STPTO	MURF-STPTO
990	62.5	12.5	3295	2	Q93X71	Q93x71 streptomyce	1063	62	12.4	464	2	Q8UZD9	Q8uzd9 streptomyce
991	62	12.4	98	2	Q9KEE3	Q9kee3 bacillus ha	1064	62	12.4	474	2	Q66GH1	Q66gh1 streptomyce
992	62	12.4	117	2	Q24440	Q24440 phaseolus v	1065	62	12.4	486	2	Q6KJ57	Q6k57 symbiobacte
993	62	12.4	128	1	RL7 CORGL	RL7 corynebacte	1066	62	12.4	488	2	Q6KJ56	Q6k56 symbiobacte
994	62	12.4	128	2	Q8FSA0	Q8fsa0 corynebacte	1067	62	12.4	494	2	Q6JN63	Q6j63 xanthomonas
995	62	12.4	137	2	Q9YF55	Q9yif5 aerypyrum p	1068	62	12.4	500	2	Q52206	Q52206 xanthomonas
996	62	12.4	142	2	Q6HIDS	Q6hid5 human adeno	1069	62	12.4	502	2	Q9HNH8	Q9hnh8 xanthomonas
997	62	12.4	144	2	Q8POV1	Q8pov1 xanthomonas	1070	62	12.4	502	2	Q74JH0	Q74jh0 rhodopseudo
998	62	12.4	150	2	Q87BW9	Q87bw9 xylella fas	1071	62	12.4	535	2	Q667A7	Q667a7 rhodopseudo
999	62	12.4	156	2	Q67K09	Q67k09 symbiobacte	1072	62	12.4	541	2	Q92243	Q92243 rhizobium m
1000	62	12.4	164	2	Q72LC1	Q72lc1 thermus tle	1073	62	12.4	544	2	Q8H4X9	Q8h4x9 oryza sativ
1001	62	12.4	188	2	Q6Z2Y5	Q6z2y5 oryza sativ	1074	62	12.4	545	2	Q8H4X9	Q8h4x9 oryza sativ
1002	62	12.4	199	1	IL11 RAT	IL11 rat	1075	62	12.4	549	2	P93076	P93076 beta vulgar
1003	62	12.4	200	2	Q65585	Q65585 raltus norv	1076	62	12.4	549	2	P93076	P93076 beta vulgar
1004	62	12.4	211	2	Q937M4	Q937m4 desulfofaba	1077	62	12.4	550	2	Q9A0H1	Q9a0h1 pseudomonas
1005	62	12.4	219	2	Q6NM02	Q6nm02 arabidopsis	1078	62	12.4	574	2	Q9HMG7	Q9hmg7 pseudomonas
1006	62	12.4	224	2	Q6ZD78	Q6z78 oryza sativ	1079	62	12.4	584	2	Q8XZC6	Q8xz6 ralestonia s
1007	62	12.4	232	2	Q6N0Q1	Q6n0q1 rhodopseudo	1080	62	12.4	585	2	Q8XZC6	Q8xz6 ralestonia s
1008	62	12.4	235	2	Q6VVD8	Q6vvd8 ustilago ma	1081	62	12.4	591	2	Q8CF81	Q8cf81 mus musculu
1009	62	12.4	237	2	Q654S3	Q654s3 oryza sativ	1082	62	12.4	594	2	Q8KBU1	Q8kb1 mus musculu
1010	62	12.4	240	2	Q8EGZ0	Q8egz0 shewanella	1083	62	12.4	609	2	Q8KBU1	Q8kb1 mus musculu
1011	62	12.4	242	1	HIS4 HALN1	HIS4 halobacteri	1084	62	12.4	620	2	Q6L5L8	Q6l5l8 coltuna
1012	62	12.4	257	1	MOAF_KLEAE	MOAF klebsiella	1085	62	12.4	637	2	SMP_COTJA	SMP_COTJA
1013	62	12.4	257	2	Q6V1Y7	Q6v1y7 uncultured	1086	62	12.4	641	2	Q67LE1	Q67le1 symbiobacte
1014	62	12.4	261	2	Q6NKI6	Q6nki6 corynebacte	1087	62	12.4	642	2	Q8YTS6	Q8yts6 anabaena sp
1015	62	12.4	265	2	Q82P8	Q82p8 streptomyce	1088	62	12.4	643	2	Q9A8N9	Q9a8n9 caulobacter
1016	62	12.4	271	2	Q6AS50	Q6as50 desulfofaba	1089	62	12.4	645	2	Q8X2A5	Q8x2a5 escherichia
1017	62	12.4	284	2	Q6MJR0	Q6mjr0 bdellovibri	1090	62	12.4	660	1	RBP2_HUMAN	RBP2_HUMAN
1018	62	12.4	287	2	Q9YAW7	Q9yaw7 aerypyrum p	1091	62	12.4	668	1	Q8UFW6	Q8ufw6
1019	62	12.4	291	2	Q8CK69	Q8ck69 streptomyce	1092	62	12.4	682	2	Q8UFW6	Q8ufw6
1020	62	12.4	293	2	Q9L0R9	Q9l0r9 streptomyce	1093	62	12.4	682	2	Q8UFW6	Q8ufw6
1021	62	12.4	295	2	Q9X8B5	Q9x8b5 oryza sativ	1094	62	12.4	694	2	Q7D048	Q7d048
1022	62	12.4	296	2	Q9X8B5	Q9x8b5 oryza sativ	1095	62	12.4	724	2	P77970	P77970
1023	62	12.4	299	1	G3P_DICD1	G3p dicystosell	1096	62	12.4	732	2	Q6CKH0	Q6ckh0
1024	62	12.4	316	2	Q7EYL9	Q7eyl9 oryza sativ	1097	62	12.4	746	2	Q9NM77	Q9nm77
1025	62	12.4	322	2	Q740Y0	Q740y0 mycobacteri	1098	62	12.4	754	2	Q6GM95	Q6gm95 xenopus lae
1026	62	12.4	335	2	Q648E6	Q648e6 uncultured	1099	62	12.4	755	2	Q6GM95	Q6gm95 xenopus lae
1027	62	12.4	335	2	Q86Y99	Q86y99 dicystosell	1100	62	12.4	775	1	YTX1_XENTLA	YTX1_XENTLA
1028	62	12.4	338	2	Q8YH6	Q8yh6 bruceella me	1101	62	12.4	829	2	Q9JND1	Q9jnd1 mus musculu
1029	62	12.4	347	2	Q89JF5	Q89jf5 bradyrhizob	1102	62	12.4	832	2	Q89JND1	Q89jnd1 mus musculu
1030	62	12.4	347	2	Q64EP2	Q64ep2 uncultured	1103	62	12.4	863	2	Q6PCY3	Q6pcy3
1031	62	12.4	347	2	Q88B32	Q88b32 pseudomonas	1104	62	12.4	877	1	E74B_DROME	E74b_DROME
1032	62	12.4	348	2	Q67SY0	Q67sy0 symbiobacte	1105	62	12.4	883	2	Q14560	Q14560 homo sapien
1033	62	12.4	349	2	Q89G81	Q89g81 bradyrhizob	1106	62	12.4	925	2	Q80207	Q80207 raltus norv
1034	62	12.4	360	2	Q72LJ1	Q72lj1 thermus the	1107	62	12.4	954	1	GCSP_AGR15	GCSP_AGR15
1035	62	12.4	363	2	Q69949	Q69949 streptomyce	1108	62	12.4	991	2	Q880F2	Q880f2 pseudomonas
1036	62	12.4	368	2	Q94KJ5	Q94kj5 ipomoea pur	1109	62	12.4	998	2	Q9S2K3	Q9s2k3 streptomyce
1037	62	12.4	370	2	Q6ZKZ7	Q6zrz7 bacillus ii	1110	62	12.4	1003	2	Q9P2P3	Q9p2p3 salmoneila
1038	62	12.4	372	2	Q6S6I9	Q6s6i9 mycobacteri	1111	62	12.4	1025	2	Q8XYF4	Q8xyf4 arabidopsis
1039	62	12.4	382	1	PE23_MYCTU	PE23 mycobacteri	1112	62	12.4	1030	2	Q9C905	Q9c905 arabidopsis
1040	62	12.4	385	2	Q03990	Q03990 dancus caro	1113	62	12.4	1030	2	Q9C905	Q9c905 arabidopsis
1041	62	12.4	388	1	Q8N467	Q8n467 ipomoea nli	1114	62	12.4	1233	2	Q7KMX7	Q7kxm7 dicystosell
1042	62	12.4	388	1	CHSD_IPONTI	CHSD ipomoea pur	1115	62	12.4	1233	2	Q881Y1	Q881y1 pseudomonas
1043	62	12.4	388	1	Q04934	Q04934 ipomoea pur	1116	62	12.4	1250	2	Q88XG7	Q88xg7 ashbya gos
1044	62	12.4	388	2	Q94KJ3	Q94kj3 ipomoea pur	1117	62	12.4	1290	2	Q7OOL6	Q7ool6 xanthomonas
1045	62	12.4	388	2	Q92PK8	Q92pk8 rhizobium m	1118	62	12.4	1300	2	Q7OOL6	Q7ool6 xanthomonas
1046	62	12.4	389	2	Q66EM6	Q66em6 yersinia ps	1119	62	12.4	1366	2	Q82MF2	Q82mf2 anopheles g
1047	62	12.4	389	2	Q9AAC8	Q9aac8 caulobacter	1120	62	12.4	1434	2	Q8K448	Q8k448 mus musculu
1048	62	12.4	393	2	Q8MR45	Q8mr45 drosophila	1121	62	12.4	1642	2	Q81OC7	Q81oc7 mus musculu
1049	62	12.4	393	2	Q914I9	Q914i9 pseudomonas	1122	62	12.4	1642	2	Q81OC7	Q81oc7 mus musculu
1050	62	12.4	398	2	Q9IRI1	Q9iri1 streptomyce	1123	62	12.4	1642	2	Q81OC7	Q81oc7 mus musculu
1051	62	12.4	407	1	PCAB_PSEPU	PCAB pseudomonas	1124	62	12.4	1642	2	Q81OC7	Q81oc7 mus musculu
1052	62	12.4	408	2	Q6W09	Q6w09 aspergillus	1125	62	12.4	1642	2	Q81OC7	Q81oc7 mus musculu
1053	62	12.4	408	2	Q6WH96	Q6wh96 bdellovibri	1126	62	12.4	2969	2	Q6M6V0	Q6m6v0 corynebacte

1127	62	12.4	2969	2	Q8NS46	O8ns46 corynebacte	1200	61.5	12.3	402	2	Q7UAX3	Q7uax3 shigella fl
1128	62	12.4	4133	2	Q6XNJ3	O6xnj3 burkholderi	1201	61.5	12.3	404	2	Q7WMV9	Q7wmv9 porphyromon
1129	61.5	12.3	75	2	Q6A4X3	O6a4x3 malus domes	1202	61.5	12.3	405	2	Q97ZT8	Q97zt8 sulfolobus
1130	61.5	12.3	124	1	RL7_BRUME	RL106 bruceella me	1203	61.5	12.3	410	2	Q9PAK8	Q9fak8 rhizobium 1
1131	61.5	12.3	127	2	Q82D06	Q82d06 streptomyce	1204	61.5	12.3	413	2	Q67T35	Q67t35 bymbiobacte
1132	61.5	12.3	133	2	Q06787	O06787 mycobacteri	1205	61.5	12.3	414	2	Q897B8	Q897b8 clostridium
1133	61.5	12.3	133	2	Q7ZN2	Q7zn2 mycobacteri	1206	61.5	12.3	416	2	Q8KJF1	Q8kuf1 actinosyane
1134	61.5	12.3	139	2	Q8CBS8	O8cb8 mus musculu	1207	61.5	12.3	417	2	Q83PE8	Q83pe8 shigella fl
1135	61.5	12.3	145	2	Q9RYG6	Q9ryg6 delnoccocu	1208	61.5	12.3	421	2	Q62KW7	Q62kw7 burkholderi
1136	61.5	12.3	153	2	Q7D815	Q7d815 mycobacteri	1209	61.5	12.3	421	2	Q63TR4	Q63tr4 burkholderi
1137	61.5	12.3	180	2	Q41878	Q41878 zea mays (m	1210	61.5	12.3	422	2	Q98AM3	Q98aw3 rhizobium 1
1138	61.5	12.3	185	2	Q93KH9	Q93kh9 uncultured	1211	61.5	12.3	425	2	Q982F8	Q982f8 rhizobium 1
1139	61.5	12.3	211	2	Q9S2U3	Q9s2u3 streptomyce	1212	61.5	12.3	431	2	Q6NEM2	Q6nem2 corynebacte
1140	61.5	12.3	217	1	RNH2_AGR75	O8h2e agrobacteri	1213	61.5	12.3	434	2	U143_HHV11	U143 HHV11
1141	61.5	12.3	221	2	Q813B5	O813b5 oryza sativ	1214	61.5	12.3	435	2	Q7TYF6	Q7tyf6 human herpe
1142	61.5	12.3	221	2	Q75H7	Q75h7 oryza sativ	1215	61.5	12.3	441	1	DHOM_MYCBO	DHOM_MYCBO
1143	61.5	12.3	223	2	Q87Z04	Q87z04 pseudomonas	1216	61.5	12.3	441	1	DHOM_MYCTU	DHOM_MYCTU
1144	61.5	12.3	230	2	Q8XHB8	O8xhb8 clostridium	1217	61.5	12.3	442	1	Q9S3J2	Q9s3j2 campylobact
1145	61.5	12.3	238	2	Q7VZM1	Q7vzm1 bordetella	1218	61.5	12.3	445	2	Q8YW88	Q8yw88 anabaena sp
1146	61.5	12.3	246	2	Q6ALB4	O6alb4 desulfocale	1219	61.5	12.3	447	2	Q98BS4	Q98bs4 rhizobium 1
1147	61.5	12.3	247	2	Q847X8	Q847x8 uncultured	1220	61.5	12.3	454	2	Q881B7	Q881b7 pseudomonas
1148	61.5	12.3	250	2	Q847X3	Q847x3 uncultured	1221	61.5	12.3	459	2	Q8XQX4	Q8xqx4 ralstonia b
1149	61.5	12.3	254	2	Q8PL43	Q8pl43 xanthomonas	1222	61.5	12.3	461	2	Q88Q46	Q88q46 pseudomonas
1150	61.5	12.3	256	2	Q76FE8	Q76fe8 diosophilla	1223	61.5	12.3	464	2	Q82D04	Q82d04 streptomyce
1151	61.5	12.3	256	2	Q92SS3	Q92ss3 rhizobium m	1224	61.5	12.3	465	2	Q7NNX3	Q7nnx3 chromobacte
1152	61.5	12.3	256	2	Q98HP6	Q98hp6 rhizobium 1	1225	61.5	12.3	470	2	Q852C2	Q852c2 oryza sativ
1153	61.5	12.3	257	2	Q54175	O54175 streptomyce	1226	61.5	12.3	480	2	Q8N3W6	Q8n3w6 homo sapien
1154	61.5	12.3	264	2	Q82AU5	Q82aus streptomyce	1227	61.5	12.3	503	1	PUR8_STRLP	P82670 streptomyce
1155	61.5	12.3	266	2	Q93UR4	Q93ur4 desulfovibr	1228	61.5	12.3	531	2	Q7V217	Q7v217 prochloroco
1156	61.5	12.3	276	2	Q7VZ71	Q7vz71 bordetella	1229	61.5	12.3	537	2	Q67L80	Q67l80 symbiobacte
1157	61.5	12.3	276	2	Q7WML1	Q7wml1 bordetella	1230	61.5	12.3	561	2	Q7W721	Q7w721 bordetella
1158	61.5	12.3	276	2	Q7WML8	Q7wml8 bordetella	1231	61.5	12.3	564	2	Q8D5V6	Q8d5v6 vibrio vuln
1159	61.5	12.3	283	2	Q27763	Q27763 methanobact	1232	61.5	12.3	587	1	DLDI_YEAST	P32891 saccharomyc
1160	61.5	12.3	296	2	Q7WNT9	Q7wn9 bordetella	1233	61.5	12.3	593	2	Q6K60	Q6k60 bacteriopho
1161	61.5	12.3	297	2	Q8RB16	Q8rb16 thermoaer	1234	61.5	12.3	616	2	Q6NOD7	Q6nod7 rhodopseudo
1162	61.5	12.3	298	2	Q64RN4	O64rn4 bacteroides	1235	61.5	12.3	620	2	Q82A11	Q82a11 streptomyce
1163	61.5	12.3	299	2	Q7W149	Q7w149 bordetella	1236	61.5	12.3	635	2	Q7MCK5	Q7mck5 vibrio vuln
1164	61.5	12.3	304	2	Q9ABZ6	Q9abz6 caulobacter	1237	61.5	12.3	643	2	Q6PLQ2	Q6plq2 chlamydomon
1165	61.5	12.3	306	1	DDL_HAEIN	P4405 haemophilus	1238	61.5	12.3	647	2	Q7Q072	Q7qct2 giardia lam
1166	61.5	12.3	313	2	Q9HQ34	Q9hq34 halobacteri	1239	61.5	12.3	663	2	Q8U4B1	Q8u4b1 pyrococcus
1167	61.5	12.3	313	2	Q8PPA1	O8ppa1 xanthomonas	1240	61.5	12.3	702	2	Q8XYJ9	Q8xyj9 ralstonia b
1168	61.5	12.3	317	2	Q8UOC1	O8uoc1 pyrococcus	1241	61.5	12.3	722	1	GLNE_CRIGR	Q7ctg49 c bifuncio
1169	61.5	12.3	318	1	K1PF_XANCP	P3334 xanthomonas	1242	61.5	12.3	739	1	SYG_HUMAN	P41250 homo sapien
1170	61.5	12.3	319	2	Q83Q66	O83q66 shigella fl	1243	61.5	12.3	741	2	Q947C1	Q947c1 zea mays (m
1171	61.5	12.3	327	2	Q6BK72	Q6bk72 debaryomyc	1244	61.5	12.3	751	2	Q7Z5H0	Q7z5h0 homo sapien
1172	61.5	12.3	333	2	Q9HS82	Q9hs82 halobacteri	1245	61.5	12.3	760	2	Q8KJPS	Q8kjp5 rhizobium 1
1173	61.5	12.3	334	2	Q9ZXS2	Q9zxs2 mycobacteri	1246	61.5	12.3	768	2	Q6C100	Q6c100 yarrowia 11
1174	61.5	12.3	338	2	Q9KDX8	Q9kdx8 bacillus ha	1247	61.5	12.3	802	1	BCB2_ACEXY	O82860 acetobacter
1175	61.5	12.3	341	2	Q7NFY3	Q7nfy3 gloebacter	1248	61.5	12.3	806	2	Q7OCU4	Q7qcu4 anopheles g
1176	61.5	12.3	344	1	NAGK_HUMAN	Q9uj70 homo sapien	1249	61.5	12.3	820	2	Q91116	Q91116 pseudomonas
1177	61.5	12.3	344	2	Q9NV37	Q9nv37 homo sapien	1250	61.5	12.3	870	1	CLB1_STRAW	Q82eu3 streptomyce
1178	61.5	12.3	346	2	Q89156	Q89156 bradyrhizob	1251	61.5	12.3	936	2	Q7Q8H4	Q7q8h4 anopheles g
1179	61.5	12.3	350	2	Q81V29	O81v29 bacillus an	1252	61.5	12.3	952	2	Q8U3N7	Q8u3n7 pyrococcus
1180	61.5	12.3	351	2	Q6NZX7	O6nzx7 rhodopseudo	1253	61.5	12.3	1024	1	T1PT_DROME	Q9u3v5 dictyophila
1181	61.5	12.3	351	2	Q9RZK5	Q9rzk5 delnoccocu	1254	61.5	12.3	1036	2	Q7U4E9	Q7u4e9 synecchococ
1182	61.5	12.3	355	1	TRPD_AZOB	P66924 azospirillum	1255	61.5	12.3	1062	2	Q9P712	Q9p712 neurospora
1183	61.5	12.3	355	2	Q98NT7	Q98nt7 rhizobium 1	1256	61.5	12.3	1066	2	Q9ASH0	Q9ash0 oryza sativ
1184	61.5	12.3	361	2	Q9YBP9	Q9ybp9 aeropyrum p	1257	61.5	12.3	1070	2	Q7RV12	Q7rv12 neurospora
1185	61.5	12.3	364	2	Q6AEV5	O6aev5 propionibac	1258	61.5	12.3	1142	1	UB40_HUMAN	Q9nves homo sapien
1186	61.5	12.3	367	1	NK61_HUMAN	P78426 homo sapien	1259	61.5	12.3	1247	2	Q7OEL0	Q7oel0 homo sapien
1187	61.5	12.3	368	1	RH23_SCHPO	O74803 schistosach	1260	61.5	12.3	1336	2	Q78392	Q78392 neurospora
1188	61.5	12.3	384	2	Q93LD7	Q93ld7 agrobacteri	1261	61.5	12.3	1363	2	Q6N355	Q6n355 equine coro
1189	61.5	12.3	386	2	Q9ASW7	Q9asw7 caulobacter	1262	61.5	12.3	1472	2	Q7M948	Q7m948 wolinnella b
1190	61.5	12.3	392	2	Q98192	Q98192 rhizobium 1	1263	61.5	12.3	1477	2	Q9C250	Q9c250 neurospora
1191	61.5	12.3	394	2	Q824E1	O824e1 salmonella	1264	61.5	12.3	1492	2	Q68724	Q68724 yersinia pe
1192	61.5	12.3	394	2	Q8ZML0	O8zml0 salmonella	1265	61.5	12.3	1513	2	Q7RVU0	Q7rvu0 neurospora
1193	61.5	12.3	396	2	Q93906	Q93906 streptomyce	1266	61.5	12.3	1545	2	Q74YR1	Q74yr1 yersinia pe
1194	61.5	12.3	396	2	Q9EWX4	Q9ewx4 streptomyce	1267	61.5	12.3	1545	2	Q7ARG4	Q7arg4 yersinia pe
1195	61.5	12.3	397	2	Q8KCT9	Q8kct9 chlorobium	1268	61.5	12.3	1545	2	Q9ZH03	Q9zh03 yersinia pe
1196	61.5	12.3	399	2	Q7SAS6	Q7saa6 neurospora	1269	61.5	12.3	1725	2	Q6Z1F2	Q6z1f2 burkholderi
1197	61.5	12.3	399	2	Q92M24	Q92m24 rhizobium m	1270	61.5	12.3	2103	2	Q9CDB1	Q9cdb1 mycobacteri
1198	61.5	12.3	400	2	Q8XK4	O8xk4 escherichia	1271	61.5	12.3	2404	2	Q90733	Q90733 wheat yellow
1199	61.5	12.3	402	1	YHUX_ECOLI	P76662 escherichia	1272	61.5	12.3	2751	2	Q8XUK0	Q8xuk0 ralstonia b

1273	61.5	12.3	3247	2	065553	065553 bovine herp	1346	61	12.2	370	2	0887D7	0887d7 pseudomonas
1274	61.5	12.3	3247	2	077CD4	077cd4 bovine herp	1347	61	12.2	370	2	0887D7	0887d7 pseudomonas
1275	61.5	12.3	3889	2	06SSB8	06sse8 chlamydomon	1348	61	12.2	377	2	09KYT3	09kyt3 ralestonia s
1276	61.5	12.3	4753	2	08PLI3	08pli3 xanthomonas	1349	61	12.2	377	2	09KYT3	09kyt3 streptomyc
1277	61.5	12.3	4881	2	09S0R3	09s0r3 streptomyc	1350	61	12.2	382	2	09KSB4	09ksb4 desulfobact
1278	61	12.2	104	2	08TFV6	08tfv6 aspergillus	1351	61	12.2	390	2	022101	022101 caenorhabd
1279	61	12.2	104	2	08TFV7	08tfv7 aspergillus	1352	61	12.2	392	2	08CCU7	08ccu7 mus musculu
1280	61	12.2	106	2	08TFV3	08tfv3 aspergillus	1353	61	12.2	394	1	Y169_SYNPX	Y169 synpx
1281	61	12.2	107	2	08TFV2	08tfv2 aspergillus	1354	61	12.2	395	2	09RVT4	09rvt4 synchococc
1282	61	12.2	115	2	05S996	05s996 neosartorya	1355	61	12.2	396	2	06GRT3	06grt3 delnocoocc
1283	61	12.2	115	2	06A9H0	06a9h0 propionibac	1356	61	12.2	398	1	SUCC_RHIME	SUCC rhime
1284	61	12.2	117	2	09KN10	09kn10 vibrio chol	1357	61	12.2	402	2	06H144	06h144 bacillus lae
1285	61	12.2	126	2	09HH11	09hh11 halobacteri	1358	61	12.2	406	2	06SFB7	06sfb7 bacillus th
1286	61	12.2	142	2	08UY87	08uy87 simian aden	1359	61	12.2	406	2	06MA90	06ma90 bacillus th
1287	61	12.2	142	2	06OPB5	06opb5 simian aden	1360	61	12.2	414	2	09KXC3	09kxc3 rhizobium m
1288	61	12.2	143	2	067R71	067r71 symbiobacte	1361	61	12.2	419	2	08G0Z7	08g0z7 bacillus th
1289	61	12.2	144	2	062AY7	062ay7 burkholderi	1362	61	12.2	419	2	097RL7	097rl7 bacillus ha
1290	61	12.2	145	2	06DB51	06db51 erwina car	1363	61	12.2	419	2	08DOF7	08dof7 bruceella su
1291	61	12.2	150	2	06NBJ3	06nbj3 rhodopseudo	1364	61	12.2	419	2	09RIT4	09rit4 streptococc
1292	61	12.2	152	2	09RNR7	09rnr7 solar lake	1365	61	12.2	419	2	09RIT4	09rit4 streptococc
1293	61	12.2	167	2	08PH36	08ph36 xanthomonas	1366	61	12.2	420	1	06MAE1	06mae1 parachlamy
1294	61	12.2	172	2	0916Y7	0916y7 pseudomonas	1367	61	12.2	420	1	09CLES	09cles deinococcus
1295	61	12.2	185	1	ADH_ANAPL	ADH anapla	1368	61	12.2	422	2	092TWO	092two pasteurella
1296	61	12.2	190	2	08HHK6	08hhk6 anas platyr	1369	61	12.2	422	2	092TWO	092two rhizobium m
1297	61	12.2	190	2	08HHK6	08hhk6 sphenodon p	1370	61	12.2	424	2	073T89	073t89 mycobacteri
1298	61	12.2	191	2	07XZ45	07xz45 sphenodon p	1371	61	12.2	430	2	0743Z9	0743z9 mycobacteri
1299	61	12.2	192	2	08RIT7	08rit7 griffithbia	1372	61	12.2	433	1	08G3M5	08g3m5 bifidobacte
1300	61	12.2	194	2	09ATC7	09atc7 mus musculu	1373	61	12.2	433	1	CITM_BACSU	CITM bacsu
1301	61	12.2	199	1	IL11_MOUSE	IL11 mus musculu	1374	61	12.2	435	2	06NEU9	06neu9 corynebacte
1302	61	12.2	203	2	070A08	070a08 mus musculu	1375	61	12.2	440	2	06LP21	06lp21 rhodopirell
1303	61	12.2	207	2	0275S8	0275s8 nonomurea	1376	61	12.2	443	2	06RPK24	06rp21 photobacter
1304	61	12.2	215	2	06C7P7	06c7p7 yarrowia li	1377	61	12.2	447	2	082510	082510 streptomyc
1305	61	12.2	228	2	08U269	08u269 yarrowia li	1378	61	12.2	449	2	045082	045082 streptomyc
1306	61	12.2	228	2	089HH9	089hh9 pyrococcus	1379	61	12.2	449	2	089IL4	089il4 burkholderi
1307	61	12.2	231	2	06N634	06n634 bradyrhizob	1380	61	12.2	462	2	06NGX8	06ngx8 bradyrhizob
1308	61	12.2	232	2	07N4F6	07n4f6 rhodopseudo	1381	61	12.2	480	2	06ASP9	06asp9 corynebacte
1309	61	12.2	234	2	093HB2	093hb2 photorhabdu	1382	61	12.2	487	2	09RV67	09rv67 propionbac
1310	61	12.2	240	2	07VZ11	07vz11 streptomyc	1383	61	12.2	493	2	09VC70	09vc70 delnocoocc
1311	61	12.2	240	2	07W559	07w559 bordetella	1384	61	12.2	499	2	08BGC6	08bgc6 aeropyrum p
1312	61	12.2	240	2	07WDB6	07wdb6 bordetella	1385	61	12.2	500	2	06N7D8	06n7d8 drosophila
1313	61	12.2	246	2	082VC7	082vc7 bordetella	1386	61	12.2	502	2	08G5A1	08g5a1 shevanelia
1314	61	12.2	247	2	08YSS1	08yss1 nitrosomona	1387	61	12.2	504	2	08G5A1	08g5a1 rhodopseudo
1315	61	12.2	259	2	026573	026573 anabaena sp	1388	61	12.2	512	2	06LTKS	06ltns bifidobacte
1316	61	12.2	261	2	06CND7	06cnd7 kluyveromyc	1389	61	12.2	520	2	08PVP6	08pvp6 photobacter
1317	61	12.2	265	2	06CND7	06cnd7 kluyveromyc	1390	61	12.2	523	2	08PVP6	08pvp6 anophelae s
1318	61	12.2	267	2	06CND7	06cnd7 kluyveromyc	1391	61	12.2	523	2	08PVP6	08pvp6 xanthomonas
1319	61	12.2	277	2	07X919	07x919 streptomyc	1392	61	12.2	525	2	080ZE2	080ze2 mus musculu
1320	61	12.2	280	2	07VT83	07vt83 streptomyc	1393	61	12.2	525	2	005685	005685 mycobacteri
1321	61	12.2	281	2	041345	041345 rhodospirill	1394	61	12.2	540	2	08EMW1	08emw1 oceanobacti
1322	61	12.2	281	2	042407	042407 silene prat	1395	61	12.2	562	1	ATKA_ALIAC	ATKA aliac
1323	61	12.2	295	1	AOP9_MOUSE	AOP9 mus musculu	1396	61	12.2	565	2	073TQ3	073tq3 mycobacteri
1324	61	12.2	305	2	06C908	06c908 mus musculu	1397	61	12.2	572	2	P87247	P87247 botrytis ci
1325	61	12.2	305	2	06C908	06c908 mus musculu	1398	61	12.2	575	2	07P9Z3	07p9z3 rickettsia
1326	61	12.2	305	2	06C908	06c908 mus musculu	1399	61	12.2	578	2	07P9Z3	07p9z3 rickettsia
1327	61	12.2	312	2	09EM29	09em29 anophelae s	1400	61	12.2	579	2	FAAH_MOUSE	FAAH mouse
1328	61	12.2	313	2	09X518	09x518 streptomyc	1401	61	12.2	582	2	08C541	08c541 mus musculu
1329	61	12.2	313	2	09X518	09x518 streptomyc	1402	61	12.2	586	1	09HT97	09ht97 pseudomonas
1330	61	12.2	313	2	07W2A6	07w2a6 neisseria m	1403	61	12.2	589	2	S132_MOUSE	S132 mouse
1331	61	12.2	313	2	07WR73	07wr73 bordetella	1404	61	12.2	615	2	09RUI5	09rui5 mus musculu
1332	61	12.2	314	2	08H110	08h110 pseudomonas	1405	61	12.2	615	2	09RUI5	09rui5 mus musculu
1333	61	12.2	314	2	07XR51	07xr51 oryza sativ	1406	61	12.2	630	1	ACHA_RAT	ACHA rat
1334	61	12.2	314	2	08PCJ3	08pcj3 xanthomonas	1407	61	12.2	637	1	PUE8_DROME	PUE8 drome
1335	61	12.2	333	2	09K0U4	09k0u4 xanthomonas	1408	61	12.2	641	2	08BVT0	08bvt0 mus musculu
1336	61	12.2	339	2	088BD8	088bd8 pseudomonas	1409	61	12.2	671	2	09N9L9	09n9l9 leishmania
1337	61	12.2	339	2	088BD8	088bd8 pseudomonas	1410	61	12.2	682	2	08C0F2	08c0f2 mus musculu
1338	61	12.2	339	2	088BD8	088bd8 pseudomonas	1411	61	12.2	685	2	06SXS1	06sxs1 oryza sativ
1339	61	12.2	345	2	06N0W8	06n0w8 corynebacte	1412	61	12.2	694	2	07W714	07w714 bordetella
1340	61	12.2	347	2	094802	094802 halococcal s	1413	61	12.2	712	2	07KUP1	07kup1 drosophila
1341	61	12.2	349	2	09FEBZ8	09febz8 streptomyc	1414	61	12.2	723	2	08Y2S0	08y2s0 ralestonia s
1342	61	12.2	355	1	LYPD_AGRIS	LYPD agrobacteri	1415	61	12.2	732	2	09KHM5	09khm5 synchococc
1343	61	12.2	359	1	Y199_MYCTU	Y199 mycobacteri	1416	61	12.2	732	2	08T6I2	08t6i2 giardia lam
1344	61	12.2	364	2	093RV8	093rv8 streptomyc	1417	61	12.2	738	2	07QDN9	07qdn9 giardia lam
1345	61	12.2	365	2	09A2P7	09a2p7 caulobacter	1418	61	12.2	738	2	060BQ3	060bq3 chlamydomon

1419	61	12.2	738	2	08XYC9	08xyc9 ralsfontia s
1420	61	12.2	745	2	08BRM1	08brml mus musculu
1421	61	12.2	754	2	080IX5	080ix5 providence
1422	61	12.2	802	1	BCB1_ACEKXY	B37716 acetoabacter
1423	61	12.2	816	2	089TK5	089tk5 bradyrhizob
1424	61	12.2	839	2	0726K4	0726k4 desulfobibtr
1425	61	12.2	861	2	09NKK3	09nkk3 bombyx mori
1426	61	12.2	877	2	099BV2	099bv2 baboon cyto
1427	61	12.2	880	2	08BKK5	08bkk5 pseudomonas
1428	61	12.2	896	2	09AN79	09an79 bradyrhizob
1429	61	12.2	900	1	CLB2_SYNPX	Q7UC33 synecchococ
1430	61	12.2	905	2	084HG5	084hg5 pseudomonas
1431	61	12.2	920	1	MMU7_MYCBO	P65370 mycobacteri
1432	61	12.2	920	1	MMU7_MYCTU	08pbag xanthomonas
1433	61	12.2	921	2	08PAK6	08pai6 rhizobium 1
1434	61	12.2	927	1	ARL2_RHIL0	065w28 mannheimia
1435	61	12.2	965	2	065W28	P28876 schizosacch
1436	61	12.2	1010	1	PM42_SCHPO	086v15 homo sapien
1437	61	12.2	1044	1	CST_HUMAN	06x249 bovine herp
1438	61	12.2	1054	2	06X249	07kra9 drosophila
1439	61	12.2	1086	2	07KRA9	09atp8 acetabulari
1440	61	12.2	1107	2	09ATP8	06awp8 drosophila
1441	61	12.2	1112	2	06AWP8	Q7KN85 drosophila
1442	61	12.2	1112	2	07KN85	Q9FNX2 acetabulari
1443	61	12.2	1112	2	09FNX2	06cve9 kluyveromyc
1444	61	12.2	1260	2	06CVER	06ieel bradyrhizob
1445	61	12.2	1261	2	06IER1	08p317 xanthomonas
1446	61	12.2	1318	2	08P317	08p316 mus musculu
1447	61	12.2	1370	2	06P9U6	089255 wheat spind
1448	61	12.2	1470	2	089255	080rt4 mus musculu
1449	61	12.2	1531	1	SLT1_MOUSE	080xj3 mus musculu
1450	61	12.2	1705	2	080XJ3	083t5 streptomyc
1451	61	12.2	1975	2	083TP5	Q9U0V2 leishmania
1452	61	12.2	2207	2	09U0V2	Q7R2Y8 giardia lam
1453	61	12.2	4561	2	07R2Y8	Q9U296 giardia lam
1454	61	12.1	99	1	RL12_METVA	P10623 methanococ
1455	60.5	12.1	105	1	RL93_SCHPO	096v33 schizosacch
1456	60.5	12.1	110	2	08Y0E4	08y0e4 ralsfontia s
1457	60.5	12.1	120	2	08G1Y9	08g1y9 brucella su
1458	60.5	12.1	133	2	06CAAI	06caai yarrowia 11
1459	60.5	12.1	138	1	CH16_DROME	P22977 drosophila
1460	60.5	12.1	138	2	09VSP4	Q9VSP4 drosophila
1461	60.5	12.1	140	2	08I7B8	08i7b8 echinococu
1462	60.5	12.1	144	2	08YF71	08yfl1 brucella me
1463	60.5	12.1	151	2	06ZPB3	06zpb3 homo sapien
1464	60.5	12.1	158	2	08PJU0	08pju0 xanthomonas
1465	60.5	12.1	159	2	09R9N6	Q9r9n6 rhizobium m
1466	60.5	12.1	162	2	065285	065285 cryza sattiv
1467	60.5	12.1	173	2	034300	034300 rhizobium e
1468	60.5	12.1	195	2	09XCD9	09xcd9 mycobacteri
1469	60.5	12.1	192	2	091658	Q9i658 pseudomonas
1470	60.5	12.1	200	2	08FZ71	08fz71 brucella su
1471	60.5	12.1	201	2	07NSI9	Q7nsi9 chromobacte
1472	60.5	12.1	203	2	09X811	09x811 streptomyc
1473	60.5	12.1	204	2	08YIP0	08yip0 brucella me
1474	60.5	12.1	208	2	063K03	063k03 burkholderi
1475	60.5	12.1	209	1	V282_ARATH	065421 arabidopsis
1476	60.5	12.1	212	2	065V57	065v57 mannheimia
1477	60.5	12.1	219	2	P71432	P71432 leptochrix
1478	60.5	12.1	223	2	08YPD3	08ypd3 anabaena sp
1479	60.5	12.1	223	2	07NTJ1	07ntl1 chromobacte
1480	60.5	12.1	225	1	B10D_MYCLE	P45466 mycobacteri
1481	60.5	12.1	227	2	09G608	Q9g608 diplophos t
1482	60.5	12.1	233	1	RNFE_YERPE	Q82d2 yerersinia p
1483	60.5	12.1	233	2	066AG9	066ag9 yerersinia ps
1484	60.5	12.1	239	2	Q7V8R1	Q7v8r1 prochloroc
1485	60.5	12.1	244	2	086530	086530 streptomyc
1486	60.5	12.1	246	2	08PGF5	08pgf5 xanthomonas
1487	60.5	12.1	254	2	Q7NUZ6	Q7nuz6 chromobacte
1488	60.5	12.1	259	2	Q922A5	Q922a5 rhizobium m
1489	60.5	12.1	259	2	Q712P6	Q712p6 mus musculu
1490	60.5	12.1	260	2	08Z6M0	08z6m0 salmoneila
1491	60.5	12.1	264	2	Q8TA14	Q8ta14 homo sapien

1492	60.5	12.1	265	2	023788	023788 cucumis sat
1493	60.5	12.1	266	2	08BL26	08bl26 mus muscula
1494	60.5	12.1	267	2	084G51	084g51 rhizobium 1
1495	60.5	12.1	267	2	08PGR6	08pgr6 xanthomonas
1496	60.5	12.1	270	2	072GR6	Q72gr6 thermus the
1497	60.5	12.1	277	2	082168	082168 streptomyces
1498	60.5	12.1	284	2	Q7WNA1	Q7wna1 bordetella
1499	60.5	12.1	292	2	Q9T2S9	Q9t2s9 plasmodium
1500	60.5	12.1	297	2	06AUF2	06auf2 oryza sativa
ALIGNMENTS						
RESULT 1						
UGR2_HUMAN	STANDARD;	PRT;	104 AA.			
ID	UGR2_HUMAN	Q96OR1; Q96PL0;				
AC	Q96OR1; Q96PL0;	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Created)	05-JUL-2004 (Rel. 44, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last sequence update)	25-JAN-2005 (Rel. 46, Last annotation update)				
DE	Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1) (Pneumo secretory protein 2) (PnSP-2) (UNQ629/PRO1245).					
DE	2) (PnSP-2) (UNQ629/PRO1245).					
GN	Name=SCGB3A1; Synonyms=HIN1, PnSP2, UGRP2;					
OS	Homo sapiens (human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=21396515; PubMed=11481438; DOI=10.1073/pnas.171138398;					
RA	Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVengle R., Seth P.,					
RA	Keelin C.M., Knei E., Boesenberg M., Schmitt S., Marks J.R., Pagon Z.,					
RA	Bellina D., Razumovic J., Polyak K.,					
RT	"HIN-1, a putative cytokine highly expressed in normal but not					
RT	cancerous mammary epithelial cells."					
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).					
RL	[2]					
RN	SEQUENCE FROM N.A.					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=21539178; PubMed=11682631; DOI=10.1210/me.15.11.2021;					
RA	Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,					
RA	Klimura S.,					
RT	"UGRP1, a uteroglobin/clara cell secretory protein-related protein, is					
RT	a novel lung-enriched downstream target gene for the T/BBP/NKX2.1					
RL	homedomain transcription factor."					
RL	Mol. Endocrinol. 15:2021-2036(2001).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RA	Clippe A., Laing I.A., Lesouef P.N., Bernard A., Knops B.,					
RT	"Molecular cloning of PnSP-1, a protein of the respiratory tract with					
RT	potential association to atopy."					
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,					
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel P.,					
RA	Raton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,					
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,					
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,					
RA	Seahagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,					
RA	Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yatsura D.,					
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment."					
RL	Genome Res. 13:2265-2270(2003).					
RN	[5]					
RP	SEQUENCE FROM N.A.					
RT	TISSUE=Brain;					
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RX						



RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shmura C.M., Schuler G.D.,  
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Diatchenko L., Manolagas S.C., Moore T., Max S.I., Wang J., Heide F.,  
 RA Stancovski I., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.W., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whitting M., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Schmutz J., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skala U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RP SEQUENCE OF 21-35.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites";  
 RL Protein Sci. 13:2819-2824(2004).  
 CC -1- FUNCTION. Potential growth inhibitory cytokine.  
 CC -1- TISSUE SPECIFICITY. Highly expressed in breast tissues. Absent in  
 CC breast cancer cell lines.  
 CC -1- SIMILARITY. Belongs to the uteroglobin family. UGRP subfamily.  
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 DR EMBL; AY040564; AAK82942.1; -  
 DR EMBL; AF313458; AAL26217.1; -  
 DR EMBL; AF316839; AAO04481.1; -  
 DR EMBL; AY350864; AAO08423.1; -  
 DR EMBL; BC029176; AAH29176.1; -  
 DR Gene; HGNC:18384; SCGB3A1.  
 DR H-InvDB; HIX0005498; -  
 DR MIM; 606500; -  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0005125; F:cytokine activity; NAS.  
 DR GO; GO:0003088; P:negative regulation of cell growth; NAS.  
 DR GO; GO:0042127; P:regulation of cell proliferation; NAS.  
 DR Cytokine; Direct protein sequencing; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 104 Uteroglobin-related protein 2.  
 FT COMPLET 19 19 A--R (in Ref. 1).  
 SQ SEQUENCE 104 AA; 10100 MM; CAA0951F8F1455F CRC64;  
 Query Match 100.0%; Score 502; DB 1; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-36;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLAALGLCVALLSCSSAAAFVSGS-APVAPVAALESAAEAGAGTLANPLGTNPL 60  
 Db 1 MKLAALGLCVALLSCSSAAAFVSGS-APVAPVAALESAAEAGAGTLANPLGTNPL 60  
 QY 61 LSSLGLIPVNHLESGSKCVAEIGPQAVGAVKALIKALLGLATVFG 104  
 Db 61 LSSLGLIPVNHLESGSKCVAEIGPQAVGAVKALIKALLGLATVFG 104

RESULT 2

Q71MT8  
 ID Q71MT8 PRELIMINARY; PRT; 104 AA.  
 AC Q71MT8  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Pseudo secretory protein 2.  
 GN Name=Psp2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mistar;  
 RA Clippe A., Laing I.A., Lesouef P.N., Bernard A., Knoops B.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF36841; AAO04483.1; -  
 SQ SEQUENCE 104 AA; 10512 MM; FDB870D75750F9E6 CRC64;  
 Query Match 52.0%; Score 261; DB 2; Length 104;  
 Best Local Similarity 59.8%; Pred. No. 2.7e-15;  
 Matches 64; Conservative 13; Mismatches 24; Indels 6; Gaps 4;  
 QY 1 MKLAALGLCVALLSCSSAAAFVSGS-APVAPVAALESAAEAGAGTLANPLGTNPL 57  
 Db 1 MKLAALGLCVALLSCSSAAAFVSGS-APVAPVAALESAAEAGAGTLANPLGTNPL 57  
 QY 61 LSSLGLIPVNHLESGSKCVAEIGPQAVGAVKALIKALLGLATVFG 104  
 Db 61 LSSLGLIPVNHLESGSKCVAEIGPQAVGAVKALIKALLGLATVFG 104  
 RESULT 3  
 UGR2\_MOUSE  
 ID UGR2\_MOUSE STANDARD; PRT; 104 AA.  
 AC Q920D7;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in  
 DE normal-1) (Secretoglobin family 3A member 1) (Pseudo secretory protein  
 DE 2) (Psp-2).  
 GN Name=Scgb3a1; Synonyms=Hn1, Psp2, UGRP2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=2139515; PubMed=11481438; DOI=10.1073/pnas.171138398;  
 RA Krop I.E., Syro D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,  
 RA Kaelin C.M., Rhee E., Rosenberg M., Schmitt S., Marks J.R., Pagon Z.,  
 RA Belina D., Razumovic J., Poljak K.;  
 RT "HIN-1, a putative cytokine highly expressed in normal but not  
 RT cancerous mammary epithelial cells";  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21539178; PubMed=11682631; DOI=10.1210/me.15.11.2021;  
 RA Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,  
 RA Kimura S.;  
 RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is  
 RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1  
 RT homeodomain transcription factor";  
 RL Mol. Endocrinol. 15:2021-2036(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WMR1;  
 RA Clippe A., Laing I.A., Lesouef P.N., Bernard A., Knoops B.;  
 RT "Molecular cloning of Psp-1, a protein of the respiratory tract with  
 RT potential association to atopy";  
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

```

CC -1- FUNCTION: Potential growth inhibitory cytokine.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
CC -----
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CC -----
CC EMBL: AF313456; AAL26216.1; -.
CC EMBL: AF436840; AAQ04482.1; -.
CC MGD; MGI:1915912; Scg33a1.
CC Cytokine; Signal.
CC SIGNL.
CC CHAIN 1 21 Potential.
CC FT 22 104 Uteroglobin-related protein 2.
CC SEQUENCE 104 AA; 10591 MW; D62F0E601FB57A6D CRC64;

Query Match 49.8%; Score 250; DB 1; Length 104;
Best Local Similarity 57.0%; Pred. No. 2.5e-14;
Matches 61; Conservative 14; Mismatches 26; Indels 6; Gaps 4;

QY 1 MKL--AALLIGCVALLSCSSAAAFVGS-AKPVAPVAALSSAAGAGTLAN-PLGTINPL 57
DB 1 MKLTTPLVLCVALLSDSGVAFPMDSLAKPAVEPVAAALPAALAAVAGAVPSPLSHLAIL 60

QY 58 KLLSLSGIPVNHILIEGOKCVAELGPQAVGAVKALKALGALTIVFG 104
DB 61 RFLIAMSIGIPLDPLIESRKCVTELGPBAVAV--KSLIGVLTIVFG 104

RESULT 4
QY 07M741 PRELIMINARY; PRT; 93 AA.
AC 07M741;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HINI (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22338213; PubMed=12406855;
RA Reynolds S.D., Reynolds P.R., Pryhuber G.S., Finder J.D., Stripp B.R.,
RT "Secretoglobins SCGB3A1 and SCGB3A2 define secretory cell subsets in
RT mouse and human airways."
RL Am. J. Respir. Crit. Care Med. 166:1498-1509(2002).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL: BK000202; DAA00359.1; -.
FT NON_TER
SQ SEQUENCE 93 AA; 9319 MW; D3E2F96A9380DF70 CRC64;

Query Match 46.2%; Score 232; DB 2; Length 93;
Best Local Similarity 57.1%; Pred. No. 8.5e-13;
Matches 56; Conservative 15; Mismatches 19; Indels 8; Gaps 4;

QY 9 LCVALSCSSAAAFVGS-AKPVAPVAALSSAAGAGTLAN-PLGTINPLKLLSLSLGI 66
DB 2 LCVAL--VGAVPLVSLAKPAVEPVAAITAAEAVAGAVPSPLSHLILRFIVSLGI 58

QY 67 PVNHILIEGOKCVAELGPQAVGAVKALKALGALTIVFG 104
DB 59 PLDPLIDGSRKCVTELGPBAVAV--KSLIGALTIVFG 93

RESULT 5
Q8CJC6

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ID 08CJC6 PRELIMINARY; PRT; 94 AA.
AC 08CJC6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE UGRP2 type B.
DE Name=Scg33a1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22326074; PubMed=12438750; DOI=10.1159/000064067;
RA Niimi T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodas A.,
RA Zimonjic D.B., Keck-Waggoner C.L., Popescu N.C., Kimura S.,
RT "Cloning, expression, and chromosomal localization of the mouse gene
RT (Scg33a1, alias Ugrp2) that encodes a member of the novel uteroglobin-
RT related protein gene family."
RL Cytogenet. Genome Res. 97:120-127(2002).
DR EMBL: AF313457; AAN62328.1; -.
DR MGD; MGI:1915912; Scg33a1.
DR GO; GO:0005615; Extracellular space; TAS.
SQ SEQUENCE 94 AA; 9578 MW; 7C84B908A6365B59 CRC64;

Query Match 44.8%; Score 225; DB 2; Length 94;
Best Local Similarity 57.3%; Pred. No. 3.5e-12;
Matches 51; Conservative 14; Mismatches 20; Indels 4; Gaps 2;

QY 17 SAAAFVGSAPVAPVAAALSSAAGAGTLAN-PLGTINPLKLLSLSGIPVNHILIEG 75
DB 9 SVAFFWDSLAKPAVEPVAAALPAALAAVAGAVPSPLSHLILRFILASMGIPLDPLIEG 68

QY 76 QKCVAEIPQAVGAVKALKALGALTIVFG 104
DB 69 RKCVELGPBAVAV--KSLIGVLTIVFG 94

RESULT 6
QY 096PL1 STANDARD; PRT; 93 AA.
ID 096PL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
DE member 2) (Pneumo secretory protein 1) (Pnsp-1) (UNQ566/PRO1128).
GN Name=SCGB3A2; Synonyms=PNSP1, UGRP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539178; PubMed=11682631; DOI=10.1210/me.15.11.2021;
RA Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
RA Kimura S.,
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1
RT homeodomain transcription factor."
RL Mol. Endocrinol. 15:2021-2036(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Clippe A., Laing I.A., Lessouef P.N., Bernard A., Knoops B.,
RT "Molecular cloning of Pnsp-1, a protein of the respiratory tract with
RT potential association to atopy."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

QY 13
RP SEQUENCE FROM N.A.
RX MEDLINE=22867296; PubMed=12915309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heidens S.,

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RA Huang A., Kim H.S., Klimewski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,  
 RA Seethagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,  
 RA Vanden R., Watson C., Wleand D., Woods K., Xie M.-H., Yansura D.,  
 RA Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P., Gray A.,  
 RT "The secreted protein discovery initiative (SDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,

RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Hsieh N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stadler M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Gitwood J., Schmitz J., Myers R.M.,

RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- SUBUNIT: Homodimer.

CC -1- TISSUE SPECIFICITY: Highly expressed in lung.

CC -1- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.

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CC -----

DR EMBL; AF313455; AAL26215.1; -

DR EMBL; AF439544; AA004559.1; -

DR EMBL; AF439545; AA004560.1; -

DR EMBL; AY388979; AA089358.1; -

DR EMBL; BC024232; AA424232.1; -

DR Genew; HGNC:18391; SCGB3A2.

DR H-invDB; HIX0005286; -

DR MIM; 606531; -

DR Signal.

KW SIGNAL.

FT CHAIN

SEQUENCE 93 AA; 10161 MW; FBD4BFC2BF3718 CRC64;

Query Match

Best Local Similarity 43.6%; Pred. No. 1.7e-06; Length 93;

Matches 44; Conservative 9; Mismatches 38; Indels 10; Gaps 2;

QY 1 MKLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 59

Db 1 MKLVITFLVLTSLSCYSATAPLANKVPLPVDKLPL-----PLDNLTPMDPLK 51

QY 60 LLSLGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 52 LKTLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

RESULT 7  
 ID 071MM7 PRELIMINARY; PRT; 93 AA.  
 AC 071MM7  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 GN Pseudo secretory protein 1.  
 OS Name=Pnsp1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mistar;  
 RA Clippe A., Laing I.A., Lesouef P.N., Bernard A., Knops B.;  
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF439547; AA004562.1; -

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62  
 Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54  
 QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100  
 Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

Query Match

Best Local Similarity 29.6%; Score 148.5; DB 2; Length 93;

Matches 40; Conservative 10; Mismatches 35; Indels 13; Gaps 2;

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54

QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

RESULT 8

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54

QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54

QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54

QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54

QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54

QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54

QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 8 LKLVITGLC-----GYSATAPFLINSVPLPVDKLPL-----PLDNLTPMDPLK 54

QY 63 STGLIPVNHLEGSOKCVAEFGPOAVGAVKALKALGAL 100

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

Db 55 TLGLISVEHLVEGLRKCVNELGPEASEAVKKLIALSHL 92

QY 3 LLAALGLCVALS-SSAAFLVGSAPVAPVVALESAAAGAGTLANPLGTINPKLT 62

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CC Name=B;
CC IsoId=Q220H1.3; Sequence=VSP_006726;
CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
CC -1- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL: AF274959; AAL25708.1; -.
DR EMBL: AF274960; AAL25709.1; -.
DR EMBL: AF274961; AAL25710.1; -.
DR EMBL: AF439546; AAQ04561.1; -.
DR MGD: MGI:2153470; Scg3a2.
DR GO: GO:0005576; C:extracellular; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR InterPro: IPR006038; Uteroglobin_supf.
DR Pfam: PF01099; Uteroglobin; 1.
KW Alternative splicing; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 139 Uteroglobin-related protein 1.
FT FT VSVLFLPMICAYPRDSKKQTFARLERVEGSKL -> EALS
FT VARSPDIC 107 139 HLV (in isoform B).
FT FT /FTId=VSP_006726.
FT VARSPDIC 85 91 VITICST -> EALSHIV (in isoform A).
FT FT /FTId=VSP_006727.
FT VARSPDIC 92 139 Missing (in isoform A).
FT FT /FTId=VSP_006728.
SQ SEQUENCE 139 AA; 15431 MW; 8A2PB08B41B6554 CRC64;

Query Match 26.9%; Score 135; DB 1; Length 139;
Best Local Similarity 35.1%; Pred. No. 0.00037;
Matches 34; Conservative 17; Mismatches 36; Indels 10; Gaps 1;

QY 1 MKLAALLGCVALLSCSSNAAPLYGSAKPPVAQPVAALESAAAGTLANPLKLL 60
DB 1 MKLVSIFFLVTTIGICGVSATALLINRLPVVDKLPV-----PLDDIIPSFDPKML 50

QY 61 LLSLGIIPVNHLEIGSQKVAELGPOAVGAVKALKLL 97
DB 51 LKTLGISVEHLVTGKKCVDELGPBAGAVKALLVII 87

RESULT 9
O82LN6 PRELIMINARY; PRT; 255 AA.
ID O82LN6;
AC 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative methionine aminopeptidase.
GN OrderedLocusNames=SAV1974.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.

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```

RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RL Nat. Biotechnol. 21:526-531(2003).
CC -1- FUNCTION: Removes the amino-terminal methionine from nascent
CC proteins (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
CC preferentially methionine, from peptides and arylamides.
CC -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family M24a.
DR EMBL: AP005029; BAC69685.1; -.
DR HSSP: Q9X117; 100X.
DR GO: GO:0004239; F:methionyl aminopeptidase activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002467; Pept_M24A_MAP.
DR InterPro: IPR001714; Pept_M24A_MAP.
DR Pfam: PF00557; Peptidase_M24_1.
DR PRINTS: PR00599; MAPEPTIDASE.
DR TIGRFAMs: TIGR00500; met_pdae_1.
KW Aminopeptidase; Cobalt; Complete proteome; Hydrolyase; Protease.
SQ SEQUENCE 255 AA; 26727 MW; 0C41CD3010F855A3 CRC64;

Query Match 17.5%; Score 88; DB 2; Length 255;
Best Local Similarity 31.6%; Pred. No. 8.2;
Matches 31; Conservative 16; Mismatches 19; Indels 32; Gaps 6;

QY 7 LGLCVA--LSCSSAAPLYGSAKPPVAQPVAALE-----SAAEGA--GTLANPL 51
DB 99 LDDAVARGGVADAAISFLVGKRP-ASVYAMIEATERALAGIAAKKGAIRIGDLSHA 157

QY 52 GTLNPPLKLLSLGIIPVNHLEIGSQKVAELGPOAVGA 89
DB 158 GT-----VLSKAGYRIN-----TEFGSHGIGS 179

RESULT 10
O8FST3 PRELIMINARY; PRT; 281 AA.
ID O8FST3;
AC 08FST3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CE0299;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Ueda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojohori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens."
RL Genome Res. 13:1572-1579(2003).
DR EMBL: AP005215; BAC17109.1; -.
DR InterPro: IPR001992; Bact_sec_systII.
DR Pfam: PF00482; GSP11_F_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 281 AA; 28188 MW; 3143B69C35048C2D CRC64;

Query Match 16.6%; Score 83.5; DB 2; Length 281;
Best Local Similarity 30.1%; Pred. No. 22;
Matches 40; Conservative 9; Mismatches 45; Indels 39; Gaps 7;

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Oy 3 LAALIGCV-----ALSCSAAFLVNGSAKPVAAVPALESAAE-----AGAGTTL 47  
 Db 106 LAGLGLGICGNLRGAPMADMDHALHRTTGSAGPTTVALTAARRVSGSGSAAYL 165  
 Oy 48 ANP-----LGLT-----NPLKLTLSSLCIPVNHILEGS-----QCVNEL-GPOAV 87  
 Db 166 IDAPTMOLRLGRTIWESEHNGIFVRLDLQ-----KHLLEAOERHROASAAOLQGPQAT 221  
 Oy 88 GAVKALKALLGAL 100  
 Db 222 AVTIALPLAGVL 234

RESULT 11  
 ID TNK1 HUMAN STANDARD; PRT, 1327 AA.  
 AC 095271; 095272;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Tankyrase 1 (EC 2.4.2.30) (TNK1) (Tankyrase I) (TNKS-1) (TRF1-  
 GN Name-TNKS; Synonyms-PARP, TIN1, TINFL, TNKSI;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RX SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Testis;  
 RX MEDLINE=99040105; PubMed=9822378; DOI=10.1126/science.282.5393.1484;  
 RA Smith S., Girtat I., Schmitz A., de Lange T.;  
 RT "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";  
 RL Science 282:1484-1487(1998).  
 [2]  
 RX SUBCELLULAR LOCATION.  
 RX MEDLINE=99454782; PubMed=10523501;  
 RA Smith S., de Lange T.;  
 RT "Cell cycle dependent localization of the telomeric PARP, tankyrase,  
 to nucleolar pore complexes and centrosomes.";  
 RL J. Cell Sci. 112:3649-3656(1999).  
 [3]  
 RX FUNCTION, AND PHOSPHORYLATION.  
 RX MEDLINE=20556282; PubMed=10988299; DOI=10.1074/jbc.M007635200;  
 RA Chi N.-W., Lodish H.F.;  
 RT "Tankyrase is a Golgi-associated mitogen-activated protein kinase  
 substrate that interacts with IRAP in GLUT4 vesicles.";  
 RL J. Biol. Chem. 275:38437-38444(2000).  
 [4]  
 RX FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.  
 RX MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002;  
 RA Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;  
 RT "Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2  
 at human telomeres.";  
 RL Mol. Cell. Biol. 22:332-342(2002).  
 [5]  
 RX IDENTIFICATION IN A COMPLEX WITH PRT1, TERF1 AND TINF2.  
 RX PubMed=12768206; DOI=10.1038/nature01688;  
 RA Loayza D., De Lange T.;  
 RT "PRT1 as a terminal transducer of TRF1 telomere length control.";  
 RL Nature 424:1013-1018(2003).  
 CC -1- FUNCTION: May regulate vesicle trafficking and modulate the  
 subcellular distribution of SLG2A4/GUT4-vesicles. Has PARP  
 activity and can modify TERP1, and thereby contribute to the  
 regulation of telomere length.  
 CC -1- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-riboseyl}(n)-acceptor =  
 nicotinamide + {ADP-D-riboseyl}(N+1)-acceptor.  
 CC -1- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with  
 the cytoplasmic domain of INPEP/Orase in SLG2A4/GUT4-vesicles.  
 CC Binds to the N-terminus of telomeric TERP1 via the ANK repeats.  
 CC Found in a complex with PRT1, TERP1 and TINF2.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and

CC with juxtanuclear SLG2A4/GUT4-vesicles. A minor proportion is  
 CC also found at nuclear pore complexes and around the pericentriolar  
 CC matrix of mitotic centrosomes. During interphase, a small fraction  
 CC of TNKS is found in the nucleus, associated with TERP1.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=095271-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=095271-2; Sequence=VSP\_004538, VSP\_004539;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.  
 CC -1- PTM: Phosphorylated on serine residues by MAPK kinases upon  
 CC insulin stimulation.  
 CC -1- PTM: ADP-ribosylated (-auto).  
 CC -1- SIMILARITY: Belongs to the PARP family.  
 CC -1- SIMILARITY: Contains 15 ANK repeats.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -----  
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 CC -----  
 CC EMBL, AF082556; AAC79841.1; -;  
 CC EMBL, AF082557; AAC79842.1; -;  
 CC EMBL, AF082558; AAC79843.1; -;  
 CC EMBL, AF082559; AAC79844.1; -;  
 CC HSSP, P6157; IN11.  
 CC GeneW, HGNC:11941; TNKS.  
 CC MIM, 603303; -;  
 CC DR GO, GO:0000781; C:chromosome, telomeric region, IDA.  
 CC DR GO, GO:0003950; F:NAD+ ADP-ribosyltransferase activity, IDA.  
 CC DR GO, GO:0005515; F:protein binding, IPI.  
 CC DR GO, GO:0007004; P:telomerase-dependent telomere maintenance; NAS.  
 CC InterPro, IPR001600; SAM.  
 CC Pfam, PF00023; ANK, 19.  
 CC SMART, SM00248; SAM, 1.  
 CC SMART, SM00248; ANK, 17.  
 CC DR PROSITE, PS50088; ANK\_REPEAT, 15.  
 CC DR PROSITE, PS50297; ANK\_REPEAT\_REGION, 1.  
 CC DR PROSITE, PS50105; SAM\_DOMAIN, 1.  
 CC ADP-ribosylation; Alternative splicing; ANK repeat;  
 CC Glycosyltransferase; Golgi stack; NAD; Nuclear protein;  
 CC Phosphorylation; Repeat; Telomere; Transferase.  
 CC REPEAT 215 247 ANK 1.  
 CC REPEAT 248 280 ANK 2.  
 CC REPEAT 281 313 ANK 3.  
 CC REPEAT 368 400 ANK 4.  
 CC REPEAT 401 433 ANK 5.  
 CC REPEAT 434 466 ANK 6.  
 CC REPEAT 521 556 ANK 7.  
 CC REPEAT 557 589 ANK 8.  
 CC REPEAT 590 622 ANK 9.  
 CC REPEAT 683 715 ANK 10.  
 CC REPEAT 716 748 ANK 11.  
 CC REPEAT 749 781 ANK 12.  
 CC REPEAT 836 868 ANK 13.  
 CC REPEAT 869 901 ANK 14.  
 CC REPEAT 902 934 ANK 15.  
 CC DOMAIN 1030 1089 SAM.  
 CC DOMAIN 1176 1327 PARP.  
 CC DOMAIN 9 14 Poly-His.  
 CC DOMAIN 27 34 Poly-Pro.  
 CC DOMAIN 128 134 Poly-Ser.  
 CC DOMAIN 137 145 Poly-Ser.  
 CC VARSPPLIC 641 643 EST -> GHS (in isoform 2).  
 CC VARSPPLIC 644 1327 /PTId=VSP\_004538.  
 CC Missing (in isoform 2).

```

FT      MUTAGEN      1184      1184      /FTId=VSP_004539.
FT      MUTAGEN      1291      1291      H->A: loss of activity; when associated
FT      MUTAGEN      1291      1291      with A-1291.
FT      SEQUENCE      1327 AA; 142010 MW; E14DE985C710B957 CRC64;
SQ
Query Match      16.5%; Score 83; DB 1; Length 1327;
Best Local Similarity 30.5%; Pred. No. 99;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY      15 CSSAAAFVGSAXPVAQPVAALESAA-----EAGAGTIANPLGTINPLKLLISLGPVN 69
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      90 CSTTSTICTVAAAPVV-PAVSTSSAGAVAPNPAAGSGNNPSSSSPTSSSSSPSSPGS 148
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      70 HLIBGSG---KCVAEIGPQAVGAVKAKLLGAL 100
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      149 SLAESPEAGVSSSTPAFGAAGPGTGVPAVSGAL 183
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
ID      Q9K3G4      PRELIMINARY;      PRT;      247 AA.
AC      Q9K3G4;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical protein SC01277.
GN      ORFNames=SCG18.24;
OS      Streptomyces coelicolor.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycineae; Streptomycetaceae; Streptomycetes.
OX      NCBI_TaxID=1902;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2) / M145;
RX      MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA      Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA      Thomson N.R., James K.D., Harris D.B., Quail M.A., Kleiser H.,
RA      Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA      Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA      Huang C.-H., Kleiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA      Rabinowitch R., Rajandream M.A., Rutherford K.M., Rutter S.,
RA      Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA      Warren T., Wietorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
RA      Hopwood D.A.;
RT      "Complete genome sequence of the model actinomycete Streptomyces
RT      coelicolor A3(2).";
RL      Nature 417:141-147(2002).
RW      EMBL: AL939108; CAB99157.1; -.
KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE 247 AA; 22950 MW; EE32ABD6146881B CRC64;

Query Match      16.4%; Score 82.5; DB 2; Length 247;
Best Local Similarity 31.8%; Pred. No. 24;
Matches 34; Conservative 10; Mismatches 40; Indels 23; Gaps 5;

QY      17 SAAAFVGSAXP-----VAQPVAALESAAEAG-----AGTIANPLGTL-----NPLKL 59
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      61 NALAAAGAVNPAATAGVTNPPLAALGGIAGAAGPLAGLAAGAAGPAGTGAAGNPPLAA 120
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      60 LLSSL--GIIVNHLIESQKVAELGPQAVGAVKAKLLGALTVP 104
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      121 LTGAAGGNPLAALGAGNPPLAALG---GAANPLAAVGAAGALG 163
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
ID      Q98CR1      PRELIMINARY;      PRT;      694 AA.
AC      Q98CR1;
DT      01-OCT-2001 (TrEMBLrel. 18, Created)
DT      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE      M15043 protein.
GN      OrededilocusNames=m15043;
OS      Rhizobium loti (Mesorhizobium loti).
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Phyllobacteriaceae; Mesorhizobium.
OX      NCBI_TaxID=381;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      SRRAIN=MAFP303099;
RX      MEDLINE=21082930; PubMed=11214968;
RA      Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA      Matanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,
RA      Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
RA      Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA      Takenuchi C., Yamada M., Tabeta S.;
RT      "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT      Mesorhizobium loti.";
RL      DNA Res. 7:331-338(2000).
DR      EMBL; AP003005; BAB51560.1; -.
DR      InterPro; IPR003781; COA_binding.
DR      InterPro; IPR001412; tRNA_synt_I.
DR      Pfam; PF02629; COA_binding; 1.
DR      PROSITE; PS00178; AA_trna_LIGASE_I; UNKNOWN_1.
KW      Complete proteome.
SQ      SEQUENCE 694 AA; 73126 MW; 19E4978531DCF6CC CRC64;

Query Match      16.4%; Score 82.5; DB 2; Length 694;
Best Local Similarity 33.3%; Pred. No. 61;
Matches 33; Conservative 11; Mismatches 42; Indels 13; Gaps 4;

QY      3 LALLGCVALLSSSAAAFVGS-APVAPQVAALESAAAGATLANPLGTINP-----L 57
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      438 MWPLFGISEMDAGAAAFGMAWAEPOAPVDT--SAAAGAG-----GHVTPDEAEA 489
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      58 KLLLSLGIPIVNHILIESQKVAELGPQAVGAVKAKAL 96
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      490 KARLIRAGLVPVPGERAGNVAEIVISSMALGFPVALKAL 528
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 14
ID      Q6H4X3      PRELIMINARY;      PRT;      117 AA.
AC      Q6H4X3;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Hypothetical protein OSJNBa0085K21.14 (Hypothetical protein
DE      OSJNBa0023117.30).
GN      Name=OSJNBa0085K21.14; Synonyms=OSJNBa0023117.30;
OS      Oryza sativa (japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaceae; Oryza.
OX      NCBI_TaxID=39947;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sasaki T., Matsumoto T., Katayose Y.;
RL      Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Sasaki T., Matsumoto T., Yamamoto K.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF005804; BAD26226.1; -.
DR      EMBL; AP004863; BAD25557.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE 117 AA; 11719 MW; 2A7303E30D68D0BD CRC64;

Query Match      16.3%; Score 82; DB 2; Length 117;
Best Local Similarity 32.9%; Pred. No. 14;
Matches 26; Conservative 9; Mismatches 34; Indels 10; Gaps 2;

QY      6 LLGLCVALLSSSAAAFVGSAXPVAQPVAALESAAEAGATLAN-----PLGT-----LN 55
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Db 17 LLSCAVAASHHTAAAAAGSTSPPAAPQLGMPRSATAGCGMRTGRTREYTPGTLPSPQLP 76  
 QY 56 PLKLLSLIGIPVNHLEIG 74  
 Db 77 PIVQFPPTLPVPPGMAAG 95

## RESULT 15

062CF0 PRELIMINARY; PRT; 540 AA.  
 ID 062CF0  
 AC 062CF0;  
 DT 25-OCT-2004 (TRENBLrel. 28, Created)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
 DE di-haem cytochrome c peroxidase family protein.  
 GN ORFNames=BMAA0945;  
 OS Burkholderia mallei ATCC 23344.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia.  
 OX NCBI\_TaxID=243160;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 23344;  
 RA Niernan W.C., Deshazer D., Kim H.S., Tetteijn H., Nelson K.E.,  
 RA Feldblyum T., Ulrich R.L., Roming C.M., Brinkac L.M., Daugherty S.C.,  
 RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,  
 RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,  
 RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarría S.,  
 RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,  
 RA Zhou L., Fraser C.M.;  
 RT "Structural flexibility in the Burkholderia mallei genome.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).  
 DR EMBL; CP000011; AAU46131.1; -.  
 KW Peroxidase.  
 SQ SEQUENCE 540 AA; 57096 MM; 298E2A368B38ED9 CRC64;

Query Match 16.3%; Score 82; DB 2; Length 540;  
 Best Local Similarity 32.0%; Pred. No. 54;  
 Matches 31; Conservative 12; Mismatches 34; Indels 20; Gaps 5;

QY 14 SCSGAAPFLVGSAPK-----VAQPVAALESAAEAGTLAN--PL-----GTINPLK 58  
 Db 55 ACASATAFASGAAPGALDAVRAHYPASSLSPTFTPGAGAAHVQEPQALRAKASPS 114  
 QY 59 LLLSLIGIPVNHLEIGS--QKCVAEIG--POAVGAV 90  
 Db 115 SLPPSPSPPTTSLPGAPQGRVAVATIGRTGPVASKV 151

Search completed: March 5, 2005, 21:27:23  
 Job time : 224 secs



GenCore version 5.1.6  
OM protein - protein search, using sw model  
Run on: March 5, 2005, 21:19:54 ; Search time 163 Seconds  
(without alignments)  
246.767 Million cell updates/sec

Title: US-09-989-731-408  
Sequence: 1 MKLAALLGLCVALLSCSSAAA.....QAVGAVKALKALLGALTVEG 104  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
2105692 segs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV65757	standard;	protein;	104	AA.	
DE	Membrane-bound protein					PRO1245.
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 3;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 2						
ID	AAV44458	standard;	protein;	104	AA.	
DE	Human lung specific gene protein					Ing107.
PN	WO960160-A1.					
PD	25-NOV-1999.					
PA	(DIAD-) DIADEXUS LLC.					
Query Match		100.0%;	Score 502;	DB 3;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 3						
ID	AAV87288	standard;	protein;	104	AA.	
DE	Human signal peptide containing protein					HSP-65 SEQ ID NO:65.
PN	WO20000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match		100.0%;	Score 502;	DB 3;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 4						
ID	AAV65280	standard;	protein;	104	AA.	
DE	Human PRO1245 (UNO629) protein sequence					SEQ ID NO:408.
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 4;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 5						
ID	AAV86141	standard;	protein;	104	AA.	
DE	Human PRO1245 polypeptide.					
PN	WO200153486-A1.					
PD	26-JUL-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 5;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 6						
ID	ABU58095	standard;	protein;	104	AA.	

DE	Human PRO polypeptide	#127.				
PN	US2003027163-A1.					
PD	06-FEB-2003.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 7						
ID	ABU59173	standard;	protein;	104	AA.	
DE	Novel human secreted or transmembrane protein					PRO1245.
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 8						
ID	ABU82685	standard;	protein;	104	AA.	
DE	Human secreted/transmembrane protein					PRO1245.
PN	US2003032023-A1.					
PD	13-FEB-2003.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 9						
ID	AAO19895	standard;	protein;	104	AA.	
DE	Human uteroglobin related protein					2.
PN	WO2003000111-A2.					
PD	03-JAN-2003.					
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 10						
ID	ABU60604	standard;	protein;	104	AA.	
DE	Human secreted/transmembrane protein,					#163.
PN	US2002160384-A1.					
PD	31-OCT-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 11						
ID	ABU13986	standard;	protein;	104	AA.	
DE	Human PRO1245 polypeptide.					
PN	US2002103125-A1.					
PD	01-AUG-2002.					
PA	(GETH ) GENENTECH LTD.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 12						
ID	ABU72571	standard;	protein;	104	AA.	
DE	Novel human secreted and transmembrane protein					PRO1245.
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 13						
ID	ABU59320	standard;	protein;	104	AA.	
DE	Human secreted/transmembrane protein,					#163.
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 14						
ID	ABO26017	standard;	protein;	104	AA.	
DE	Human PRO1245 polypeptide.					
PN	US2002127576-A1.					
PD	12-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 502;	DB 6;	Length 104;	
Best Local Similarity		100.0%;	Pred. No. 2e-48;			
RESULT 15						
ID	ABU59026	standard;	protein;	104	AA.	
DE	Human secreted/transmembrane protein,					#163.
PN	US2002142961-A1.					
PD	03-OCT-2002.					
PA	(GETH ) GENENTECH INC.					

Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 16  
ID ABU92404 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 17  
ID ABU59469 standard; protein; 104 AA.  
DE Novel human secreted or transmembrane protein PRO1358.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 18  
ID ABU92235 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 19  
ID ABU10941 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 20  
ID ABU81693 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 21  
ID ABU8632 standard; protein; 104 AA.  
DE Human secreted and transmembrane polypeptide PRO1245.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 22  
ID ABO34146 standard; protein; 104 AA.  
DE Human PRO1245 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 23  
ID ADA37919 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 24  
ID ADA21605 standard; protein; 104 AA.  
DE Human secreted/transmembrane polypeptide PRO1245.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 25  
ID ADA10392 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein, PRO1245.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 26  
ID ADA17936 standard; protein; 104 AA.  
DE Human PRO1245 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 27  
ID ADA28044 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 28  
ID ADA94624 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 29  
ID ADA38849 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 30  
ID ADA2970 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 31  
ID ABO53232 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 32  
ID ADA2531 standard; protein; 104 AA.  
DE Human secreted/transmembrane polypeptide PRO1245.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 502; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 33  
ID ABO22602 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 502; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 34  
ID ADA0697 standard; protein; 104 AA.  
DE Human secreted/transmembrane PRO polypeptide #127.  
PN US2003049658-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 502; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 35  
ID ADA39390 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 502; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;

RESULT 36  
ID ADB96416 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 37  
ID ADC57888 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 38  
ID ADC53522 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 39  
ID ADC12119 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 40  
ID ADC65541 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 41  
ID ADC65541 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 42  
ID ADC07596 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 43  
ID ADC14708 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 44  
ID ADD08240 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 45  
ID ADC82065 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 46  
ID ADD07707 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.

PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 47  
ID ADC82598 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 48  
ID ADD08778 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 49  
ID ADD07027 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 50  
ID ADC83274 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 51  
ID ADD55381 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 52  
ID ADD56339 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 53  
ID ADD54777 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 54  
ID ADE26931 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 55  
ID ADE26398 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 7; Length 104;  
Pred. No. 2e-48;  
RESULT 56  
ID ADF67335 standard; protein; 104 AA.  
DE Human PRO1245 amino acid sequence SEQ ID NO:408.

PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 57  
ID ADI35589 standard; protein; 104 AA.  
DE Human PRO polypeptide #127.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 502; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 58  
ID ADJ37309 standard; protein; 104 AA.  
DE Human tumour therapy associated PRO1245.  
PN US2003211096-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 59  
ID ADI00082 standard; protein; 104 AA.  
DE Novel human secreted and transmembrane protein PRO1245.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 502; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 60  
ID ADF35534 standard; protein; 104 AA.  
DE Human PRO1245 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 502; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 61  
ID ADG11784 standard; protein; 104 AA.  
DE Human PRO1245 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 62  
ID ADH19654 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 63  
ID ADG68233 standard; protein; 104 AA.  
DE Human PRO polypeptide #114.  
PN US2003170228-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 64  
ID ADH21147 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 502; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 65  
ID ADH20187 standard; protein; 104 AA.  
DE Human secreted/transmembrane protein PRO1245.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 502; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;

RESULT 66  
ID ADP07777 standard; protein; 104 AA.  
DE Human secreted protein, seq id 260.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 502; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2e-48;  
RESULT 67  
ID AAW5868 standard; protein; 104 AA.  
DE IUI05 polypeptide sequence.  
PN WO9833926-A1.  
PD 06-AUG-1998.  
PA (ABBO ) ABBOTT LAB.  
Query Match 99.2%; Score 498; DB 2; Length 104;  
Best Local Similarity 99.0%; Pred. No. 5.6e-48;  
RESULT 68  
ID ADI36315 standard; protein; 104 AA.  
DE Full-length hTIN-1 polypeptide, seq id 1.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 99.0%; Score 497; DB 7; Length 104;  
Best Local Similarity 99.0%; Pred. No. 7.2e-48;  
RESULT 69  
ID ADJ75657 standard; protein; 104 AA.  
DE Marker gene related amino acid sequence SEQ ID NO.909.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 99.0%; Score 497; DB 8; Length 104;  
Best Local Similarity 99.0%; Pred. No. 7.2e-48;  
RESULT 70  
ID ADI36316 standard; protein; 86 AA.  
DE Mature hTIN-1 polypeptide, seq id 2.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 82.1%; Score 412; DB 7; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.1e-38;  
RESULT 71  
ID ADI36317 standard; protein; 84 AA.  
DE Mature hTIN-1 polypeptide, seq id 22.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 81.3%; Score 408; DB 7; Length 84;  
Best Local Similarity 100.0%; Pred. No. 5.7e-38;  
RESULT 72  
ID AAO19893 standard; protein; 104 AA.  
DE Murine uteroglobin related protein 2.  
PN WO2003000111-A2.  
PD 03-JAN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 49.8%; Score 250; DB 6; Length 104;  
Best Local Similarity 57.0%; Pred. No. 4.6e-20;  
RESULT 73  
ID ADI36321 standard; protein; 104 AA.  
DE Full-length hTIN-1 polypeptide, seq id 5.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 49.8%; Score 250; DB 7; Length 104;  
Best Local Similarity 57.0%; Pred. No. 4.6e-20;  
RESULT 74  
ID ADI36326 standard; peptide; 93 AA.  
DE Full-length hTIN-1 polypeptide, seq id 21.  
PN WO200268673-A2.  
PD 06-SEP-2002.

PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 46.2%; Score 232; DB 7; Length 93;  
Best Local Similarity 57.1%; Pred. No. 4.2e-18;  
RESULT 75  
ID ADI36328 standard; peptide; 83 AA.  
DE Mature rHIN-1 polypeptide, seq id 27.  
PN WO200266873-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 44.9%; Score 225.5; DB 7; Length 83;  
Best Local Similarity 60.5%; Pred. No. 2e-17;  
RESULT 76  
ID ADI36322 standard; protein; 85 AA.  
DE Mature rHIN-1 polypeptide, seq id 6.  
PN WO200266873-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 44.0%; Score 221; DB 7; Length 85;  
Best Local Similarity 57.5%; Pred. No. 6.5e-17;  
RESULT 77  
ID ADI36323 standard; protein; 83 AA.  
DE Mature rHIN-1 polypeptide, seq id 24.  
PN WO200266873-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 43.6%; Score 219; DB 7; Length 83;  
Best Local Similarity 57.6%; Pred. No. 1.1e-16;  
RESULT 78  
ID AAM62068 standard; protein; 93 AA.  
DE Human lung tissue gene LUI03 protein.  
PN WO9820143-A1.  
PD 14-MAY-1998.  
PA (ABRO ) ABBOTT LAB.  
Query Match 31.9%; Score 160; DB 2; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 79  
ID AAY28334 standard; protein; 93 AA.  
DE LUI03 specific amino acid consensus sequence.  
PN US939265-A.  
PD 17-AUG-1999.  
PA (ABRO ) ABBOTT LAB.  
Query Match 31.9%; Score 160; DB 2; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 80  
ID AAY44456 standard; protein; 93 AA.  
DE Human lung specific gene protein Lng101.  
PN WO960160-A1.  
PD 25-NOV-1999.  
PA (DIAD-) DIADEXUS LLC.  
Query Match 31.9%; Score 160; DB 3; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 81  
ID AAY87289 standard; protein; 93 AA.  
DE Human signal peptide containing protein HSP-66 SEQ ID NO:66.  
PN WO200000610-A2.  
PD 06-JAN-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 31.9%; Score 160; DB 3; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 82  
ID AAU29145 standard; protein; 93 AA.  
DE Human PRO polypeptide sequence #122.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GENTH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 4; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 83  
ID ABUS8521 standard; protein; 93 AA.

DE Human PRO polypeptide #122.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 84  
ID ABUS8069 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 85  
ID ABUS4384 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 86  
ID ABR66258 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 87  
ID ABR65648 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 88  
ID ABUS9588 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 89  
ID ABUS2827 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 90  
ID ABUS9948 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 91  
ID ABR68197 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 92  
ID AAO19894 standard; protein; 93 AA.  
DE Human uteroglobin related protein 1.  
PN WO2003000111-A2.  
PD 03-JAN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 93  
ID ABUS9250 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003036144-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 94 43.6%; Pred. No. 5.4e-10;

ID ABU92681 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003036149-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 95 43.6%; Pred. No. 5.4e-10;

ID ABO08758 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003044923-A1.

PD 06-MAR-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 96 43.6%; Pred. No. 5.4e-10;

ID ABO02810 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003040062-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 97 43.6%; Pred. No. 5.4e-10;

ID ABR74964 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003040056-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 98 43.6%; Pred. No. 5.4e-10;

ID ABR94726 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003044926-A1.

PD 06-MAR-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 99 43.6%; Pred. No. 5.4e-10;

ID ABU85699 standard; protein; 93 AA.

DE Human PRO polypeptide #122.

PN US2003036140-A1.

PD 20-FEB-2003.

Query Match

PA (GETH ) GENENTECH INC.

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 100 43.6%; Pred. No. 5.4e-10;

ID ABO98859 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.

PN US2003013153-A1.

PD 16-JAN-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 101 43.6%; Pred. No. 5.4e-10;

ID ABO98074 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.

PN US2003017544-A1.

PD 23-JAN-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 102 43.6%; Pred. No. 5.4e-10;

ID ABU91780 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.

PN US2003027277-A1.

PD 06-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 103 43.6%; Pred. No. 5.4e-10;

ID ABU89473 standard; protein; 93 AA.

DE Human PRO polypeptide #122.

PN US2003036141-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
PD 13-FEB-2003.Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 104 43.6%; Pred. No. 5.4e-10;

ID ABU86314 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003036146-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 105 43.6%; Pred. No. 5.4e-10;

ID ABU67527 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003036162-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 106 43.6%; Pred. No. 5.4e-10;

ID ABU80555 standard; protein; 93 AA.

DE Human PRO protein #122.

PN US2003036137-A1.

PD 20-FEB-2003.

Query Match

PA (GETH ) GENENTECH INC.

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 107 43.6%; Pred. No. 5.4e-10;

ID ABR9473 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003040063-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 108 43.6%; Pred. No. 5.4e-10;

ID ABR98863 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003040064-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 109 43.6%; Pred. No. 5.4e-10;

ID ABO16386 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003027267-A1.

PD 06-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 110 43.6%; Pred. No. 5.4e-10;

ID ABR92286 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003036160-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 111 43.6%; Pred. No. 5.4e-10;

ID ABO16927 standard; protein; 93 AA.

DE Human secreted/transmembrane protein (PRO) #122.

PN US2003044925-A1.

PD 06-MAR-2003.

Query Match

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 112 43.6%; Pred. No. 5.4e-10;

ID ABR78348 standard; protein; 93 AA.

DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003054474-A1.

PD 20-MAR-2003.

Query Match

PA (GETH ) GENENTECH INC.

Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 113 43.6%; Pred. No. 5.4e-10;

ID ABU85084 standard; protein; 93 AA.

DE Novel human secreted and transmembrane protein PRO1128.

PN US2003032114-A1.

PD 13-FEB-2003.

Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 114				
ID ABO00223 standard; protein; 93 AA.				
ID DE Novel human secreted and transmembrane protein PRO1128.				
PN US2003032101-A1.				
PD 13-FEB-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 115				
ID ABO11555 standard; protein; 93 AA.				
ID DE Human secreted/transmembrane protein (PRO) #122.				
PN US2003036124-A1.				
PD 20-FEB-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 116				
ID ABO02200 standard; protein; 93 AA.				
ID DE Human secreted/transmembrane protein (PRO) #122.				
PN US2003040054-A1.				
PD 27-FEB-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 117				
ID AB08774 standard; protein; 93 AA.				
ID DE Novel human secreted and transmembrane protein PRO1128.				
PN US2003036133-A1.				
PD 20-FEB-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 118				
ID AB063469 standard; protein; 93 AA.				
ID DE Human secreted/transmembrane protein (PRO) #122.				
PN US2003036134-A1.				
PD 20-FEB-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 119				
ID ABO06270 standard; protein; 93 AA.				
ID DE Novel human secreted and transmembrane protein PRO1128.				
PN US2003022824-A1.				
PD 30-JAN-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 120				
ID ABR59306 standard; protein; 93 AA.				
ID DE Human secreted polypeptide PRO1128, SEQ ID NO:244.				
PN US2003027275-A1.				
PD 06-FEB-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 121				
ID ABO09368 standard; protein; 93 AA.				
ID DE Human secreted/transmembrane protein (PRO) #122.				
PN US2003027324-A1.				
PD 06-FEB-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 122				
ID ABO19232 standard; protein; 93 AA.				
ID DE Novel human secreted and transmembrane protein PRO1128.				
PN US2003036118-A1.				
PD 20-FEB-2003.				
PA (GENTH ) GEMENTECH INC.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		
RESULT 123				
ID ABO11250 standard; protein; 93 AA.				
ID DE Human secreted/transmembrane protein (PRO) #122.				
PN US2003036123-A1.				
PD 20-FEB-2003.				
Query Match	31.9%;	Score 160;	DB 6;	Length 93;
Best Local Similarity	43.6%;	Pred. No. 5.4e-10;		

RESULT 124	ID	ABR66868 standard; protein; 93 AA.	
DE	Human secreted polypeptide PRO1128, SEQ ID NO:244.		
PN	US2003036148-A1.		
PD	20-FEB-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 125	ID	ABO16081 standard; protein; 93 AA.	
DE	Human secreted/transmembrane protein (PRO) #122.		
PN	US2003040060-A1.		
PD	27-FEB-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 126	ID	ABO13787 standard; protein; 93 AA.	
DE	Human secreted/transmembrane protein (PRO) #122.		
PN	US2003044916-A1.		
PD	06-MAR-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 127	ID	ABU65690 standard; protein; 93 AA.	
DE	Human secreted/transmembrane protein, SEQ ID 244.		
PN	US2003036156-A1.		
PD	20-FEB-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 128	ID	ABO07538 standard; protein; 93 AA.	
DE	Human PRO polypeptide #122.		
PN	US2003032117-A1.		
PD	13-FEB-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 129	ID	ABO03725 standard; protein; 93 AA.	
DE	Human secreted/transmembrane protein (PRO) #122.		
PN	US2003036128-A1.		
PD	20-FEB-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 130	ID	ABR67173 standard; protein; 93 AA.	
DE	Human secreted polypeptide PRO1128, SEQ ID NO:244.		
PN	US2003027266-A1.		
PD	06-FEB-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 131	ID	ABO15776 standard; protein; 93 AA.	
DE	Human secreted/transmembrane protein (PRO) #122.		
PN	US2003054483-A1.		
PD	20-MAR-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
PA	(GETH) GENENTECH INC.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 132	ID	ABU56057 standard; protein; 93 AA.	
DE	Human secreted/transmembrane protein, PRO1128.		
PN	US200302298-A1.		
PD	30-JAN-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 133	ID	ABU63385 standard; protein; 93 AA.	
DE	Human PRO polypeptide #122.		
PN	US2003032102-A1.		
PD	13-FEB-2003.		
Query Match		31.9%; Score 160; DB 6; Length 93;	
Best Local Similarity		43.6%; Pred. No. 5.4e-10;	
RESULT 134	ID	ABU95330 standard; protein; 93 AA.	



DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 135 43.6%; Pred. No. 5.4e-10;  
ID ABR71233 standard; protein, 93 AA.  
DE Human PRO1128 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 136 43.6%; Pred. No. 5.4e-10;  
ID ABO07843 standard; protein, 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 137 43.6%; Pred. No. 5.4e-10;  
ID ABR70084 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 138 43.6%; Pred. No. 5.4e-10;  
ID ABR69417 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 139 43.6%; Pred. No. 5.4e-10;  
ID ABO01558 standard; protein, 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 140 43.6%; Pred. No. 5.4e-10;  
ID ABR61360 standard; protein, 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 141 43.6%; Pred. No. 5.4e-10;  
ID ABR60157 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 142 43.6%; Pred. No. 5.4e-10;  
ID ABR67892 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 143 43.6%; Pred. No. 5.4e-10;  
ID ABR65280 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 144 43.6%; Pred. No. 5.4e-10;  
ID ABR6502 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN 06-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 145 43.6%; Pred. No. 5.4e-10;  
ID ABR71914 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 146 43.6%; Pred. No. 5.4e-10;  
ID ABR65394 standard; protein, 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 147 43.6%; Pred. No. 5.4e-10;  
ID ABR89084 standard; protein, 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 148 43.6%; Pred. No. 5.4e-10;  
ID ABR83164 standard; protein, 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 149 43.6%; Pred. No. 5.4e-10;  
ID ABR95020 standard; protein, 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 150 43.6%; Pred. No. 5.4e-10;  
ID ABR90568 standard; protein, 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 151 43.6%; Pred. No. 5.4e-10;  
ID ABR84079 standard; protein, 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 152 43.6%; Pred. No. 5.4e-10;  
ID ABR93730 standard; protein, 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 153 43.6%; Pred. No. 5.4e-10;  
ID ABR64975 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 154 43.6%; Pred. No. 5.4e-10;  
ID ABR68807 standard; protein, 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003027271-A1.

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PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 155
ID ABO06623 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 156
ID ABR99168 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 157
ID ABU57052 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 158
ID ABU86004 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 159
ID ABU82291 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 160
ID ABU87302 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 161
ID ABU83774 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 162
ID ABO08148 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 163
ID ABU81859 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 164
ID ABU66023 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 165
ID ABR59852 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 166
ID ABU94040 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 167
ID ABU93893 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 168
ID ABR66563 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 169
ID ABR90981 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 170
ID ABU94408 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 171
ID ABU79290 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 172
ID ABU86619 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 173
ID ABU85924 standard; protein; 93 AA.
DE Novel human secreted and transmembrane protein PRO1128.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 174
ID ABU94713 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 31.9%; Score 160; DB 6; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 175
ID ABO04640 standard; protein; 93 AA.
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DE Human PRO polypeptide #122.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 176  
ID ABR70389 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 177  
ID ABR98554 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 178  
ID ABR65953 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
PA (GENTH ) GEMENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 179  
ID ABR64670 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 180  
ID ABR79595 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 181  
ID ABR92986 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 182  
ID ABR95945 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 183  
ID ABR91165 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 184  
ID ABR90258 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 185  
ID ABO09673 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003044931-A1.

PD 06-MAR-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 186  
ID ABO10945 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 187  
ID ABR70999 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 188  
ID ABR87607 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 189  
ID ABR91475 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 190  
ID ABR84689 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 191  
ID ABR69779 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 192  
ID ABR80156 standard; protein; 93 AA.  
DE Human PRO protein #122.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 193  
ID ABR93425 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 194  
ID ABO09978 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 195  
ID ABO09063 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;

RESULT 196  
ID ABU10631 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein #122.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 197  
ID ABU95640 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 198  
ID ABU96849 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 199  
ID ABR70694 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 200  
ID ABO05045 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 201  
ID ABO08453 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US200304922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 202  
ID ABO05660 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 203  
ID ABR74049 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 204  
ID ABR95641 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US200305445-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 205  
ID ABR80938 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 206  
ID ABR81243 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 207  
ID ABM00939 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 208  
ID ABR88541 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 209  
ID ABM77362 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 210  
ID ABO28846 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 211  
ID ABO31591 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 212  
ID ABM08008 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 213  
ID ABO40488 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 214  
ID ABO35913 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;

Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 215  
ID ABO44052 standard; protein: 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 216  
ID ADA77996 standard; protein: 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 217  
ID ABM24847 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 218  
ID ABO03115 standard; protein: 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 219  
ID ABR90371 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 220  
ID ABM17285 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 221  
ID ABR95031 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 222  
ID ABR95336 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 223  
ID ABO21574 standard; protein: 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 224  
ID ABR97838 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064452-A1.  
PA (GETH ) GENENTECH INC.

03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 225  
ID ABR87626 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 226  
ID ABM77667 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 227  
ID ABM27897 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 228  
ID ABM06178 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 229  
ID ABM03684 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 230  
ID ABM35135 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 231  
ID ABM26372 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 232  
ID ABO48154 standard; protein: 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 233  
ID ABR92896 standard; protein: 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 234  
ID ABO424657 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 235  
ID ABM11668 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 236  
ID ABM02769 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 237  
ID ABM16065 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 238  
ID ABO27626 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 239  
ID ABM29117 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 240  
ID ABM07093 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 241  
ID ABM21187 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 242  
ID ABM09533 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;

Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 243  
ID ABO41403 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 244  
ID ABO36218 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 245  
ID ABO43747 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 246  
ID ABM76447 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 247  
ID ABM76143 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 248  
ID ABM25762 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 249  
ID ABM26067 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 250  
ID ABO03420 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 251  
ID ABO02505 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 252  
ID ABR9676 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003036130-A1.  
PD 20-FEB-2003.

Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 253  
ID ABR73744 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 254  
ID ABO16996 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 255  
ID ABR94421 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 256  
ID ABR75928 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 257  
ID ABR71304 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 258  
ID ABR93201 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 259  
ID ABR93506 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 260  
ID ABR87931 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 261  
ID ABO27931 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 262

ID ABO30066 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 263  
ID ABO33275 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 264  
ID ABO4963 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 265  
ID ABO8923 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 266  
ID ABO36523 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 267  
ID ABO35608 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 268  
ID ABO39573 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 269  
ID ABO10448 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 270  
ID ABO11973 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;  
RESULT 271  
ID ABO52119 standard; protein; 93 AA.



DE Human PRO polypeptide #122.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 272  
ID ABO52424 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 273  
ID ABO23742 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 274  
ID ABR97228 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 275  
ID ABR87016 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 276  
ID ABM1058 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 277  
ID ABM28202 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 278  
ID ABO32201 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 279  
ID ABM15328 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 280  
ID ABM06483 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068709-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 281  
ID ABM04294 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 282  
ID ABM22407 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 283  
ID ABM07703 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 284  
ID ABO40793 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 285  
ID ABM35440 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 286  
ID ABM33203 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 287  
ID ABO52729 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 288  
ID ABO50289 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 289  
ID ABU9283 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;

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Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 290
ID ABO04335 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 291
ID ABO05965 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 292
ID ABO18505 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 293
ID ABR9753 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 294
ID ABR8063 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 295
ID ABM0124 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 296
ID ABR8884 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 297
ID ABM1349 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 298
ID ABM2088 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 299
ID ABO4203 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 300
ID ABO4262 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 301
ID ABM1014 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 302
ID ABO3865 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 303
ID ABM3289 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 304
ID ABM2272 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 305
ID ABM7492 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 306
ID ADA7978 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 307
ID ABR9631 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 308
ID ABM0246 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
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RESULT 309  
ID ABR86406 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 310  
ID ABR86711 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 311  
ID ABR16675 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 312  
ID ABR29727 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 313  
ID ABO29151 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 314  
ID ABR23932 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 315  
ID ABR23322 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 316  
ID ABR22102 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 317  
ID ABO37743 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 318

ID ABR28507 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 319  
ID ABR28812 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 320  
ID ABR66456 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 321  
ID ABR75838 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 322  
ID ABR3418 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 323  
ID ABR34423 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 324  
ID ABO20354 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 325  
ID ABO21269 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 326  
ID ABO22184 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 327  
ID ABR96618 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 328
ID ABR85796 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 329
ID ABR9778 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 330
ID ABM00329 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 331
ID ABM00634 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 332
ID ABO29761 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 333
ID ABM23627 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 334
ID ABM29422 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 335
ID ABO38353 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 336
ID ABO45653 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 337
ID ABR89761 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 338
ID ADA8155 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 339
ID ABO16691 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 340
ID ABO18317 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 341
ID ABO22744 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003027255-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 342
ID ABO23049 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 343
ID ABR92591 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 344
ID ABR81548 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003048744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 345
ID ABM77972 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 346
ID ABR89761 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
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Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 347  
ID ABM2677 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 348  
ID ABM13803 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 349  
ID ABO28541 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 350  
ID ABO30371 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 351  
ID ABM07398 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 352  
ID ABM03989 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 353  
ID ABO37133 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 354  
ID ABO41708 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 355  
ID ABO35303 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;

RESULT 356  
ID ABM25152 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 357  
ID ABO47544 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 358  
ID ABO47849 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 359  
ID ABO48459 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 360  
ID ABO51509 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 361  
ID ABO51814 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 362  
ID ABO50594 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003048779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 363  
ID ABR79718 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 364  
ID ABM16980 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 365  
ID ABO18012 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.

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PN US2003044918-A1.
ID 06-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 366
ID ABO20964 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 367
ID ABR6923 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 368
ID ABM12278 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 369
ID ABM16370 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 370
ID ABM24237 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 371
ID ABM14718 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 372
ID ABM04599 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 373
ID ABM06788 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 374
ID ABM09228 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
PN 43.6%; Pred. No. 5.4e-10;

RESULT 375
ID ABO39268 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 376
ID ABM75533 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 377
ID ABM25457 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 378
ID ABM19667 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 379
ID ABO46873 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 380
ID ABO47178 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 381
ID ADA83313 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 382
ID ABR71609 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 383
ID ABR72219 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 384
ID ABR98558 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036129-A1.
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PD 20-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 385  
ID ABO06928 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 386  
ID ABR84881 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 387  
ID ABR73439 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 388  
ID ABR7653 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 389  
ID ABR73134 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 390  
ID ABM18200 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 391  
ID ABO20659 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 392  
ID ABO25402 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 393  
ID ABO25707 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 394  
ID ABR94116 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.

PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 395  
ID ABR80023 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 396  
ID ABM1363 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 397  
ID ABO32970 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 398  
ID ABO30676 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 399  
ID ABO30981 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 400  
ID ABM27287 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 401  
ID ABM30032 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 402  
ID ABM05568 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 6; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 403  
ID ABM1633 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068698-A1.  
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 404
ID ABM08618 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 405
ID ABO42318 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 406
ID ABO38048 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 407
ID ABO45958 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 408
ID ABM66761 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 409
ID ADB20356 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 410
ID ABM19662 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 411
ID ABO49374 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 412
ID ABO49679 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 413
ID ADA78608 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 414
ID ABR88236 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 415
ID ABM26982 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 416
ID ABM03379 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 417
ID ABO39878 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 6; Length 93;
RESULT 418
ID ABO49984 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 419
ID ABO50899 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 420
ID ABO05355 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 421
ID ABR74659 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 422
ID ABR77138 standard; protein; 93 AA.
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DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US200304927-A1.  
PD 06-MAR-2003.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 423  
ID ABM17895 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 424  
ID ABR95946 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 425  
ID ABO21879 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 426  
ID ABO20049 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 427  
ID ABO24352 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 428  
ID ABR6101 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 429  
ID ABM10753 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 430  
ID ABM76752 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 431  
ID ABR9456 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;

RESULT 432  
ID ABM12583 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 433  
ID ABM05873 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 434  
ID ABO3498 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 435  
ID ABM03074 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 436  
ID ABM19052 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 437  
ID ABM19357 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 438  
ID ABO4656 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 439  
ID ABO49069 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 440  
ID ABR69112 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003072273-A1.  
PD 06-FEB-2003.  
Query Match 31.9%; Score 160; DB 7; Length 93;  
Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 441  
ID ABR89151 standard; protein; 93 AA.

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DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 442
  ID ABR72524 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003036120-A1.
  PD 20-FEB-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 443
  ID ABR74354 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003036161-A1.
  PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 444
  ID ABO29651 standard; protein; 93 AA.
  DE Human HIN-2 protein.
  PN WO2003046125-A2.
  PD 05-JUN-2003.
PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 445
  ID ABO18622 standard; protein; 93 AA.
  DE Human secreted/transmembrane protein (PRO) #122.
  PN US2003044921-A1.
  PD 06-MAR-2003.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 446
  ID ABR80328 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003049739-A1.
  PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 447
  ID ABO01549 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003059882-A1.
  PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 448
  ID ABO02159 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003059884-A1.
  PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 449
  ID ABR87321 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003066887-A1.
  PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 450
  ID ABR1288 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003073186-A1.
  PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 451
  ID ABR30642 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003064443-A1.
  PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 452
  ID ABR24542 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003064444-A1.
  PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 453
  ID ABO29456 standard; protein; 93 AA.
  DE Human secreted/transmembrane protein (PRO) #122.
  PN US2003068697-A1.
  PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 454
  ID ABO31286 standard; protein; 93 AA.
  DE Human secreted/transmembrane protein (PRO) #122.
  PN US2003068710-A1.
  PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 455
  ID ABR14413 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003068686-A1.
  PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 456
  ID ABO09838 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003073178-A1.
  PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 457
  ID ABO38963 standard; protein; 93 AA.
  DE Human secreted/transmembrane protein (PRO) #122.
  PN US2003068774-A1.
  PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 458
  ID ABR34728 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003104538-A1.
  PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 459
  ID ABO51204 standard; protein; 93 AA.
  DE Human secreted/transmembrane protein (PRO) #122.
  PN US2003049781-A1.
  PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
  RESULT 460
  ID ABR1288 standard; protein; 93 AA.
  DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
  PN US2003073186-A1.
  PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
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RESULT 460
ID ABO4030 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 461
ID ABO10500 standard; protein; 93 AA.
DE Human PRO polypeptide #122.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 462
ID ABR77743 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 463
ID ABR78953 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 464
ID ABO24047 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003054482-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 465
ID ABR93811 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054457-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 466
ID ABO1854 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003059883-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 467
ID ABM78277 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049764-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 468
ID ABR90066 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003073177-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 469
ID ABM7592 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 470
ID ABM13193 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003064450-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 471
ID ABO31896 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068731-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 472
ID ABM14108 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 473
ID ABM08313 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068754-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 474
ID ABO40183 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 475
ID ABM74618 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096351-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 476
ID ABM3813 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096358-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 477
ID ABM20272 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104556-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
RESULT 478
ID ABO48764 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003049756-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 31.9%; Score 160; DB 7; Length 93;
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RESULT 479
ID ABR72829 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 480
ID ABO15471 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 481
ID ABR85186 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 482
ID ABO15166 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 483
ID ABO17301 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 484
ID ABO17590 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 485
ID ABR85491 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 486
ID ABO77057 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 487
ID ABO28236 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 488
ID ABO23017 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 491
ID ABO21492 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 492
ID ABO15023 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 493
ID ABO41098 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 494
ID ABO36828 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 495
ID ABO37438 standard; protein; 93 AA.
DE Human secreted/transmembrane protein (PRO) #122.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 496
ID ABO75228 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
RESULT 497
ID ABO33508 standard; protein; 93 AA.
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.9%; Score 160; DB 7; Length 93;
Best Local Similarity 43.6%; Pred. No. 5.4e-10;
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Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 498  
ID ABO46263 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 499  
ID ADA82679 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 500  
ID ABM31862 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 501  
ID ABM31252 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 502  
ID ADB85987 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 503  
ID ABM32167 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 504  
ID ABM32472 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 505  
ID ABM31557 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 506  
ID ABM30947 standard; protein; 93 AA.  
DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 507

ID ADD05717 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 508  
ID ADG02712 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 509  
ID ADG01419 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 510  
ID ADF95594 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 511  
ID ADG12409 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 512  
ID ADH09069 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 513  
ID ADL32850 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 514  
ID ADM30384 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 515  
ID ADN39907 standard; protein; 93 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C277.  
PN WC2003042661-A2.  
PD 22-MAY-2003.  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 43.6%; Pred. No. 5.4e-10; Length 93;  
RESULT 516  
ID ADE74381 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.

PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 517  
ID ADE74993 standard; protein; 93 AA.  
DE Human secreted/transmembrane protein (PRO) #122.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 518  
ID ADP6206 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 519  
ID ADG04477 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 520  
ID ADG00637 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 521  
ID ADG82893 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 522  
ID ADH26174 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 523  
ID ADH33143 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 524  
ID ADJ54882 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 525  
ID ADJ64653 standard; protein; 93 AA.  
DE Human PRO polypeptide #122.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
31.9%; Score 160; DB 8; Length 93;  
PD (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Best Local Similarity 43.6%; Pred. No. 5.4e-10;  
RESULT 526  
ID ADM31549 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 527  
ID ADM36596 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 528  
ID ADJ40401 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 529  
ID ADN38009 standard; protein; 93 AA.  
DE Novel human secreted and transmembrane protein PRO1128.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 31.9%; Score 160; DB 8; Length 93;  
RESULT 530  
ID ADO78100 standard; protein; 93 AA.  
DE Human SCGB3A2.  
PN DE10254601-A1.  
PD 03-JUN-2004.  
PA (GANV-) GANNVED PHARM AG.  
Query Match  
Best Local Similarity 30.1%; Score 151; DB 8; Length 93;  
RESULT 531  
ID AAU14471 standard; protein; 87 AA.  
DE Human novel protein #342.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 28.9%; Score 145; DB 4; Length 87;  
RESULT 532  
ID ADH80789 standard; protein; 87 AA.  
DE Human polypeptide #106.  
PN US2003232054-A1.  
PD 18-DEC-2003.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (CHEN/) CHEN R.  
PA (QIAN/) QIAN X B.  
PA (WANG/) WANG Z W.  
PA (WEHR/) WEHRMAN T.  
PA (ZHAN/) ZHANG J.  
PA (ZHOU/) ZHOU P.  
PA (CAOY/) CAO Y.  
PA (DRMA/) DRMANC R T.  
Query Match  
Best Local Similarity 28.9%; Score 145; DB 8; Length 87;  
RESULT 533  
ID AAO19892 standard; protein; 91 AA.  
DE Murine uteroglobin related protein 1 type A.  
PN WO2003000111-A2.  
PD 03-JAN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Query Match 26.9%; Score 135; DB 6; Length 91;  
Best Local Similarity 36.0%; Pred. No. 3.4e-07;  
RESULT 534  
ID AAO29652 standard; protein; 91 AA.  
DE Mouse HTN-2 protein.  
PN W02003046125-A2.  
PD 05-JUN-2003.  
PA (NAJF-) NAT JEWISH MEDICAL & RES CENT.  
Query Match 26.9%; Score 135; DB 7; Length 91;  
Best Local Similarity 36.0%; Pred. No. 3.4e-07;  
RESULT 535  
ID AD136329 standard; peptide; 93 AA.  
DE Human UGRF-1 polypeptide, seq id 32.  
PN W0200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Query Match 26.9%; Score 135; DB 7; Length 93;  
Best Local Similarity 40.6%; Pred. No. 3.5e-07;  
RESULT 536  
ID AAU14235 standard; protein; 137 AA.  
DE Human novel protein #106.  
PN W0200155437-A2.  
PD 02-AUG-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 26.9%; Score 135; DB 4; Length 137;  
Best Local Similarity 41.9%; Pred. No. 5.8e-07;  
RESULT 537  
ID AAW75869 standard; protein; 26 AA.  
DE LUI105 polypeptide derived peptide sequence 1.  
PN W09833926-A1.  
PD 06-AUG-1998.  
PA (ABBO ) ABBOTT LAB.  
Query Match 23.5%; Score 118; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
RESULT 538  
ID AAW75871 standard; protein; 21 AA.  
DE LUI105 polypeptide derived peptide sequence 3.  
PN W09833926-A1.  
PD 06-AUG-1998.  
PA (ABBO ) ABBOTT LAB.  
Query Match 19.9%; Score 100; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.00043;  
RESULT 539  
ID AAW75870 standard; protein; 19 AA.  
DE LUI105 polypeptide derived peptide sequence 2.  
PN W09833926-A1.  
PD 06-AUG-1998.  
PA (ABBO ) ABBOTT LAB.  
Query Match 18.3%; Score 92; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
RESULT 540  
ID AAW75872 standard; protein; 18 AA.  
DE LUI105 polypeptide derived peptide sequence 4.  
PN W09833926-A1.  
PD 06-AUG-1998.  
PA (ABBO ) ABBOTT LAB.  
Query Match 17.7%; Score 89; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.0061;  
RESULT 541  
ID AAW75873 standard; protein; 19 AA.  
DE LUI105 polypeptide derived peptide sequence 5.  
PN W09833926-A1.  
PD 06-AUG-1998.  
PA (ABBO ) ABBOTT LAB.  
Query Match 16.5%; Score 83; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
RESULT 542  
ID AAY44403 standard; protein; 673 AA.  
DE Human truncated tankyrase-1.  
PN W0964606-A1.  
PD 16-DEC-1999.  
PA (UYRQ ) UNIV ROCKEFELLER.

Query Match 16.5%; Score 83; DB 3; Length 673;  
Best Local Similarity 30.5%; Pred. No. 3.4;  
RESULT 543  
ID AAV79538 standard; protein; 673 AA.  
DE Truncated human tankyrase #1.  
PN W0200229017-A2.  
PD 11-APR-2002.  
PA (UYRQ ) UNIV ROCKEFELLER.  
Query Match 16.5%; Score 83; DB 5; Length 673;  
Best Local Similarity 30.5%; Pred. No. 3.4;  
RESULT 544  
ID AAY44404 standard; protein; 949 AA.  
DE Human truncated tankyrase-2.  
PN W0964606-A1.  
PD 16-DEC-1999.  
PA (UYRQ ) UNIV ROCKEFELLER.  
Query Match 16.5%; Score 83; DB 3; Length 949;  
Best Local Similarity 30.5%; Pred. No. 5.3;  
RESULT 545  
ID AAV79539 standard; protein; 949 AA.  
DE Truncated human tankyrase #2.  
PN W0200229017-A2.  
PD 11-APR-2002.  
PA (UYRQ ) UNIV ROCKEFELLER.  
Query Match 16.5%; Score 83; DB 5; Length 949;  
Best Local Similarity 30.5%; Pred. No. 5.3;  
RESULT 546  
ID AAY44402 standard; protein; 1327 AA.  
DE Human tankyrase.  
PN W0964606-A1.  
PD 16-DEC-1999.  
PA (UYRQ ) UNIV ROCKEFELLER.  
Query Match 16.5%; Score 83; DB 3; Length 1327;  
Best Local Similarity 30.5%; Pred. No. 8.3;  
RESULT 547  
ID AAB27212 standard; protein; 1327 AA.  
DE Human tankyrase I protein sequence SEQ ID NO: 8.  
PN W0200061813-A1.  
PD 19-OCT-2000.  
PA (GERO-) GERON CORP.  
Query Match 16.5%; Score 83; DB 3; Length 1327;  
Best Local Similarity 30.5%; Pred. No. 8.3;  
RESULT 548  
ID AAB66279 standard; protein; 1327 AA.  
DE Human tankyrase1 SEQ ID NO: 4.  
PN W0200100849-A1.  
PD 04-JAN-2001.  
PA (ICOS-) ICOS CORP.  
Query Match 16.5%; Score 83; DB 4; Length 1327;  
Best Local Similarity 30.5%; Pred. No. 8.3;  
RESULT 549  
ID AAV79537 standard; protein; 1327 AA.  
DE Human tankyrase.  
PN W0200229017-A2.  
PD 11-APR-2002.  
PA (UYRQ ) UNIV ROCKEFELLER.  
Query Match 16.5%; Score 83; DB 5; Length 1327;  
Best Local Similarity 30.5%; Pred. No. 8.3;  
RESULT 550  
ID ADR14791 standard; protein; 1327 AA.  
DE Amino acid sequence of human MAPCAX orthologue #23.  
PN W02004066948-A2.  
PD 12-AUG-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 16.5%; Score 83; DB 8; Length 1327;  
Best Local Similarity 30.5%; Pred. No. 8.3;  
RESULT 551  
ID ABO76950 standard; protein; 718 AA.  
DE Pseudomonas aeruginosa polypeptide #9125.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 16.4%; Score 82.5; DB 7; Length 718;

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Best Local Similarity 37.3%; Pred. No. 4.2;
RESULT 552
ID ABR63120 standard; protein: 439 AA.
DE Penicillium lypc1i phytaase.
PN WO2003062409-A2.
PD 31-JUL-2003.
PA (HOPE) ROCHE VITAMINS AG.
Query Match 15.8%; Score 79.5; DB 7; Length 439;
Best Local Similarity 29.9%; Pred. No. 4.6;
RESULT 553
ID ABO73010 standard; protein: 255 AA.
DE Pseudomonas aeruginosa polypeptide #5185.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.6%; Score 78.5; DB 7; Length 255;
Best Local Similarity 24.1%; Pred. No. 3;
RESULT 554
ID ABO80397 standard; protein: 540 AA.
DE Pseudomonas aeruginosa polypeptide #12572.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.3%; Score 77; DB 7; Length 540;
Best Local Similarity 30.0%; Pred. No. 12;
RESULT 555
ID ABU22766 standard; protein: 561 AA.
DE Protein encoded by prokaryotic essential gene #8293.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 15.1%; Score 76; DB 6; Length 561;
Best Local Similarity 26.4%; Pred. No. 16;
RESULT 556
ID ABP66002 standard; protein: 889 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:746.
PN EPI227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 15.1%; Score 76; DB 5; Length 889;
Best Local Similarity 25.7%; Pred. No. 30;
RESULT 557
ID ABP66269 standard; protein: 496 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:1013.
PN EPI227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 15.0%; Score 75.5; DB 5; Length 496;
Best Local Similarity 30.3%; Pred. No. 16;
RESULT 558
ID ADS21025 standard; protein: 855 AA.
DE Bacterial polypeptide #10058.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
DE (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 15.0%; Score 75.5; DB 8; Length 855;
Best Local Similarity 32.9%; Pred. No. 32;
RESULT 559
ID AAB42153 standard; protein: 361 AA.
DE Human ORFX ORF1917 polypeptide sequence SEQ ID NO:3834.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 14.9%; Score 75; DB 3; Length 361;
Best Local Similarity 35.4%; Pred. No. 12;
RESULT 560
ID ADN99707 standard; protein: 362 AA.
DE Novel human protein sequence #523.
PN WO2004038003-A2.

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PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 14.9%; Score 75; DB 8; Length 362;
Best Local Similarity 35.4%; Pred. No. 12;
RESULT 561
ID ADO20269 standard; protein: 362 AA.
DE Human PRO polypeptide #585.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 14.9%; Score 75; DB 8; Length 362;
Best Local Similarity 35.4%; Pred. No. 12;
RESULT 562
ID AEM81662 standard; protein: 362 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82491, SEQ:4297.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 14.9%; Score 75; DB 8; Length 362;
Best Local Similarity 35.4%; Pred. No. 12;
RESULT 563
ID AAM68511 standard; protein: 469 AA.
DE B. flavum fumase protein.
PN JP10262684-A.
PD 06-OCT-1998.
PA (MITU) MITSUBISHI CHEM CORP.
Query Match 14.7%; Score 74; DB 2; Length 469;
Best Local Similarity 25.0%; Pred. No. 22;
RESULT 564
ID AAB76752 standard; protein: 358 AA.
DE Corynebacterium glutamicum MCF protein SEQ ID NO:486.
PN WO200100805-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 14.6%; Score 73.5; DB 4; Length 358;
Best Local Similarity 26.5%; Pred. No. 17;
RESULT 565
ID AAG91541 standard; protein: 358 AA.
DE C glutamicum protein fragment SEQ ID NO: 5295.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOM) KYOMA HAKKO KOGYO KK.
Query Match 14.6%; Score 73.5; DB 4; Length 358;
Best Local Similarity 26.5%; Pred. No. 17;
RESULT 566
ID AAB66866 standard; protein: 443 AA.
DE Human peptidyl-prolyl isomerase-2.
PN US6171843-B1.
PD 09-JAN-2001.
PA (INCY-) INCYTE PHARM INC.
Query Match 14.6%; Score 73.5; DB 4; Length 443;
Best Local Similarity 34.1%; Pred. No. 23;
RESULT 567
ID ABU62206 standard; protein: 447 AA.
DE Human peptidyl-prolyl isomerase 2 (HPIP2).
PN US6524838-B1.
PD 25-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 73.5; DB 6; Length 447;
Best Local Similarity 34.1%; Pred. No. 23;
RESULT 568
ID ADB87811 standard; protein: 447 AA.
DE Human peptidyl-prolyl isomerase, HPIP-2.
PN US2003087390-A1.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 73.5; DB 7; Length 447;
Best Local Similarity 34.1%; Pred. No. 23;
RESULT 569
ID ADC34766 standard; protein: 776 AA.
DE Rat salt inducible kinase seq id 34.
PN US2003087317-A1.
PD 08-MAY-2003.

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PA (INCY-) INCYTE GENOMICS INC.  
Query Match 14.6%; Score 73.5; DB 7; Length 776;  
Best Local Similarity 33.7%; Pred. No. 48;  
RESULT 570  
ID ADS43317 standard; protein; 739 AA.  
DE Bacterial polypeptide #21747.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.5%; Score 73; DB 8; Length 739;  
Best Local Similarity 27.1%; Pred. No. 51;  
RESULT 571  
ID ABB65719 standard; protein; 1279 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 23949.  
PN WO200171042-A2.  
PD 27-SBP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 14.5%; Score 73; DB 4; Length 1279;  
Best Local Similarity 31.6%; Pred. No. 1.1e+02;  
RESULT 572  
ID AAM49674 standard; protein; 421 AA.  
DE T. thermophilus HB8 O-acetylhomoserine sulphydase.  
PN JP2002010787-A.  
PD 15-JAN-2002.  
PA (RIKA ) RIKAGAKU KENKYUSHO.  
PA (IKED-) IKEDA SHOKKEN KK.  
Query Match 14.4%; Score 72.5; DB 5; Length 421;  
Best Local Similarity 37.5%; Pred. No. 28;  
RESULT 573  
ID AAU42386 standard; protein; 122 AA.  
DE Propionibacterium acnes immunogenic protein #3282.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 14.3%; Score 72; DB 4; Length 122;  
Best Local Similarity 39.4%; Pred. No. 6.2;  
RESULT 574  
ID ABM38905 standard; protein; 122 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #3581.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 14.3%; Score 72; DB 6; Length 122;  
Best Local Similarity 39.4%; Pred. No. 6.2;  
RESULT 575  
ID AAR72643 standard; protein; 236 AA.  
DE Leishmania donovani A2 protein of the ORF1 domain.  
PN CA2105538-A.  
PD 04-MAR-1995.  
PA (UYMC-) UNIV MCGILL.  
Query Match 14.3%; Score 72; DB 2; Length 236;  
Best Local Similarity 29.8%; Pred. No. 15;  
RESULT 576  
ID AAR71477 standard; protein; 236 AA.  
DE Leishmania donovani A2 protein.  
PN WO9506729-A1.  
PD 09-MAR-1995.  
PA (UYMC-) UNIV MCGILL.  
Query Match 14.3%; Score 72; DB 2; Length 236;  
Best Local Similarity 29.8%; Pred. No. 15;  
RESULT 577  
ID ADS25292 standard; protein; 395 AA.  
DE Bacterial polypeptide #1325.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.2%; Score 72; DB 8; Length 395;  
Best Local Similarity 26.1%; Pred. No. 37;  
RESULT 584  
ID ADS25416 standard; protein; 438 AA.

PA (GOLD/) GOLDMAN B S.  
Query Match 14.3%; Score 72; DB 8; Length 395;  
Best Local Similarity 36.2%; Pred. No. 29;  
RESULT 578  
ID ADS25842 standard; protein; 395 AA.  
DE Bacterial polypeptide #14875.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.3%; Score 72; DB 8; Length 395;  
Best Local Similarity 36.2%; Pred. No. 29;  
RESULT 579  
ID ADS22407 standard; protein; 395 AA.  
DE Bacterial polypeptide #11440.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.3%; Score 72; DB 8; Length 395;  
Best Local Similarity 36.2%; Pred. No. 29;  
RESULT 580  
ID ADS25457 standard; protein; 395 AA.  
DE Bacterial polypeptide #14490.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.3%; Score 72; DB 8; Length 395;  
Best Local Similarity 36.2%; Pred. No. 29;  
RESULT 581  
ID ABJ04701 standard; protein; 528 AA.  
DE Mycobacterium tuberculosis protein 36.  
PN WO200244406-A2.  
PD 06-JUN-2002.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 14.3%; Score 72; DB 5; Length 528;  
Best Local Similarity 28.4%; Pred. No. 43;  
RESULT 582  
ID ADJ48924 standard; protein; 405 AA.  
DE O11-associated gene related protein #424.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDERNAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 14.2%; Score 71.5; DB 8; Length 405;  
Best Local Similarity 27.8%; Pred. No. 34;  
RESULT 583  
ID ADS25947 standard; protein; 432 AA.  
DE Bacterial polypeptide #14980.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.2%; Score 71.5; DB 8; Length 432;  
Best Local Similarity 26.1%; Pred. No. 37;  
RESULT 584  
ID ADS25416 standard; protein; 438 AA.

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DE Bacterial polypeptide #14449.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 14.2%; Score 71.5; DB 8; Length 438;
RESULT 585
ID ADS25098 standard; protein; 450 AA.
DE Bacterial polypeptide #14131.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 14.2%; Score 71.5; DB 8; Length 450;
RESULT 586
ID ADS22360 standard; protein; 859 AA.
DE Bacterial polypeptide #11393.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 14.2%; Score 71.5; DB 8; Length 859;
RESULT 587
ID ABG15241 standard; protein; 342 AA.
DE Novel human diagnostic protein #15232.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 14.1%; Score 71; DB 4; Length 342;
RESULT 588
ID ABU22662 standard; protein; 1395 AA.
DE Protein encoded by Prokaryotic essential gene #8189.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 14.1%; Score 71; DB 6; Length 1395;
RESULT 589
ID ADP30057 standard; protein; 578 AA.
DE Human secreted protein SEQ ID #824.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 14.0%; Score 70.5; DB 8; Length 578;
RESULT 590
ID AAM31666 standard; protein; 668 AA.
DE Arabidopsis thaliana heat shock protein like (GenBank: CAB46061).
PN WO200170929-A2.
PD 27-SEP-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match
Best Local Similarity 14.0%; Score 70.5; DB 4; Length 668;
RESULT 591
ID ADN93904 standard; protein; 902 AA.
DE Novel human protein sequence #620.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
14.0%; Score 70.5; DB 8; Length 902;

Best Local Similarity 35.0%; Pred. No. 1.3e+02;
RESULT 592
ID ADN99803 standard; protein; 902 AA.
DE Novel human protein sequence #619.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 14.0%; Score 70.5; DB 8; Length 902;
RESULT 593
ID ABU49383 standard; protein; 477 AA.
DE Protein encoded by Prokaryotic essential gene #34910.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 13.9%; Score 70; DB 6; Length 477;
RESULT 594
ID ADS23013 standard; protein; 689 AA.
DE Bacterial polypeptide #12046.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 13.9%; Score 70; DB 8; Length 689;
RESULT 595
ID ABU40129 standard; protein; 362 AA.
DE Protein encoded by Prokaryotic essential gene #25656.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 13.8%; Score 69.5; DB 6; Length 362;
RESULT 596
ID AAM73657 standard; protein; 423 AA.
DE M. tuberculosis antigen clone mTCC#2 protein sequence.
PN WO9853076-A2.
PD 26-NOV-1998.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 13.8%; Score 69.5; DB 2; Length 423;
RESULT 597
ID AAM73767 standard; protein; 423 AA.
DE M. tuberculosis antigen clone mTCC#2 protein sequence.
PN WO9853075-A2.
PD 26-NOV-1998.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 13.8%; Score 69.5; DB 2; Length 423;
RESULT 598
ID AAU08228 standard; protein; 423 AA.
DE Polypeptide encoded by Mycobacterium tuberculosis clone mTCC#2.
PN WO200162893-A2.
PD 30-AUG-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 13.8%; Score 69.5; DB 4; Length 423;
RESULT 599
ID AAU01891 standard; protein; 423 AA.
DE M. tuberculosis antigen mTCC#2 (Mtb41).
PN WO200124820-A1.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 13.8%; Score 69.5; DB 4; Length 423;
RESULT 600
ID AAE29715 standard; protein; 423 AA.
DE Mycobacterium sp. mTCC#1 antigenic protein.
PN WO200272792-A2.
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PD 19-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 13.8%; Score 69.5; DB 5; Length 423;  
Best Local Similarity 31.8%; Pred. No. 61;  
RESULT 601  
ID AAE17579 standard; protein; 423 AA.  
DE Mycobacterium species MTR41 (MTCC #1) protein.  
PN W0200198460-A2.  
PD 27-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 13.8%; Score 69.5; DB 5; Length 423;  
Best Local Similarity 31.8%; Pred. No. 61;  
RESULT 602  
ID AAB07585 standard; protein; 427 AA.  
DE Protein encoded by the bleomycin (BLM) gene cluster ORF31.  
PN W0200040704-A1.  
PD 13-JUL-2000.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 13.8%; Score 69.5; DB 3; Length 427;  
Best Local Similarity 32.0%; Pred. No. 62;  
RESULT 603  
ID AB021233 standard; protein; 458 AA.  
DE Protein encoded by Prokaryotic essential gene #6760.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITRA) PHARM INC.  
Query Match 13.8%; Score 69.5; DB 6; Length 458;  
Best Local Similarity 26.5%; Pred. No. 68;  
RESULT 604  
ID ADL65715 standard; protein; 492 AA.  
DE C. glutamicum RXA-associated protein #36.  
PN DE10154177-A1.  
PD 08-MAY-2003.  
PA (BADI) BASF AG.  
Query Match 13.8%; Score 69.5; DB 7; Length 492;  
Best Local Similarity 29.1%; Pred. No. 74;  
RESULT 605  
ID AAG90047 standard; protein; 495 AA.  
DE C glutamicum protein fragment SEQ ID NO: 3801.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOM) KYOMA HAKKO KOGYO KK.  
Query Match 13.8%; Score 69.5; DB 4; Length 495;  
Best Local Similarity 29.1%; Pred. No. 75;  
RESULT 606  
ID AAY32066 standard; protein; 710 AA.  
DE Mycobacterium tuberculosis antigen fusion protein MCB71F.  
PN W09951748-A2.  
PD 14-OCT-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 13.8%; Score 69.5; DB 2; Length 710;  
Best Local Similarity 31.8%; Pred. No. 1.2e+02;  
RESULT 608  
ID AAE17588 standard; protein; 710 AA.  
DE Mycobacterium species MTR31F fusion protein.  
PN W0200198460-A2.  
PD 27-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 13.8%; Score 69.5; DB 5; Length 710;  
Best Local Similarity 31.8%; Pred. No. 1.2e+02;  
RESULT 609  
ID ADF69767 standard; protein; 710 AA.  
DE Fusion protein #8 of M. tuberculosis antigen.  
PN US2003147911-A1.  
PD 07-AUG-2003.

PA (CORI-) CORIXA CORP.  
Query Match 13.8%; Score 69.5; DB 7; Length 710;  
Best Local Similarity 31.8%; Pred. No. 1.2e+02;  
RESULT 610  
ID AAU74595 standard; protein; 723 AA.  
DE Antigenic fusion protein DPV-MTI-MSL-MTCC2 (Mcb71F).  
PN US2002009459-A1.  
PD 24-JAN-2002.  
PA (REED/) REED S G.  
PA (SKET/) SKETKY Y A.  
PA (DILL/) DILLON D C.  
PA (ALDE/) ALDERSON M.  
PA (CAMP/) CAMPOS-NETO A.  
Query Match 13.8%; Score 69.5; DB 5; Length 723;  
Best Local Similarity 31.8%; Pred. No. 1.2e+02;  
RESULT 611  
ID AAY32064 standard; protein; 856 AA.  
DE Mycobacterium tuberculosis antigen fusion protein MCB86F.  
PN W09951748-A2.  
PD 14-OCT-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 13.8%; Score 69.5; DB 2; Length 856;  
Best Local Similarity 31.8%; Pred. No. 1.5e+02;  
RESULT 612  
ID ADF69763 standard; protein; 856 AA.  
DE Fusion protein #6 of M. tuberculosis antigen.  
PN US2003147911-A1.  
PD 07-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 13.8%; Score 69.5; DB 7; Length 856;  
Best Local Similarity 31.8%; Pred. No. 1.5e+02;  
RESULT 613  
ID AAU74593 standard; protein; 859 AA.  
DE Antigenic fusion protein Erid14-DPV-MTI-MSL-MTCC2 (Mcb86F).  
PN US2002009459-A1.  
PD 24-JAN-2002.  
PA (REED/) REED S G.  
PA (SKET/) SKETKY Y A.  
PA (DILL/) DILLON D C.  
PA (ALDE/) ALDERSON M.  
PA (CAMP/) CAMPOS-NETO A.  
Query Match 13.8%; Score 69.5; DB 5; Length 859;  
Best Local Similarity 31.8%; Pred. No. 1.5e+02;  
RESULT 614  
ID ADA26368 standard; protein; 1154 AA.  
DE Mycobacterium MTR72F-MTCC#2 (fusion MTR114F) protein.  
PN W02003070187-A2.  
PD 28-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 13.8%; Score 69.5; DB 8; Length 1154;  
Best Local Similarity 31.8%; Pred. No. 2.3e+02;  
RESULT 615  
ID ADU49404 standard; protein; 124 AA.  
DE O11-associated gene related protein #904.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 13.7%; Score 69; DB 8; Length 124;  
Best Local Similarity 31.8%; Pred. No. 14;  
RESULT 616  
ID ADR89163 standard; protein; 250 AA.  
DE Amino acid sequence of a reductase.  
PN EP1452588-A1.  
PD 01-SEP-2004.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 13.7%; Score 69; DB 8; Length 250;  
Best Local Similarity 26.2%; Pred. No. 35;  
RESULT 617  
ID ADM19851 standard; protein; 291 AA.

DE Protein encoded by novel human channel/transporter gene #169.  
PN WO200154472-A2.  
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 13.7%; Score 69; DB 4; Length 291;  
Best Local Similarity 32.1%; Pred. No. 42;

RESULT 618

ID AD541606 standard; protein; 424 AA.  
DE Bacterial polypeptide #20036.

PN US200323675-A1.

PD 18-DEC-2003.

PA (CAOY/) CNO Y.

PA (HUNK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

Query Match

Best Local Similarity 13.7%; Score 69; DB 8; Length 424;  
Best Local Similarity 33.7%; Pred. No. 69;

RESULT 619

ID AAB43214 standard; protein; 431 AA.  
DE Human ORF2978 polypeptide sequence SEQ ID NO:5956.

PN WO200058473-A2.

PD 05-OCT-2000.

PA (CURA-) CURAGEN CORP.

Query Match

Best Local Similarity 13.7%; Score 69; DB 3; Length 431;  
Best Local Similarity 24.1%; Pred. No. 71;

RESULT 620

ID ABO79368 standard; protein; 468 AA.  
DE Pseudomonas aeruginosa polypeptide #11543.

PN US651795-B1.

PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match

Best Local Similarity 13.7%; Score 69; DB 7; Length 468;  
Best Local Similarity 34.5%; Pred. No. 79;

RESULT 621

ID ABU19788 standard; protein; 470 AA.  
DE Protein encoded by Prokaryotic essential gene #5315.

PN WO200277183-A2.

PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match

Best Local Similarity 13.7%; Score 69; DB 6; Length 470;  
Best Local Similarity 27.0%; Pred. No. 80;

RESULT 622

ID ADG33826 standard; protein; 479 AA.  
DE Actinomyces dual condensation/epimerisation NRPS domain protein ID 85.

PN WO2003089641-A2.

PD 30-OCT-2003.

PA (ECOP-) ECOPIA BIOSCIENCES INC.

Query Match

Best Local Similarity 13.7%; Score 69; DB 7; Length 479;  
Best Local Similarity 35.5%; Pred. No. 82;

RESULT 623

ID ABB63462 standard; protein; 569 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 17178.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE-) PE CORP NY.

Query Match

Best Local Similarity 13.7%; Score 69; DB 4; Length 569;  
Best Local Similarity 25.2%; Pred. No. 1e+02;

RESULT 624

ID AAU61320 standard; protein; 628 AA.  
DE Propionibacterium acnes immunogenic protein #22216.

PN WO200181581-A2.

PD 01-NOV-2001.

PA (CORI-) CORIXA CORP.

Query Match

Best Local Similarity 13.7%; Score 69; DB 4; Length 628;  
Best Local Similarity 30.3%; Pred. No. 1.2e+02;

RESULT 625

ID ABM57839 standard; protein; 628 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #22515.

PN WO2003033515-A1.

PD 24-APR-2003.

PA (CORI-) CORIXA CORP.

Query Match

Best Local Similarity 13.7%; Score 69; DB 6; Length 628;

Best Local Similarity 30.3%; Pred. No. 1.2e+02;

RESULT 626

ID ABO73535 standard; protein; 163 AA.  
DE Pseudomonas aeruginosa polypeptide #5710.

PN US6551795-B1.

PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match

Best Local Similarity 13.6%; Score 68.5; DB 7; Length 163;  
Best Local Similarity 34.3%; Pred. No. 22;

RESULT 627

ID ABP6027 standard; protein; 377 AA.  
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:771.

PN EPI227152-A1.

PD 31-JUL-2002.

PA (NEST-) SOC PROD NESTLE SA.

Query Match

Best Local Similarity 13.6%; Score 68.5; DB 5; Length 377;  
Best Local Similarity 28.1%; Pred. No. 68;

RESULT 628

ID ABU33873 standard; protein; 404 AA.  
DE Protein encoded by Prokaryotic essential gene #19400.

PN WO200277183-A2.

PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match

Best Local Similarity 13.6%; Score 68.5; DB 6; Length 404;  
Best Local Similarity 31.0%; Pred. No. 74;

RESULT 629

ID ABU33816 standard; protein; 434 AA.  
DE Protein encoded by Prokaryotic essential gene #19343.

PN WO200277183-A2.

PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match

Best Local Similarity 13.6%; Score 68.5; DB 6; Length 434;  
Best Local Similarity 31.3%; Pred. No. 82;

RESULT 630

ID ABM65499 standard; protein; 436 AA.  
DE Propionibacterium acnes immunogenic polypeptide #30175.

PN WO2003033515-A1.

PD 24-APR-2003.

PA (CORI-) CORIXA CORP.

Query Match

Best Local Similarity 13.6%; Score 68.5; DB 6; Length 436;  
Best Local Similarity 34.8%; Pred. No. 82;

RESULT 631

ID ABU42281 standard; protein; 556 AA.  
DE Protein encoded by Prokaryotic essential gene #27808.

PN WO200277183-A2.

PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match

Best Local Similarity 13.6%; Score 68.5; DB 6; Length 556;  
Best Local Similarity 26.9%; Pred. No. 1.1e+02;

RESULT 632

ID AAE32018 standard; protein; 1445 AA.  
DE Human blood cell surface antigen, CD109 #2.

PN WO200285942-A2.

PD 31-OCT-2002.

PA (IVMC-) UNIV MCGILL.

Query Match

Best Local Similarity 13.6%; Score 68.5; DB 6; Length 1445;  
Best Local Similarity 25.5%; Pred. No. 4e+02;

RESULT 633

ID AAU50922 standard; protein; 101 AA.  
DE Propionibacterium acnes immunogenic protein #11818.

PN WO200181581-A2.

PD 01-NOV-2001.

PA (CORI-) CORIXA CORP.

Query Match

Best Local Similarity 13.5%; Score 68; DB 4; Length 101;  
Best Local Similarity 35.3%; Pred. No. 14;

RESULT 634

ID ABM47441 standard; protein; 101 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12117.

PN WO2003033515-A1.

PD 24-APR-2003.

PA (CORI-) CORIXA CORP.

Query Match

Best Local Similarity 13.5%; Score 68; DB 6; Length 101;  
Best Local Similarity 35.3%; Pred. No. 14;

RESULT 635  
ID ABU25976 standard; protein; 126 AA.  
DE Protein encoded by Prokaryotic essential gene #11503.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 13.5%; Score 68; DB 6; Length 126;  
Best Local Similarity 33.3%; Pred. No. 18;  
RESULT 636  
ID AAU27346 standard; protein; 206 AA.  
DE Novel bone marrow polypeptide #24.  
PN WO200164840-A2.  
PD 07-SEP-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 13.5%; Score 68; DB 4; Length 206;  
Best Local Similarity 40.0%; Pred. No. 35;  
RESULT 637  
ID ABG29616 standard; protein; 339 AA.  
DE Novel human diagnostic protein #29607.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 13.5%; Score 68; DB 4; Length 339;  
Best Local Similarity 29.7%; Pred. No. 67;  
RESULT 638  
ID ABR42493 standard; protein; 377 AA.  
DE Connermycin A1 biosynthetic decarboxylase.  
PN WO2003014352-A2.  
PD 20-FEB-2003.  
PA (UYTU-) UNIV TUEBINGEN.  
Query Match 13.5%; Score 68; DB 6; Length 377;  
Best Local Similarity 28.7%; Pred. No. 77;  
RESULT 639  
ID ABU40451 standard; protein; 466 AA.  
DE Protein encoded by Prokaryotic essential gene #25978.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 13.5%; Score 68; DB 6; Length 466;  
Best Local Similarity 31.8%; Pred. No. 1e+02;  
RESULT 640  
ID ADP04395 standard; protein; 480 AA.  
DE Bacterial polypeptide #508.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.5%; Score 68; DB 7; Length 480;  
Best Local Similarity 31.8%; Pred. No. 1.1e+02;  
RESULT 641  
ID ABM68704 standard; protein; 590 AA.  
DE Photocorhabdus luminescens protein sequence #1801.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 13.5%; Score 68; DB 6; Length 590;  
Best Local Similarity 29.3%; Pred. No. 1.4e+02;  
RESULT 642  
ID ABG28816 standard; protein; 896 AA.  
DE Novel human diagnostic protein #28807.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 13.5%; Score 68; DB 4; Length 896;  
Best Local Similarity 29.7%; Pred. No. 2.4e+02;  
RESULT 643  
ID AAB36119 standard; protein; 9510 AA.  
DE Streptomyces nodosus amphi gene encoded protein.  
PN WO200297082-A2.  
PD 05-DEC-2002.  
PA (UYDU-) UNIV COLLEGE DUBLIN.  
Query Match 13.5%; Score 68; DB 6; Length 9510;  
Best Local Similarity 30.8%; Pred. No. 5.4e+03;

RESULT 644  
ID APP65533 standard; protein; 227 AA.  
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:277.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST) SOC PROD NESTLE SA.  
Query Match 13.4%; Score 67.5; DB 5; Length 227;  
Best Local Similarity 29.6%; Pred. No. 45;  
RESULT 645  
ID AAU40714 standard; protein; 478 AA.  
DE Propionibacterium acnes immunogenic protein #1610.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 13.4%; Score 67.5; DB 4; Length 478;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 646  
ID ABM37233 standard; protein; 478 AA.  
DE Propionibacterium acnes membrane-related polypeptide #1909.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 13.4%; Score 67.5; DB 6; Length 478;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 647  
ID ABU36139 standard; protein; 1206 AA.  
DE Protein encoded by Prokaryotic essential gene #21666.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 13.4%; Score 67.5; DB 6; Length 1206;  
Best Local Similarity 29.4%; Pred. No. 4.1e+02;  
RESULT 648  
ID ABU26237 standard; protein; 1486 AA.  
DE Aspergillus fumigatus essential gene protein #895.  
PN WO200286090-A2.  
PD 31-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 13.4%; Score 67.5; DB 6; Length 1486;  
Best Local Similarity 30.6%; Pred. No. 5.3e+02;  
RESULT 649  
ID ADP56158 standard; protein; 2000 AA.  
DE Human PRO protein sequence SEQ ID NO:2134.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 13.4%; Score 67.5; DB 8; Length 2000;  
Best Local Similarity 29.2%; Pred. No. 7.9e+02;  
RESULT 650  
ID ABG79533 standard; protein; 2035 AA.  
DE Human tumour suppressor protein #19.  
PN WO200264775-A1.  
PD 22-AUG-2002.  
PA (BION-) BIONOMICS LTD.  
Query Match 13.4%; Score 67.5; DB 5; Length 2035;  
Best Local Similarity 29.2%; Pred. No. 8.1e+02;  
RESULT 651  
ID ADQ96094 standard; protein; 2035 AA.  
DE T cell activation associated protein #136.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAMI KASEI PHARMA CORP.  
Query Match 13.4%; Score 67.5; DB 8; Length 2035;  
Best Local Similarity 29.4%; Pred. No. 8.1e+02;  
RESULT 652  
ID ADR66316 standard; protein; 2035 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 170 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ) HINZMANN B.  
PA (DAHL) DAHL E.  
PA (ROSE) ROSENTHAL A.  
PA (HERM) HERMANN K.

PA (PITA/) PILARSKY C.  
Query Match 13.4%; Score 67.5; DB 8; Length 2035;  
Best Local Similarity 29.2%; Pred. No. 8.1e+02;  
RESULT 653  
ID ADP66658 standard; protein; 2035 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 170 #3.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PITA/) PILARSKY C.  
Query Match 13.4%; Score 67.5; DB 8; Length 2035;  
Best Local Similarity 29.2%; Pred. No. 8.1e+02;  
RESULT 654  
ID ADP5975 standard; protein; 2428 AA.  
DE Arabidopsis thaliana root extension-induction protein #2.  
PN JP2004187564-A.  
PD 08-JUL-2004.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
Query Match 13.4%; Score 67.5; DB 8; Length 2428;  
Best Local Similarity 32.1%; Pred. No. 1e+03;  
RESULT 655  
ID ABB67747 standard; protein; 109 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 30033.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 13.3%; Score 67; DB 4; Length 109;  
Best Local Similarity 40.0%; Pred. No. 20;  
RESULT 656  
ID ADI36330 standard; peptide; 109 AA.  
DE Drosophila CG13068 polypeptide, seq id 28.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND-) DANA FARBER CANCER INST INC.  
PA (GENO-) GEN HOSPITAL CORP.  
Query Match 13.3%; Score 67; DB 7; Length 109;  
Best Local Similarity 40.0%; Pred. No. 20;  
RESULT 657  
ID AAY52205 standard; protein; 351 AA.  
DE Mycobacterium leprae y3D protein.  
PN WO9954470-A2.  
PD 28-OCT-1999.  
PA (GLAX-) GLAXO GROUP LTD.  
Query Match 13.3%; Score 67; DB 3; Length 351;  
Best Local Similarity 34.5%; Pred. No. 91;  
RESULT 658  
ID ABU35772 standard; protein; 351 AA.  
DE Protein encoded by Prokaryotic essential gene #21299.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.3%; Score 67; DB 6; Length 351;  
Best Local Similarity 34.5%; Pred. No. 91;  
RESULT 659  
ID ABO78075 standard; protein; 419 AA.  
DE Pseudomonas aeruginosa polypeptide #10250.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.3%; Score 67; DB 7; Length 419;  
Best Local Similarity 29.9%; Pred. No. 1.1e+02;  
RESULT 660  
ID ADS28907 standard; protein; 423 AA.  
DE Bacterial polypeptide #1940.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.3%; Score 67; DB 8; Length 423;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 661  
ID ADC50032 standard; protein; 469 AA.  
DE Human macroprotein-51.59.  
PN CN1382720-A.  
PD 04-DEC-2002.  
PA (BIOW-) BOWINDOM GENE DEV INC SHANGHAI.  
Query Match 13.3%; Score 67; DB 7; Length 469;  
Best Local Similarity 36.4%; Pred. No. 1.3e+02;  
RESULT 662  
ID ADG3784 standard; protein; 469 AA.  
DE Actinomyces dual condensation/epimerisation NRPS domain protein ID 43.  
PN WO2003089641-A2.  
PD 30-OCT-2003.  
PA (ECOP-) ECOPRIA BIOSCIENCES INC.  
Query Match 13.3%; Score 67; DB 7; Length 469;  
Best Local Similarity 28.3%; Pred. No. 1.3e+02;  
RESULT 663  
ID ADS21155 standard; protein; 624 AA.  
DE Bacterial polypeptide #10186.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.3%; Score 67; DB 8; Length 624;  
Best Local Similarity 35.8%; Pred. No. 1.9e+02;  
RESULT 664  
ID ADS27851 standard; protein; 724 AA.  
DE Bacterial polypeptide #16884.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.3%; Score 67; DB 8; Length 724;  
Best Local Similarity 30.4%; Pred. No. 2.4e+02;  
RESULT 665  
ID ABU40135 standard; protein; 854 AA.  
DE Protein encoded by Prokaryotic essential gene #25662.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.3%; Score 67; DB 6; Length 854;  
Best Local Similarity 28.6%; Pred. No. 2.9e+02;  
RESULT 666  
ID ABM85277 standard; protein; 1249 AA.  
DE Human protein sequence hCP1635124.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 13.3%; Score 67; DB 7; Length 1249;  
Best Local Similarity 36.4%; Pred. No. 4.8e+02;  
RESULT 667  
ID AAR14108 standard; protein; 180 AA.  
DE Zea mays 15 kd seed storage protein.  
PN WO9113993-A.  
PD 19-SEP-1991.  
PA (UPUC-) UPJOHN CO.  
Query Match 13.2%; Score 66.5; DB 2; Length 180;  
Best Local Similarity 38.6%; Pred. No. 43;  
RESULT 668  
ID ABU41499 standard; protein; 322 AA.  
DE Protein encoded by Prokaryotic essential gene #27026.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.

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Query Match      13.2%; Score 66.5; DB 6; Length 322;
Best Local Similarity 27.4%; Pred. No. 92;
RESULT 669
ID ABO67390 standard; protein; 323 AA.
DE Klebsiella pneumoniae polypeptide seqid 13907.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match      13.2%; Score 66.5; DB 7; Length 323;
Best Local Similarity 30.9%; Pred. No. 93;
RESULT 670
ID ADB75312 standard; protein; 465 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match      13.2%; Score 66.5; DB 7; Length 465;
Best Local Similarity 28.9%; Pred. No. 1.5e+02;
RESULT 671
ID ABB93369 standard; protein; 491 AA.
DE Herbicidally active polypeptide SEQ ID NO 2580.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB ) BAYER AG.
Query Match      13.2%; Score 66.5; DB 5; Length 491;
Best Local Similarity 28.3%; Pred. No. 1.6e+02;
RESULT 672
ID ADN24365 standard; protein; 667 AA.
DE Bacterial polypeptide #7018.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match      13.2%; Score 66.5; DB 8; Length 667;
Best Local Similarity 31.6%; Pred. No. 2.4e+02;
RESULT 673
ID ADF61855 standard; protein; 115 AA.
DE G3-2H6 protein which is derived from DNA antisense to human DDX9 DNA.
PN WO2003088910-A2.
PD 30-OCT-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match      13.1%; Score 66; DB 7; Length 115;
Best Local Similarity 32.8%; Pred. No. 27;
RESULT 674
ID ABO66080 standard; protein; 310 AA.
DE Klebsiella pneumoniae polypeptide seqid 12597.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match      13.1%; Score 66; DB 7; Length 310;
Best Local Similarity 28.6%; Pred. No. 1e+02;
RESULT 675
ID ABU45577 standard; protein; 330 AA.
DE Protein encoded by Prokaryotic essential gene #35104.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      13.1%; Score 66; DB 6; Length 330;
Best Local Similarity 31.5%; Pred. No. 1.1e+02;
RESULT 676
ID ABM85476 standard; protein; 332 AA.
DE Mouse protein sequence mcp5983.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match      13.1%; Score 66; DB 7; Length 332;
Best Local Similarity 38.6%; Pred. No. 1.1e+02;
RESULT 677
ID ADR06365 standard; protein; 370 AA.
DE N meningitidis P1:22,14 PorA protein SeqID25.

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PN WO2004065603-A2.
PD 05-AUG-2004.
PA (AMHP ) WYETH HOLDINGS CORP.
Query Match      13.1%; Score 66; DB 8; Length 370;
Best Local Similarity 28.7%; Pred. No. 1.3e+02;
RESULT 678
ID AAY42520 standard; protein; 390 AA.
DE Maize anthranilate phosphoribosyltransferase.
PN WO9949013-A2.
PD 30-SEP-1999.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match      13.1%; Score 66; DB 2; Length 390;
Best Local Similarity 23.5%; Pred. No. 1.4e+02;
RESULT 679
ID ABU20063 standard; protein; 440 AA.
DE Protein encoded by Prokaryotic essential gene #5590.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      13.1%; Score 66; DB 6; Length 440;
Best Local Similarity 27.5%; Pred. No. 1.6e+02;
RESULT 680
ID AAU62614 standard; protein; 543 AA.
DE Propionibacterium acnes immunogenic protein #23510.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match      13.1%; Score 66; DB 4; Length 543;
Best Local Similarity 29.1%; Pred. No. 2.1e+02;
RESULT 681
ID ABM59133 standard; protein; 543 AA.
DE Propionibacterium acnes membrane-related polypeptide #23809.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match      13.1%; Score 66; DB 6; Length 543;
Best Local Similarity 29.1%; Pred. No. 2.1e+02;
RESULT 682
ID ADS23240 standard; protein; 581 AA.
DE Bacterial polypeptide #12273.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match      13.1%; Score 66; DB 8; Length 581;
Best Local Similarity 27.9%; Pred. No. 2.3e+02;
RESULT 683
ID ABO82733 standard; protein; 587 AA.
DE Pseudomonas aeruginosa polypeptide #14908.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match      13.1%; Score 66; DB 7; Length 587;
Best Local Similarity 30.6%; Pred. No. 2.3e+02;
RESULT 684
ID AAR32007 standard; protein; 638 AA.
DE Herbicide sensitive AHAS.
PN EP525384-A2.
PD 03-FEB-1993.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match      13.1%; Score 66; DB 2; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
RESULT 685
ID AAR32008 standard; protein; 638 AA.
DE Herbicide sensitive AHAS.
PN EP525384-A2.
PD 03-FEB-1993.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match      13.1%; Score 66; DB 2; Length 638;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;

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RESULT 686
ID AAR32006 standard; protein; 638 AA.
DE Herbicide resistant AHAS.
PN EP525384-A2.
PD 03-FEB-1993.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match
Best Local Similarity 13.1%; Score 66; DB 2; Length 638;
Pred. No. 2.6e+02;
ID AAW54055 standard; protein; 638 AA.
DE AHAS clone.
PN US5767361-A.
PD 16-JUN-1998.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match
Best Local Similarity 13.1%; Score 66; DB 2; Length 638;
Pred. No. 2.6e+02;
RESULT 688
ID AAW54054 standard; protein; 638 AA.
DE AHAS clone.
PN US5767361-A.
PD 16-JUN-1998.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match
Best Local Similarity 13.1%; Score 66; DB 2; Length 638;
Pred. No. 2.6e+02;
RESULT 689
ID AAW54053 standard; protein; 638 AA.
DE AHAS clone.
PN US5767361-A.
PD 16-JUN-1998.
PA (AMCY ) AMERICAN CYANAMID CO.
Query Match
Best Local Similarity 13.1%; Score 66; DB 2; Length 638;
Pred. No. 2.6e+02;
RESULT 690
ID ABG7110 standard; protein; 638 AA.
DE Maize acetohydroxy acid synthase enzyme (AHAS) mutant #2.
PN US6444875-B1.
PD 03-SEP-2002.
PA (BADT ) BASF AG.
Query Match
Best Local Similarity 13.1%; Score 66; DB 5; Length 638;
Pred. No. 2.6e+02;
RESULT 691
ID ABG71108 standard; protein; 638 AA.
DE Maize acetohydroxy acid synthase enzyme (AHAS) .
PN US6444875-B1.
PD 03-SEP-2002.
PA (BADT ) BASF AG.
Query Match
Best Local Similarity 13.1%; Score 66; DB 5; Length 638;
Pred. No. 2.6e+02;
RESULT 692
ID ABG71109 standard; protein; 638 AA.
DE Maize acetohydroxy acid synthase enzyme (AHAS) mutant #1.
PN US6444875-B1.
PD 03-SEP-2002.
PA (BADT ) BASF AG.
Query Match
Best Local Similarity 13.1%; Score 66; DB 5; Length 638;
Pred. No. 2.6e+02;
RESULT 693
ID AAW18306 standard; protein; 1043 AA.
DE Photorhabdus luminescens insect toxin Tccc.
PN WO9717432-A1.
PD 15-MAY-1997.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
Query Match
Best Local Similarity 13.1%; Score 66; DB 2; Length 1043;
Pred. No. 4.9e+02;
RESULT 694
ID AAW56569 standard; protein; 1043 AA.
DE Toxin Tccc, encoded by the tccc gene from genomic region tcc.
PN WO9808932-A1.
PD 05-MAR-1998.
PA (DOMC ) DOWELANCO.
Query Match
Best Local Similarity 13.1%; Score 66; DB 2; Length 1043;
Pred. No. 4.9e+02;
RESULT 695
ID ADR21577 standard; protein; 1043 AA.
DE Photorhabdus Tccci toxin.
PN WO2004067727-A2.
PD 12-AUG-2004.
PA (DOMC ) DOW AGROSCIENCES LLC.
Query Match
Best Local Similarity 13.1%; Score 66; DB 8; Length 1043;
Pred. No. 4.9e+02;
RESULT 696
ID ABU05722 standard; protein; 1400 AA.
DE M. tuberculosis and M. leprae marker protein #373.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP ) INST PASTEUR.
Query Match
Best Local Similarity 13.1%; Score 66; DB 5; Length 1400;
Pred. No. 7.3e+02;
RESULT 697
ID ABB58564 standard; protein; 1664 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2484.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 13.1%; Score 66; DB 4; Length 1664;
Pred. No. 9.1e+02;
RESULT 698
ID ADR09003 standard; protein; 119 AA.
DE Human protein useful for treating neurological disease Seq 2509.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 8; Length 119;
Pred. No. 32;
RESULT 699
ID AAU76435 standard; protein; 319 AA.
DE Novel desulphurising microbe associated protein #2.
PN JP2001309788-A.
PD 06-NOV-2001.
PA (SEKI-) ZH SEKIYU SANGYO KASSERIKA CENTER.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 5; Length 319;
Pred. No. 1.2e+02;
RESULT 700
ID AAU55341 standard; protein; 321 AA.
DE Enterococcus faecalis cellular proliferation protein #628.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 4; Length 321;
Pred. No. 1.2e+02;
RESULT 701
ID ABU29413 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #14940.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 6; Length 321;
Pred. No. 1.2e+02;
RESULT 702
ID ADH86584 standard; protein; 346 AA.
DE Enterococcus faecalis polypeptide #1064.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC) DOUCETTE-STAMM L A.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 7; Length 346;
Pred. No. 1.3e+02;
RESULT 703
ID ABO64338 standard; protein; 407 AA.
DE Klebsiella pneumoniae polypeptide seqid 10855.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 13.0%; Score 65.5; DB 7; Length 407;
Pred. No. 1.6e+02;
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RESULT 704
ID ABU0589 standard; protein; 491 AA.
DE M. tuberculosis and M. leprae marker protein #540.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSE-) INSR PASTEUR.
Query Match 13.0%; Score 65.5; DB 5; Length 491;
Best Local Similarity 36.7%; Pred. No. 2.1e+02;
RESULT 705
ID ADL2268 standard; protein; 529 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 137.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.0%; Score 65.5; DB 7; Length 529;
Best Local Similarity 34.7%; Pred. No. 2.3e+02;
RESULT 706
ID ADF0585 standard; protein; 645 AA.
DE Bacterial polypeptide #1968.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 65.5; DB 7; Length 645;
Best Local Similarity 33.3%; Pred. No. 3e+02;
RESULT 707
ID ADC9736 standard; protein; 803 AA.
DE Rhizobitoxine rtxc gene derived protein, SEQ ID No 9.
PN JP2003093069-A.
PD 02-APR-2003.
PA (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.
Query Match 13.0%; Score 65.5; DB 7; Length 803;
Best Local Similarity 31.4%; Pred. No. 4e+02;
RESULT 708
ID ABU23297 standard; protein; 808 AA.
DE Protein encoded by Prokaryotic essential gene #8824.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.0%; Score 65.5; DB 6; Length 808;
Best Local Similarity 28.9%; Pred. No. 4e+02;
RESULT 709
ID ABU3614 standard; protein; 848 AA.
DE Protein encoded by Prokaryotic essential gene #21641.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.0%; Score 65.5; DB 6; Length 848;
Best Local Similarity 28.8%; Pred. No. 4.3e+02;
RESULT 710
ID ADS42058 standard; protein; 857 AA.
DE Bacterial polypeptide #20488.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.0%; Score 65.5; DB 8; Length 857;
Best Local Similarity 23.9%; Pred. No. 4.3e+02;
RESULT 711
ID ADN26721 standard; protein; 857 AA.
DE Bacterial polypeptide #9374.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.0%; Score 65.5; DB 8; Length 857;
Best Local Similarity 33.3%; Pred. No. 4.3e+02;
RESULT 712
ID ADM48067 standard; protein; 861 AA.
DE Polypeptide sequence #117 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 13.0%; Score 65.5; DB 8; Length 861;
Best Local Similarity 33.3%; Pred. No. 4.4e+02;
RESULT 713
ID ADS28481 standard; protein; 861 AA.
DE Bacterial polypeptide #17514.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.0%; Score 65.5; DB 8; Length 861;
Best Local Similarity 33.3%; Pred. No. 4.4e+02;
RESULT 714
ID ABG06406 standard; protein; 974 AA.
DE Novel human diagnostic protein #6397.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 65.5; DB 4; Length 974;
Best Local Similarity 28.8%; Pred. No. 5.1e+02;
RESULT 715
ID ABO59456 standard; protein; 1633 AA.
DE Human genome derived single exon protein #5690.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 13.0%; Score 65.5; DB 8; Length 1633;
Best Local Similarity 29.5%; Pred. No. 1e+03;
RESULT 716
ID ADO97066 standard; protein; 2250 AA.
DE Human cancer associated sequence HP11-012, SEQ ID 42.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.0%; Score 65.5; DB 8; Length 2250;
Best Local Similarity 27.6%; Pred. No. 1.5e+03;
RESULT 717
ID ABR58648 standard; protein; 2303 AA.
DE Human cancer related protein SEQ ID NO.305.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match 13.0%; Score 65.5; DB 6; Length 2303;
Best Local Similarity 29.5%; Pred. No. 1.6e+03;
RESULT 718
ID ADO08045 standard; protein; 2303 AA.
DE Human polypeptide #46.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 13.0%; Score 65.5; DB 8; Length 2303;
Best Local Similarity 29.5%; Pred. No. 1.6e+03;
RESULT 719
ID AAB70968 standard; protein; 4924 AA.
DE S. spinoza protein fragment encoded by ORF21, SEQ ID 48.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (PARB-) BAYER AG.
Query Match 13.0%; Score 65.5; DB 4; Length 4924;
Best Local Similarity 28.6%; Pred. No. 4.3e+03;
RESULT 720
ID AAV39300 standard; protein; 4928 AA.
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DE Spnd a polyketide synthase.  
PN WO9946387-A1.  
PD 16-SEP-1999.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Query Match 13.0%; Score 65.5; DB 2; Length 4928;  
Best Local Similarity 28.6%; Pred. No. 4.3e+03;  
RESULT 721  
ID AAG53754 standard; protein; 178 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66467.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.9%; Score 65; DB 3; Length 178;  
Best Local Similarity 30.1%; Pred. No. 63;  
RESULT 722  
ID ABO65795 standard; protein; 180 AA.  
DE Klebsiella pneumoniae polypeptide seqid 12312.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.9%; Score 65; DB 7; Length 180;  
Best Local Similarity 26.3%; Pred. No. 63;  
RESULT 723  
ID ABU34031 standard; protein; 260 AA.  
DE Protein encoded by Prokaryotic essential gene #19558.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 12.9%; Score 65; DB 6; Length 260;  
Best Local Similarity 26.6%; Pred. No. 1e+02;  
RESULT 724  
ID AAB79808 standard; protein; 267 AA.  
DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:350.  
PN WO200100843-A2.  
PD 04-JAN-2001.  
PA (BADT) BASF AG.  
Query Match 12.9%; Score 65; DB 4; Length 267;  
Best Local Similarity 34.8%; Pred. No. 1.1e+02;  
RESULT 725  
ID AAG89997 standard; protein; 267 AA.  
DE C glutamicum protein fragment SEQ ID NO: 3751.  
PN EP108790-A2.  
PD 20-JUN-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Query Match 12.9%; Score 65; DB 4; Length 267;  
Best Local Similarity 34.8%; Pred. No. 1.1e+02;  
RESULT 726  
ID ADC96055 standard; protein; 269 AA.  
DE E. faecium protein sequence SEQ ID 5682.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.9%; Score 65; DB 7; Length 269;  
Best Local Similarity 26.6%; Pred. No. 1.1e+02;  
RESULT 727  
ID AAB12308 standard; protein; 329 AA.  
DE Human secreted protein encoded by gene 8 clone HCWEM59.  
PN WO200029422-A1.  
PD 25-MAY-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.9%; Score 65; DB 3; Length 329;  
Best Local Similarity 31.9%; Pred. No. 1.4e+02;  
RESULT 728  
ID ABO72875 standard; protein; 350 AA.  
DE Pseudomonas aeruginosa polypeptide #5050.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.9%; Score 65; DB 7; Length 350;  
Best Local Similarity 29.5%; Pred. No. 1.5e+02;  
RESULT 729  
ID AAG4542 standard; protein; 452 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55808.  
PN EP1033405-A2.

PD 06-SEP-2000.  
Query Match 12.9%; Score 65; DB 3; Length 452;  
Best Local Similarity 30.1%; Pred. No. 2.1e+02;  
RESULT 730  
ID AAM52126 standard; protein; 457 AA.  
DE Human alpha-2CAR variant protein.  
PN WO200179561-A2.  
PD 25-OCT-2001.  
PA (LIGG/) LIGGETT S. B.  
PA (SMAL/) SMALL K M.  
Query Match 12.9%; Score 65; DB 4; Length 457;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 731  
ID AAR54834 standard; protein; 458 AA.  
DE Human derived adrenalinine alpha 2CII receptor.  
PN JP6121686-A.  
PD 06-MAY-1994.  
PA (ASAH) ASAH KASEI KOGYO KK.  
Query Match 12.9%; Score 65; DB 2; Length 458;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 732  
ID ADM37054 standard; protein; 458 AA.  
DE Human alpha-2C adrenergic receptor variant protein SEQ ID NO:7.  
PN WO2004023101-A2.  
PD 18-MAR-2004.  
PA (UYCT-) UNIV CINCINNATI.  
Query Match 12.9%; Score 65; DB 8; Length 458;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 733  
ID AAM52124 standard; protein; 461 AA.  
DE Human alpha-2CAR protein.  
PN WO200179561-A2.  
PD 25-OCT-2001.  
PA (LIGG/) LIGGETT S. B.  
PA (SMAL/) SMALL K M.  
Query Match 12.9%; Score 65; DB 4; Length 461;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 734  
ID ABP81781 standard; protein; 461 AA.  
DE Human alpha 2c-adrenoceptor protein SEQ ID NO:44.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 12.9%; Score 65; DB 6; Length 461;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 735  
ID ADP68565 standard; protein; 461 AA.  
DE Human heart mitochondrial protein as a therapeutic target SeqID371.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 12.9%; Score 65; DB 7; Length 461;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 736  
ID ADO29175 standard; protein; 461 AA.  
DE Human GPCR ADRA2C, SEQ ID NO:276.  
PN WO200404000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 12.9%; Score 65; DB 8; Length 461;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 737  
ID ADQ18949 standard; protein; 461 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1768.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 12.9%; Score 65; DB 8; Length 461;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 738  
ID ADM37052 standard; protein; 462 AA.  
DE Human alpha-2C adrenergic receptor protein SEQ ID NO:5.

PN WO2004023101-A2.  
PD 18-MAR-2004.  
PA (UYCI-) UNIV CINCINNATI.  
Query Match 12.9%; Score 65; DB 8; Length 462;  
Best Local Similarity 32.6%; Pred. No. 2.2e+02;  
RESULT 739  
ID ABG10418 standard; protein; 553 AA.  
DE Novel human diagnostic protein #10409.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.9%; Score 65; DB 4; Length 553;  
Best Local Similarity 30.2%; Pred. No. 2.8e+02;  
RESULT 740  
ID ABG08254 standard; protein; 622 AA.  
DE Novel human diagnostic protein #8245.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.9%; Score 65; DB 4; Length 622;  
Best Local Similarity 30.6%; Pred. No. 3.2e+02;  
RESULT 741  
ID AAR05588 standard; protein; 638 AA.  
DE Acetylcholinesterase (AChE) from maize C1 genome.  
PN EP360750-A.  
PD 28-MAR-1990.  
PA (CIBA) CIBA GEIGY AG.  
Query Match 12.9%; Score 65; DB 2; Length 638;  
Best Local Similarity 25.3%; Pred. No. 3.4e+02;  
RESULT 742  
ID AAG98345 standard; protein; 693 AA.  
DE Escherichia coli protein sequence SEQ ID NO:193.  
PN WO200148209-A2.  
PD 05-JUL-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.9%; Score 65; DB 4; Length 693;  
Best Local Similarity 30.2%; Pred. No. 3.7e+02;  
RESULT 743  
ID ABO71319 standard; protein; 703 AA.  
DE Pseudomonas aeruginosa polypeptide #3494.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.9%; Score 65; DB 7; Length 703;  
Best Local Similarity 28.1%; Pred. No. 3.8e+02;  
RESULT 744  
ID ABP43735 standard; protein; 725 AA.  
DE DKFZP434E192 protein.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.9%; Score 65; DB 5; Length 725;  
Best Local Similarity 30.6%; Pred. No. 4e+02;  
RESULT 745  
ID ABU22751 standard; protein; 757 AA.  
DE Protein encoded by Prokaryotic essential gene #8278.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.9%; Score 65; DB 6; Length 757;  
Best Local Similarity 31.9%; Pred. No. 4.2e+02;  
RESULT 746  
ID ABG79521 standard; protein; 832 AA.  
DE Human tumour suppressor protein #7.  
PN WO200264775-A1.  
PD 22-AUG-2002.  
PA (BIOM-) BIOMONICS LTD.  
Query Match 12.9%; Score 65; DB 5; Length 832;  
Best Local Similarity 30.6%; Pred. No. 4.8e+02;  
RESULT 747  
ID ABG08255 standard; protein; 852 AA.  
DE Novel human diagnostic protein #8246.  
PN WO200175067-A2.

PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.9%; Score 65; DB 4; Length 852;  
Best Local Similarity 30.6%; Pred. No. 4.9e+02;  
RESULT 748  
ID AAU40390 standard; protein; 885 AA.  
DE Propionibacterium acnes immunogenic protein #1286.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 12.9%; Score 65; DB 4; Length 885;  
Best Local Similarity 23.0%; Pred. No. 5.2e+02;  
RESULT 749  
ID ABM36909 standard; protein; 885 AA.  
DE Propionibacterium acnes protease/proteinase-related polypeptide #1585.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 12.9%; Score 65; DB 6; Length 885;  
Best Local Similarity 23.0%; Pred. No. 5.2e+02;  
RESULT 750  
ID ABG97452 standard; protein; 1892 AA.  
DE S. aerocolonigenes PKSE protein.  
PN CA2387401-A1.  
PD 04-SEP-2002.  
PA (ECOP-) ECORIA BIOSCIENCES INC.  
Query Match 12.9%; Score 65; DB 5; Length 1892;  
Best Local Similarity 28.4%; Pred. No. 1.4e+03;  
RESULT 751  
ID ADN20770 standard; protein; 2081 AA.  
DE Bacterial polypeptide #3423.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.9%; Score 65; DB 8; Length 2081;  
Best Local Similarity 23.5%; Pred. No. 1.6e+03;  
RESULT 752  
ID ADE55508 standard; protein; 2622 AA.  
DE Rat Protein AACT8143, SEQ ID NO 1325.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO-) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 12.9%; Score 65; DB 7; Length 2622;  
Best Local Similarity 27.7%; Pred. No. 2.2e+03;  
RESULT 753  
ID ABB64188 standard; protein; 2857 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 19356.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.9%; Score 65; DB 4; Length 2857;  
Best Local Similarity 32.7%; Pred. No. 2.4e+03;  
RESULT 754  
ID ABG99872 standard; protein; 4106 AA.  
DE S. cinamonensis MonAV/polyketide synthase multi-enzyme MONS5.  
PN WO200168867-A1.  
PD 20-SEP-2001.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
Query Match 12.9%; Score 65; DB 4; Length 4106;  
Best Local Similarity 27.7%; Pred. No. 3.9e+03;  
RESULT 755  
ID ABG00972 standard; protein; 4274 AA.  
DE Novel human diagnostic protein #963.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.9%; Score 65; DB 4; Length 4274;  
Best Local Similarity 26.2%; Pred. No. 4.1e+03;

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RESULT 756
ID ABG07375 standard; protein; 4386 AA.
DE Novel human diagnostic protein #7366.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 4; Length 4386;
RESULT 757
ID ABG21944 standard; protein; 4397 AA.
DE Novel human diagnostic protein #21935.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 4; Length 4397;
RESULT 758
ID ADG91698 standard; protein; 8147 AA.
DE Polyketide synthase ORF10 protein, SEQ ID 21.
PN WO2004065401-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOP1A BIOSCIENCES INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 8; Length 8147;
RESULT 759
ID ADP31311 standard; protein; 10944 AA.
DE Human secreted protein SEQ ID #2078.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 8; Length 10944;
RESULT 760
ID ADP31310 standard; protein; 11328 AA.
DE Human secreted protein SEQ ID #2077.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 12.9%; Score 65; DB 8; Length 11328;
RESULT 761
ID ABB06921 standard; protein; 159 AA.
DE Micromonospora carbonacea evernimycin locus protein ORF 40.
PN WO200151801-A2.
PD 02-AUG-2001.
PA (ECOP-) ECOP1A BIOSCIENCES INC.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 4; Length 159;
RESULT 762
ID AAG81022 standard; protein; 203 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:3138.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 4; Length 203;
RESULT 763
ID AAP82484 standard; protein; 294 AA.
DE Tropoelactin.
PN JF63014694-A.
PD 21-JAN-1988.
PA (SHIS) SHISEIDO CO LTD.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 1; Length 294;
RESULT 764
ID ABO69335 standard; protein; 308 AA.
DE Pseudomonas aeruginosa polypeptide #1510.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 308;
RESULT 765
ID ABO79277 standard; protein; 310 AA.
DE Pseudomonas aeruginosa polypeptide #11452.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 310;
RESULT 766
ID ABU43211 standard; protein; 321 AA.
DE Protein encoded by Prokaryotic essential gene #28738.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 6; Length 321;
RESULT 767
ID ABP39992 standard; protein; 326 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4837.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 5; Length 326;
RESULT 768
ID ADS07056 standard; protein; 326 AA.
DE Staphylococcus epidermidis polypeptide seqid 6351.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 326;
RESULT 769
ID ABO83285 standard; protein; 342 AA.
DE Pseudomonas aeruginosa polypeptide #15460.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 342;
RESULT 770
ID ADN22084 standard; protein; 416 AA.
DE Bacterial polypeptide #4737.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 416;
RESULT 771
ID ADN24843 standard; protein; 416 AA.
DE Bacterial polypeptide #7496.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 416;
RESULT 772
ID ABU47347 standard; protein; 433 AA.
DE Protein encoded by Prokaryotic essential gene #32874.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 6; Length 433;
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Best Local Similarity 32.1%; Pred. No. 2.3e+02;  
RESULT 773  
ID ABU21899 standard; protein; 493 AA.  
DE Protein encoded by Prokaryotic essential gene #7426.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.8%; Score 64.5; DB 6; Length 493;  
Best Local Similarity 30.3%; Pred. No. 2.7e+02;  
RESULT 774  
ID ABG70144 standard; protein; 548 AA.  
DE Human prey protein for Shigella ipac #8.  
PN WO200257303-A2.  
PD 25-JUL-2002.  
PA (HYBR-) HYBRIGENICS.  
Query Match 12.8%; Score 64.5; DB 5; Length 548;  
Best Local Similarity 24.3%; Pred. No. 3.1e+02;  
RESULT 775  
ID ADO80215 standard; protein; 594 AA.  
DE Actinobacillus pleuropneumoniae Aprt exotoxin.  
PN WO2004045639-A1.  
PD 03-JUN-2004.  
PA (HIPR-) LAB HIPRA SA.  
Query Match 12.8%; Score 64.5; DB 8; Length 594;  
Best Local Similarity 29.6%; Pred. No. 3.5e+02;  
RESULT 776  
ID ADS42744 standard; protein; 620 AA.  
DE Bacterial polypeptide #21174.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.8%; Score 64.5; DB 8; Length 620;  
Best Local Similarity 34.4%; Pred. No. 3.7e+02;  
RESULT 777  
ID ABU41121 standard; protein; 624 AA.  
DE Protein encoded by Prokaryotic essential gene #26648.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.8%; Score 64.5; DB 6; Length 624;  
Best Local Similarity 33.3%; Pred. No. 3.7e+02;  
RESULT 778  
ID ADP31265 standard; protein; 642 AA.  
DE Human secreted protein SEQ ID #2032.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.8%; Score 64.5; DB 8; Length 642;  
Best Local Similarity 40.0%; Pred. No. 3.8e+02;  
RESULT 779  
ID ABG70135 standard; protein; 698 AA.  
DE Human prey protein for Shigella ipad #12.  
PN WO200257303-A2.  
PD 25-JUL-2002.  
PA (HYBR-) HYBRIGENICS.  
Query Match 12.8%; Score 64.5; DB 5; Length 698;  
Best Local Similarity 24.3%; Pred. No. 4.3e+02;  
RESULT 780  
ID ABM65192 standard; protein; 805 AA.  
DE Propionibacterium acnes immunogenic polypeptide #29868.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 12.8%; Score 64.5; DB 6; Length 805;  
Best Local Similarity 29.0%; Pred. No. 5.2e+02;  
RESULT 781  
ID ADN26513 standard; protein; 857 AA.  
DE Bacterial polypeptide #9166.  
PN US2003233675-A1.

PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.8%; Score 64.5; DB 8; Length 857;  
Best Local Similarity 33.3%; Pred. No. 5.6e+02;  
RESULT 782  
ID AAV60702 standard; protein; 890 AA.  
DE Propionibacterium acnes immunogenic protein #21598.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 12.8%; Score 64.5; DB 4; Length 890;  
Best Local Similarity 29.0%; Pred. No. 5.9e+02;  
RESULT 783  
ID ABM57221 standard; protein; 890 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #21897.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 12.8%; Score 64.5; DB 6; Length 890;  
Best Local Similarity 29.0%; Pred. No. 5.9e+02;  
RESULT 784  
ID ABO82712 standard; protein; 906 AA.  
DE Pseudomonas aeruginosa polypeptide #14887.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.8%; Score 64.5; DB 7; Length 906;  
Best Local Similarity 30.0%; Pred. No. 6.1e+02;  
RESULT 785  
ID ADC00492 standard; protein; 952 AA.  
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 537.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Query Match 12.8%; Score 64.5; DB 7; Length 952;  
Best Local Similarity 29.9%; Pred. No. 6.5e+02;  
RESULT 786  
ID AAM22152 standard; protein; 1022 AA.  
DE Apxia protein.  
PN CA2170839-A.  
PD 02-SEP-1996.  
PA (UYGU-) UNIV GUELPH.  
Query Match 12.8%; Score 64.5; DB 2; Length 1022;  
Best Local Similarity 29.6%; Pred. No. 7.1e+02;  
RESULT 787  
ID AAY51406 standard; protein; 1022 AA.  
DE A. pleuropneumoniae apxia protein.  
PN US6019984-A.  
PD 01-FEB-2000.  
PA (UYGU-) UNIV GUELPH.  
Query Match 12.8%; Score 64.5; DB 3; Length 1022;  
Best Local Similarity 29.6%; Pred. No. 7.1e+02;  
RESULT 788  
ID AAR76991 standard; protein; 1023 AA.  
DE Lhaa (low homology to appA) protein.  
PN JP07138185-A.  
PD 30-MAY-1995.  
PA (NISK) NIPPON SEIBUNSU KAGAKU KENKYUSHO ZH.  
Query Match 12.8%; Score 64.5; DB 2; Length 1023;  
Best Local Similarity 29.6%; Pred. No. 7.1e+02;  
RESULT 789  
ID ADC00339 standard; protein; 1026 AA.  
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 384.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Query Match 12.8%; Score 64.5; DB 7; Length 1026;  
Best Local Similarity 29.9%; Pred. No. 7.1e+02;  
RESULT 790

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ID ADN20624 standard; protein; 1026 AA.
DE Bacterial polypeptide #3277.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
ID (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 1026;
RESULT 791
ID ADC00043 standard; protein; 1080 AA.
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 88.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 1080;
RESULT 792
ID ABO74881 standard; protein; 1413 AA.
DE Pseudomonas aeruginosa polypeptide #7056.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 1413;
RESULT 793
ID AAY92060 standard; protein; 1674 AA.
DE Murine APC-2 polypeptide.
PN WO20018913-A1.
PD 06-APR-2000.
PA (UYUT-) RIJKSUNIV UTRECHT.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 3; Length 1674;
RESULT 794
ID AAB50674 standard; protein; 2274 AA.
DE Mouse APC-2 protein sequence SEQ ID NO:65.
PN WO200073328-A2.
PD 07-DEC-2000.
PA (DEVG-) DEVGEN NV.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 4; Length 2274;
RESULT 795
ID ADO08047 standard; protein; 2274 AA.
DE Mouse polypeptide #43.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 2274;
RESULT 796
ID ABB71657 standard; protein; 2328 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41763.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 4; Length 2328;
RESULT 797
ID AAB41087 standard; protein; 2541 AA.
DE Human ORFX ORF851 polypeptide sequence SEQ ID NO:1702.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 3; Length 2541;
RESULT 798
ID ADD45522 standard; protein; 2541 AA.
DE Human Protein Q9Y490, SEQ ID NO 11186.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 2541;
RESULT 799
ID ADE58868 standard; protein; 2541 AA.
DE Human Protein Q9Y490, SEQ ID NO 4756.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 2541;
RESULT 800
ID ADE65318 standard; protein; 2541 AA.
DE Human talin 1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 7; Length 2541;
RESULT 801
ID AEM81037 standard; protein; 2541 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81738, SEQ:2683.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.8%; Score 64.5; DB 8; Length 2541;
RESULT 802
ID ADF58806 standard; protein; 61 AA.
DE Human polypeptide sequence SEQ ID NO:1214.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.7%; Score 64; DB 7; Length 61;
RESULT 803
ID ADC67221 standard; protein; 277 AA.
DE Human GPCR protein SEQ ID NO:1674.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NMT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match
Best Local Similarity 12.7%; Score 64; DB 7; Length 277;
RESULT 804
ID ADS28888 standard; protein; 278 AA.
DE Bacterial polypeptide #17921.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.7%; Score 64; DB 8; Length 278;
RESULT 805
ID ABB06890 standard; protein; 314 AA.
DE Micromonospora carbonacea evernimycin locus protein ORF 10.
PN WO200155180-A2.
PD 02-AUG-2001.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (FARN/) FARNET C.
Query Match
Best Local Similarity 12.7%; Score 64; DB 4; Length 314;
RESULT 806
ID ABB99214 standard; protein; 314 AA.
DE Orthomycin biosynthetic polypeptide SEQ ID NO 15.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match
Best Local Similarity 12.7%; Score 64; DB 6; Length 314;
```

Best Local Similarity 29.9%; Pred. No. 1.7e+02;  
RESULT 807  
ID ABJ2589 standard; protein; 335 AA.  
DE Aspergillus fumigatus essential gene protein #557.  
PN W0200286090-A2.  
PD 31-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.7%; Score 64; DB 6; Length 335;  
Best Local Similarity 26.9%; Pred. No. 1.9e+02;  
RESULT 808  
ID ABO82719 standard; protein; 346 AA.  
DE Pseudomonas aeruginosa polypeptide #14894.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.7%; Score 64; DB 7; Length 346;  
Best Local Similarity 35.5%; Pred. No. 1.9e+02;  
RESULT 809  
ID ABJ26499 standard; protein; 392 AA.  
DE Aspergillus fumigatus essential gene protein #1157.  
PN W0200286090-A2.  
PD 31-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.7%; Score 64; DB 6; Length 392;  
Best Local Similarity 26.9%; Pred. No. 2.3e+02;  
RESULT 810  
ID ADN20982 standard; protein; 395 AA.  
DE Bacterial polypeptide #3635.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.7%; Score 64; DB 8; Length 395;  
Best Local Similarity 25.0%; Pred. No. 2.3e+02;  
RESULT 811  
ID ABO71901 standard; protein; 416 AA.  
DE Pseudomonas aeruginosa polypeptide #4076.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.7%; Score 64; DB 7; Length 416;  
Best Local Similarity 30.5%; Pred. No. 2.5e+02;  
RESULT 812  
ID ABU34364 standard; protein; 445 AA.  
DE Protein encoded by Prokaryotic essential gene #19891.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.7%; Score 64; DB 6; Length 445;  
Best Local Similarity 29.7%; Pred. No. 2.7e+02;  
RESULT 813  
ID AAY75759 standard; protein; 464 AA.  
DE Neisseria meningitidis ORF 989 protein sequence SEQ ID NO:2990.  
PN W09557280-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 12.7%; Score 64; DB 3; Length 464;  
Best Local Similarity 26.2%; Pred. No. 2.9e+02;  
RESULT 814  
ID ABU37723 standard; protein; 464 AA.  
DE Protein encoded by Prokaryotic essential gene #23250.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.7%; Score 64; DB 6; Length 464;  
Best Local Similarity 26.2%; Pred. No. 2.9e+02;  
RESULT 815  
ID AAB01258 standard; protein; 466 AA.  
DE Neisseria meningitidis BASB044 protein #1.

PN W0200034482-A2.  
PD 15-JUN-2000.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 12.7%; Score 64; DB 3; Length 466;  
Best Local Similarity 26.2%; Pred. No. 2.9e+02;  
RESULT 816  
ID ABG1694 standard; protein; 605 AA.  
DE Novel human diagnostic protein #19685.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.7%; Score 64; DB 4; Length 605;  
Best Local Similarity 37.3%; Pred. No. 4.1e+02;  
RESULT 817  
ID ADS27968 standard; protein; 693 AA.  
DE Bacterial polypeptide #17001.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.7%; Score 64; DB 8; Length 693;  
Best Local Similarity 25.6%; Pred. No. 4.8e+02;  
RESULT 818  
ID ABO79385 standard; protein; 836 AA.  
DE Pseudomonas aeruginosa polypeptide #10560.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.7%; Score 64; DB 7; Length 836;  
Best Local Similarity 22.4%; Pred. No. 6.2e+02;  
RESULT 819  
ID ABO79850 standard; protein; 996 AA.  
DE Pseudomonas aeruginosa polypeptide #12025.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.7%; Score 64; DB 7; Length 996;  
Best Local Similarity 30.9%; Pred. No. 7.8e+02;  
RESULT 820  
ID ABM69055 standard; protein; 1044 AA.  
DE Photorhabdus luminescens protein sequence #2152.  
PN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP-) INST PASTEUR.  
PA (CNRS-) CNRS CENT NAT RECH SCI.  
Query Match 12.7%; Score 64; DB 6; Length 1044;  
Best Local Similarity 26.4%; Pred. No. 8.3e+02;  
RESULT 821  
ID AAB07563 standard; protein; 1218 AA.  
DE Protein encoded by the bleomycin (BLM) gene cluster ORF30.  
PN W0200040704-A1.  
PD 13-JUL-2000.  
PA (REGC-) UNIV CALIFORNIA.  
Query Match 12.7%; Score 64; DB 3; Length 1218;  
Best Local Similarity 48.0%; Pred. No. 1e+03;  
RESULT 822  
ID AAM70381 standard; protein; 1481 AA.  
DE Photorhabdus luminescens protein sequence #3478.  
PN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP-) INST PASTEUR.  
PA (CNRS-) CNRS CENT NAT RECH SCI.  
Query Match 12.7%; Score 64; DB 6; Length 1481;  
Best Local Similarity 26.6%; Pred. No. 1.3e+02;  
RESULT 823  
ID ABG06301 standard; protein; 2017 AA.  
DE Novel human diagnostic protein #6292.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 12.7%; Score 64; DB 4; Length 2017;  
 Best Local Similarity 27.0%; Pred. No. 2e+03;  
 RESULT 824  
 ID ADS27816 standard; protein; 2479 AA.  
 DE Bacterial polypeptide #16849.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 12.7%; Score 64; DB 8; Length 2479;  
 Best Local Similarity 27.6%; Pred. No. 2.6e+03;  
 RESULT 825  
 ID ADI39289 standard; protein; 6842 AA.  
 DE S. hygroscopicus geldanamycin gene cluster-encoded protein, SEQ ID:131.  
 PN WO2003106653-A2.  
 PD 24-DEC-2003.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 PA (REID/) REID R C.  
 Query Match 12.7%; Score 64; DB 8; Length 6842;  
 Best Local Similarity 25.2%; Pred. No. 9.9e+03;  
 RESULT 826  
 ID AAG89188 standard; protein; 105 AA.  
 DE Human secreted protein, SEQ ID NO: 308.  
 PN WO200142451-A2.  
 PD 14-JUN-2001.  
 PA (GEST) GENSET.  
 Query Match 12.6%; Score 63.5; DB 4; Length 105;  
 Best Local Similarity 26.5%; Pred. No. 46;  
 RESULT 827  
 ID AAE20199 standard; protein; 106 AA.  
 DE Human mature haematopoietic growth factor-like protein.  
 PN WO200214491-A2.  
 PD 21-FEB-2002.  
 PA (PHAA) PHARMACIA CORP.  
 Query Match 12.6%; Score 63.5; DB 5; Length 106;  
 Best Local Similarity 26.5%; Pred. No. 47;  
 RESULT 828  
 ID ABG66722 standard; protein; 115 AA.  
 DE Human novel polypeptide #57.  
 PN WO200244340-A2.  
 PD 06-JUN-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 12.6%; Score 63.5; DB 5; Length 115;  
 Best Local Similarity 26.5%; Pred. No. 52;  
 RESULT 829  
 ID AAE67973 standard; protein; 128 AA.  
 DE Propionibacterium acnes immunogenic protein #28869.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 12.6%; Score 63.5; DB 4; Length 128;  
 Best Local Similarity 28.7%; Pred. No. 60;  
 RESULT 830  
 ID ABM64492 standard; protein; 128 AA.  
 DE Propionibacterium acnes Predicted ORF-encoded polypeptide #29168.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 12.6%; Score 63.5; DB 6; Length 128;  
 Best Local Similarity 28.7%; Pred. No. 60;  
 RESULT 831  
 ID AAE20198 standard; protein; 130 AA.  
 DE Human haematopoietic growth factor-like protein.  
 PN WO200214491-A2.  
 PD 21-FEB-2002.  
 PA (PHAA) PHARMACIA CORP.  
 Query Match 12.6%; Score 63.5; DB 5; Length 130;  
 Best Local Similarity 26.5%; Pred. No. 61;  
 RESULT 832  
 ID ABU36045 standard; protein; 130 AA.

DE Protein encoded by Prokaryotic essential gene #21572.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 12.6%; Score 63.5; DB 6; Length 130;  
 Best Local Similarity 27.1%; Pred. No. 61;  
 RESULT 833  
 ID ADS44437 standard; protein; 175 AA.  
 DE Bacterial polypeptide #22867.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 12.6%; Score 63.5; DB 8; Length 175;  
 Best Local Similarity 32.1%; Pred. No. 90;  
 RESULT 834  
 ID AAB79884 standard; protein; 225 AA.  
 DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:502.  
 PN WO200100843-A2.  
 PD 04-JAN-2001.  
 PA (BADI) BASF AG.  
 Query Match 12.6%; Score 63.5; DB 4; Length 225;  
 Best Local Similarity 30.4%; Pred. No. 1.3e+02;  
 RESULT 835  
 ID AAB79697 standard; protein; 225 AA.  
 DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:128.  
 PN WO200100843-A2.  
 PD 04-JAN-2001.  
 PA (BADI) BASF AG.  
 Query Match 12.6%; Score 63.5; DB 4; Length 225;  
 Best Local Similarity 30.4%; Pred. No. 1.3e+02;  
 RESULT 836  
 ID ADL65943 standard; protein; 262 AA.  
 DE C. glutamicum RXA-associated protein #150.  
 PN DE10154177-A1.  
 PD 08-MAY-2003.  
 PA (BADI) BASF AG.  
 Query Match 12.6%; Score 63.5; DB 7; Length 262;  
 Best Local Similarity 34.0%; Pred. No. 1.5e+02;  
 RESULT 837  
 ID AAG91330 standard; protein; 263 AA.  
 DE C glutamicum protein fragment SEQ ID NO: 5084.  
 PN EPI108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 Query Match 12.6%; Score 63.5; DB 4; Length 263;  
 Best Local Similarity 34.0%; Pred. No. 1.5e+02;  
 RESULT 838  
 ID ADN20914 standard; protein; 284 AA.  
 DE Bacterial polypeptide #3567.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 12.6%; Score 63.5; DB 8; Length 284;  
 Best Local Similarity 30.1%; Pred. No. 1.7e+02;  
 RESULT 839  
 ID ABU23091 standard; protein; 303 AA.  
 DE Protein encoded by Prokaryotic essential gene #8618.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 12.6%; Score 63.5; DB 6; Length 303;  
 Best Local Similarity 30.9%; Pred. No. 1.9e+02;  
 RESULT 840  
 ID AAB86984 standard; protein; 367 AA.  
 DE C. glutamicum ATCC 13032 dapC variant protein.



PN EP136559-A2.  
PD 26-SEP-2001.  
PA (DEGS ) DEGUSSA-HUELS AG.  
Query Match 12.6%; Score 63.5; DB 4; Length 367;  
Best Local Similarity 30.4%; Pred. No. 2.4e+02;  
RESULT 841  
ID AAB86983 standard; protein; 367 AA.  
DE C. glutamicum ATCC 13032 dapc protein.  
PN EP136559-A2.  
PD 26-SEP-2001.  
PA (DEGS ) DEGUSSA-HUELS AG.  
Query Match 12.6%; Score 63.5; DB 4; Length 367;  
Best Local Similarity 30.4%; Pred. No. 2.4e+02;  
RESULT 842  
ID AAG90972 standard; protein; 367 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4726.  
PN EP108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 12.6%; Score 63.5; DB 4; Length 367;  
Best Local Similarity 30.4%; Pred. No. 2.4e+02;  
RESULT 843  
ID ADI3565 standard; protein; 367 AA.  
DE C. glutamicum metabolic pathway protein RXA03003.  
PN W02003040681-A2.  
PD 15-MAY-2003.  
PA (BADI ) BASF AG.  
Query Match 12.6%; Score 63.5; DB 7; Length 367;  
Best Local Similarity 30.4%; Pred. No. 2.4e+02;  
RESULT 844  
ID AAU16363 standard; protein; 375 AA.  
DE Human novel secreted protein, Seq ID 1316.  
PN W0200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.6%; Score 63.5; DB 4; Length 375;  
Best Local Similarity 35.8%; Pred. No. 2.5e+02;  
RESULT 845  
ID ABUS5432 standard; protein; 375 AA.  
DE Human novel polypeptide #519.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 12.6%; Score 63.5; DB 6; Length 375;  
Best Local Similarity 35.8%; Pred. No. 2.5e+02;  
RESULT 846  
ID AAU15910 standard; protein; 378 AA.  
DE Human novel secreted protein, Seq ID 863.  
PN W0200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.6%; Score 63.5; DB 4; Length 378;  
Best Local Similarity 35.8%; Pred. No. 2.5e+02;  
RESULT 847  
ID ABUS4979 standard; protein; 378 AA.  
DE Human novel polypeptide #66.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 12.6%; Score 63.5; DB 6; Length 378;  
Best Local Similarity 35.8%; Pred. No. 2.5e+02;  
RESULT 848  
ID AAM43037 standard; protein; 394 AA.  
DE Alcaligenes eutrophus beta-ketochiolase (BktB).  
PN W09800557-A2.  
PD 08-JAN-1998.  
PA (MONS ) MONSANTO CO.  
Query Match 12.6%; Score 63.5; DB 2; Length 394;  
Best Local Similarity 30.3%; Pred. No. 2.6e+02;

RESULT 849  
ID AAY29664 standard; protein; 394 AA.  
DE A. eutrophus beta-ketochiolase protein.  
PN US5942660-A.  
PD 24-AUG-1999.  
PA (MONS ) MONSANTO CO.  
Query Match 12.6%; Score 63.5; DB 2; Length 394;  
Best Local Similarity 30.3%; Pred. No. 2.6e+02;  
RESULT 850  
ID AAB10567 standard; protein; 394 AA.  
DE A. eutrophus BktB protein.  
PN US6091002-A.  
PD 18-JUL-2000.  
PA (MONS ) MONSANTO CO.  
Query Match 12.6%; Score 63.5; DB 3; Length 394;  
Best Local Similarity 30.3%; Pred. No. 2.6e+02;  
RESULT 851  
ID AAE05083 standard; protein; 394 AA.  
DE Alcaligenes eutrophus BktB beta-ketochiolase.  
PN US6228623-B1.  
PD 08-MAY-2001.  
PA (MONS ) MONSANTO CO.  
Query Match 12.6%; Score 63.5; DB 4; Length 394;  
Best Local Similarity 30.3%; Pred. No. 2.6e+02;  
RESULT 852  
ID ADN17447 standard; protein; 398 AA.  
DE Bacterial polypeptide #100.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.6%; Score 63.5; DB 8; Length 398;  
Best Local Similarity 30.0%; Pred. No. 2.7e+02;  
RESULT 853  
ID ABU35789 standard; protein; 407 AA.  
DE Protein encoded by Prokaryotic essential gene #21316.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.6%; Score 63.5; DB 6; Length 407;  
Best Local Similarity 35.4%; Pred. No. 2.7e+02;  
RESULT 854  
ID ABU39863 standard; protein; 458 AA.  
DE Protein encoded by Prokaryotic essential gene #25390.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.6%; Score 63.5; DB 6; Length 458;  
Best Local Similarity 27.7%; Pred. No. 3.2e+02;  
RESULT 855  
ID ABO80983 standard; protein; 467 AA.  
DE Pseudomonas aeruginosa polypeptide #13158.  
PN US651795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.6%; Score 63.5; DB 7; Length 467;  
Best Local Similarity 32.1%; Pred. No. 3.3e+02;  
RESULT 856  
ID ABB06143 standard; protein; 475 AA.  
DE Human NS protein sequence SEQ ID NO:235.  
PN W0200206315-A2.  
PD 24-JAN-2002.  
PA (COMP-) COMPUGEN LTD.  
Query Match 12.6%; Score 63.5; DB 5; Length 475;  
Best Local Similarity 23.6%; Pred. No. 3.4e+02;  
RESULT 857  
ID ABB92709 standard; protein; 519 AA.  
DE Herbicidally active polypeptide SEQ ID NO 1920.  
PN W0200210210-A2.  
PD 07-FEB-2002.

PA (FARB ) BAYER AG.  
Query Match 12.6%; Score 63.5; DB 5; Length 519;  
Best Local Similarity 31.6%; Pred. No. 3.8e+02;  
RESULT 858  
ID AAB19783 standard; protein; 529 AA.  
DE Protein encoded by Prokaryotic essential gene #5310.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITRA ) ELITRA PHARM INC.  
Query Match 12.6%; Score 63.5; DB 6; Length 529;  
Best Local Similarity 30.9%; Pred. No. 3.9e+02;  
RESULT 859  
ID AAB79045 standard; protein; 537 AA.  
DE Corynebacterium glutamicum HA protein sequence SEQ ID NO:46.  
PN WO200100842-A2.  
PD 04-JAN-2001.  
PA (BADI ) BASF AG.  
Query Match 12.6%; Score 63.5; DB 4; Length 537;  
Best Local Similarity 36.1%; Pred. No. 3.9e+02;  
RESULT 860  
ID ABO68319 standard; protein; 545 AA.  
DE Pseudomonas aeruginosa polypeptide #494.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.6%; Score 63.5; DB 7; Length 545;  
Best Local Similarity 30.1%; Pred. No. 4e+02;  
RESULT 861  
ID ABO68791 standard; protein; 594 AA.  
DE Novel human diagnostic protein #8782.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.6%; Score 63.5; DB 4; Length 594;  
Best Local Similarity 29.7%; Pred. No. 4.5e+02;  
RESULT 862  
ID ABU25746 standard; protein; 630 AA.  
DE Protein encoded by Prokaryotic essential gene #11273.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITRA ) ELITRA PHARM INC.  
Query Match 12.6%; Score 63.5; DB 6; Length 630;  
Best Local Similarity 27.6%; Pred. No. 4.9e+02;  
RESULT 863  
ID AAW23036 standard; protein; 631 AA.  
DE Human cytomegalovirus combined antigen.  
PN WO9731117-A2.  
PD 28-AUG-1997.  
PA (UYMA-) UNIV MAASTRICHT.  
Query Match 12.6%; Score 63.5; DB 2; Length 631;  
Best Local Similarity 29.9%; Pred. No. 4.9e+02;  
RESULT 864  
ID AAB79044 standard; protein; 642 AA.  
DE Corynebacterium glutamicum HA protein sequence SEQ ID NO:44.  
PN WO200100842-A2.  
PD 04-JAN-2001.  
PA (BADI ) BASF AG.  
Query Match 12.6%; Score 63.5; DB 4; Length 642;  
Best Local Similarity 36.1%; Pred. No. 5e+02;  
RESULT 865  
ID AAG89921 standard; protein; 689 AA.  
DE C glutamicum protein fragment SEQ ID NO: 3675.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 12.6%; Score 63.5; DB 4; Length 689;  
Best Local Similarity 36.1%; Pred. No. 5.5e+02;  
RESULT 866  
ID ABB64835 standard; protein; 692 AA.  
DE Drosophila melanogaster polypeptide SHQ ID NO 21297.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.

Query Match 12.6%; Score 63.5; DB 4; Length 692;  
Best Local Similarity 27.3%; Pred. No. 5.5e+02;  
RESULT 867  
ID ABO74992 standard; protein; 728 AA.  
DE Pseudomonas aeruginosa polypeptide #7167.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.6%; Score 63.5; DB 7; Length 728;  
Best Local Similarity 30.4%; Pred. No. 5.9e+02;  
RESULT 868  
ID ADP31648 standard; protein; 889 AA.  
DE Human secreted protein SEQ ID #2415.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.6%; Score 63.5; DB 8; Length 889;  
Best Local Similarity 24.0%; Pred. No. 7.7e+02;  
RESULT 869  
ID ABO83590 standard; protein; 937 AA.  
DE Pseudomonas aeruginosa polypeptide #15765.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.6%; Score 63.5; DB 7; Length 937;  
Best Local Similarity 27.6%; Pred. No. 8.2e+02;  
RESULT 870  
ID ADC00868 standard; protein; 1026 AA.  
DE Enterohaemorrhagic E. coli O157:H7-specific protein SHQ ID NO: 913.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Query Match 12.6%; Score 63.5; DB 7; Length 1026;  
Best Local Similarity 29.9%; Pred. No. 9.2e+02;  
RESULT 871  
ID ADJ92012 standard; protein; 1046 AA.  
DE Human herpesvirus 5 UL32 protein.  
PN WO2003053332-A2.  
PD 03-JUL-2003.  
PA (MYRI-) MYRIAD GENETICS INC.  
Query Match 12.6%; Score 63.5; DB 7; Length 1046;  
Best Local Similarity 29.9%; Pred. No. 9.5e+02;  
RESULT 872  
ID AAR20637 standard; protein; 1048 AA.  
DE Human cytomegalovirus antigen pp150.  
PN WO9200323-A.  
PD 09-JAN-1992.  
PA (WELL ) WELLCOME FOUND LTD.  
Query Match 12.6%; Score 63.5; DB 2; Length 1048;  
Best Local Similarity 29.9%; Pred. No. 9.5e+02;  
RESULT 873  
ID AAW27277 standard; protein; 1048 AA.  
DE Human cytomegalovirus tegument protein pp150.  
PN WO9740165-A1.  
PD 30-OCT-1997.  
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.  
Query Match 12.6%; Score 63.5; DB 2; Length 1048;  
Best Local Similarity 29.9%; Pred. No. 9.5e+02;  
RESULT 874  
ID ADR70657 standard; protein; 1048 AA.  
DE Human cytomegalovirus phosphoprotein pp150 SHQ ID NO:16.  
PN WO2004076645-A2.  
PD 10-SEP-2004.  
PA (UYMA-) UNIV MASSACHUSETTS.  
Query Match 12.6%; Score 63.5; DB 8; Length 1048;  
Best Local Similarity 29.9%; Pred. No. 9.5e+02;  
RESULT 875  
ID ABB66662 standard; protein; 1064 AA.  
DE Drosophila melanogaster polypeptide SHQ ID NO 26776.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.6%; Score 63.5; DB 4; Length 1064;

Best Local Similarity 33.0%; Pred. No. 9.7e+02;  
RESULT 876  
ID ADC87585 standard; protein; 1237 AA.  
DE Human GPCR protein SEQ ID NO:2038.  
PN EPI270724-A2.  
PD 02-JAN-2003.  
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 12.6%; Score 63.5; DB 7; Length 1232;  
Best Local Similarity 28.3%; Pred. No. 1.2e+03;  
RESULT 877  
ID AAB07564 standard; protein; 2675 AA.  
DE Protein encoded by the bleomycin (BLM) gene cluster ORF30.  
PN WO200040704-A1.  
PD 13-JUL-2000.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 12.6%; Score 63.5; DB 3; Length 2675;  
Best Local Similarity 29.1%; Pred. No. 3.3e+03;  
RESULT 878  
ID ABG25572 standard; protein; 148 AA.  
DE Novel human diagnostic protein #25563.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.5%; Score 63; DB 4; Length 148;  
Best Local Similarity 33.3%; Pred. No. 82;  
RESULT 879  
ID ABG27610 standard; protein; 191 AA.  
DE Novel human diagnostic protein #27601.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.5%; Score 63; DB 4; Length 191;  
Best Local Similarity 27.3%; Pred. No. 1.2e+02;  
RESULT 880  
ID ADF06072 standard; protein; 231 AA.  
DE Bacterial polypeptide #2185.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.5%; Score 63; DB 7; Length 231;  
Best Local Similarity 27.2%; Pred. No. 1.5e+02;  
RESULT 881  
ID ABJ19731 standard; protein; 234 AA.  
DE Human secreted protein amino acid sequence - SEQ ID NO 199.  
PN WO200277188-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.5%; Score 63; DB 6; Length 234;  
Best Local Similarity 27.8%; Pred. No. 1.5e+02;  
RESULT 882  
ID ABP99802 standard; protein; 234 AA.  
DE Human secreted protein SEQ ID NO 746.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.5%; Score 63; DB 6; Length 234;  
Best Local Similarity 27.8%; Pred. No. 1.5e+02;  
RESULT 883  
ID ADC20538 standard; protein; 234 AA.  
DE Human secreted protein - amino acid sequence #219.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.5%; Score 63; DB 7; Length 234;  
Best Local Similarity 27.8%; Pred. No. 1.5e+02;  
RESULT 884  
ID AAB51653 standard; protein; 235 AA.  
DE Human secreted protein sequence encoded by gene 34 SEQ ID NO:93.  
PN WO200061620-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.

Query Match 12.5%; Score 63; DB 3; Length 235;  
Best Local Similarity 27.8%; Pred. No. 1.5e+02;  
RESULT 885  
ID ADS14819 standard; protein; 239 AA.  
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 374.  
PN WO2004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA) UNIV IOWA RES FOUND.  
Query Match 12.5%; Score 63; DB 8; Length 239;  
Best Local Similarity 28.6%; Pred. No. 1.5e+02;  
RESULT 886  
ID ADN22097 standard; protein; 260 AA.  
DE Bacterial polypeptide #4750.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOT/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.5%; Score 63; DB 8; Length 260;  
Best Local Similarity 30.1%; Pred. No. 1.7e+02;  
RESULT 887  
ID ADN24856 standard; protein; 260 AA.  
DE Bacterial polypeptide #7509.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOT/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.5%; Score 63; DB 8; Length 260;  
Best Local Similarity 30.1%; Pred. No. 1.7e+02;  
RESULT 888  
ID ABB55068 standard; protein; 307 AA.  
DE Lactococcus lactis protein petd.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 12.5%; Score 63; DB 5; Length 307;  
Best Local Similarity 28.6%; Pred. No. 2.2e+02;  
RESULT 889  
ID ABG07376 standard; protein; 314 AA.  
DE Novel human diagnostic protein #7367.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.5%; Score 63; DB 4; Length 314;  
Best Local Similarity 26.2%; Pred. No. 2.2e+02;  
RESULT 890  
ID ABG18917 standard; protein; 316 AA.  
DE Novel human diagnostic protein #18908.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.5%; Score 63; DB 4; Length 316;  
Best Local Similarity 39.5%; Pred. No. 2.2e+02;  
RESULT 891  
ID ABU31572 standard; protein; 321 AA.  
DE Protein encoded by Prokaryotic essential gene #17099.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITRA) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 6; Length 321;  
Best Local Similarity 27.0%; Pred. No. 2.3e+02;  
RESULT 892  
ID ADC96915 standard; protein; 325 AA.  
DE E faecium protein sequence SEQ ID 6542.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.5%; Score 63; DB 7; Length 325;

Best Local Similarity 25.3%; Pred. No. 2.3e+02;  
RESULT 893  
ID ABO67512 standard; protein; 329 AA.  
DE Klebsiella pneumoniae polypeptide segid 14029.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.5%; Score 63; DB 7; Length 329;  
Best Local Similarity 27.0%; Pred. No. 2.4e+02;  
RESULT 894  
ID ABO67956 standard; protein; 360 AA.  
DE Pseudomonas aeruginosa polypeptide #131.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.5%; Score 63; DB 7; Length 360;  
Best Local Similarity 28.6%; Pred. No. 2.7e+02;  
RESULT 895  
ID ABO28808 standard; protein; 366 AA.  
DE Novel human diagnostic protein #28799.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.5%; Score 63; DB 4; Length 366;  
Best Local Similarity 29.9%; Pred. No. 2.7e+02;  
RESULT 896  
ID ABO22269 standard; protein; 373 AA.  
DE Protein encoded by Prokaryotic essential gene #7796.  
PN WO200271183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 6; Length 373;  
Best Local Similarity 29.9%; Pred. No. 2.8e+02;  
RESULT 897  
ID AUJ3669 standard; protein; 410 AA.  
DE Staphylococcus aureus cellular proliferation protein #145.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 4; Length 410;  
Best Local Similarity 29.3%; Pred. No. 3.1e+02;  
RESULT 898  
ID ABO82741 standard; protein; 410 AA.  
DE Pseudomonas aeruginosa polypeptide #14916.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.5%; Score 63; DB 7; Length 410;  
Best Local Similarity 26.7%; Pred. No. 3.1e+02;  
RESULT 899  
ID ADF14023 standard; protein; 413 AA.  
DE Human endometrial-specific protein - SRQ ID 654.  
PN WO2003059927-A1.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 12.5%; Score 63; DB 7; Length 413;  
Best Local Similarity 27.8%; Pred. No. 3.2e+02;  
RESULT 900  
ID AUJ37217 standard; protein; 414 AA.  
DE Staphylococcus aureus cellular proliferation protein #1387.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 4; Length 414;  
Best Local Similarity 29.3%; Pred. No. 3.2e+02;  
RESULT 901  
ID AUJ36936 standard; protein; 414 AA.  
DE Staphylococcus aureus cellular proliferation protein #1106.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 4; Length 414;  
Best Local Similarity 29.3%; Pred. No. 3.2e+02;

RESULT 902  
ID AAE02198 standard; protein; 414 AA.  
DE Staphylococcus aureus beta-ketoacyl-ACP synthase II (FabF).  
PN WO200130988-A1.  
PD 03-MAY-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 12.5%; Score 63; DB 4; Length 414;  
Best Local Similarity 29.3%; Pred. No. 3.2e+02;  
RESULT 903  
ID AAB62056 standard; protein; 414 AA.  
DE S. aureus fabF polypeptide.  
PN WO200116173-A1.  
PD 08-MAR-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 12.5%; Score 63; DB 4; Length 414;  
Best Local Similarity 29.3%; Pred. No. 3.2e+02;  
RESULT 904  
ID ABE16217 standard; protein; 414 AA.  
DE Protein encoded by Prokaryotic essential gene #1744.  
PN WO200271183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 6; Length 414;  
Best Local Similarity 29.3%; Pred. No. 3.2e+02;  
RESULT 905  
ID ABW73213 standard; protein; 414 AA.  
DE Staphylococcus aureus protein #2453.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 12.5%; Score 63; DB 6; Length 414;  
Best Local Similarity 29.3%; Pred. No. 3.2e+02;  
RESULT 906  
ID ADJ49574 standard; protein; 414 AA.  
DE Oil-associated gene related protein #1074.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C. C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDENUX J. R.  
PA (ROGE/) ROGERS J. A.  
Query Match 12.5%; Score 63; DB 8; Length 414;  
Best Local Similarity 29.3%; Pred. No. 3.2e+02;  
RESULT 907  
ID ADJ49181 standard; protein; 414 AA.  
DE Oil-associated gene related protein #681.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C. C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDENUX J. R.  
PA (ROGE/) ROGERS J. A.  
Query Match 12.5%; Score 63; DB 8; Length 414;  
Best Local Similarity 29.3%; Pred. No. 3.2e+02;  
RESULT 908  
ID ADS21831 standard; protein; 428 AA.  
DE Bacterial polypeptide #10864.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G. J.  
PA (SLAT/) SLATER S. C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B. S.  
Query Match 12.5%; Score 63; DB 8; Length 428;  
Best Local Similarity 26.6%; Pred. No. 3.3e+02;  
RESULT 909  
ID AAB66451 standard; protein; 434 AA.  
DE Protein encoded by Mycobacterium tuberculosis Rv3018c gene.

PN W0200102555-A1.  
PD 11-JAN-2001.  
PA (INST ) INST PASTEUR.  
Query Match 12.5%; Score 63; DB 4; Length 434;  
Best Local Similarity 29.7%; Pred. No. 3.4e+02;  
RESULT 910  
ID ABU6905 standard; protein; 434 AA.  
DE Protein encoded by prokaryotic essential gene #22432.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 6; Length 434;  
Best Local Similarity 29.7%; Pred. No. 3.4e+02;  
RESULT 911  
ID ABU45582 standard; protein; 454 AA.  
DE Protein encoded by prokaryotic essential gene #31109.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 6; Length 454;  
Best Local Similarity 23.1%; Pred. No. 3.6e+02;  
RESULT 912  
ID ABU3234 standard; protein; 494 AA.  
DE Protein encoded by prokaryotic essential gene #17761.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 6; Length 494;  
Best Local Similarity 29.4%; Pred. No. 4e+02;  
RESULT 913  
ID ABU19717 standard; protein; 513 AA.  
DE Protein encoded by prokaryotic essential gene #5244.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 6; Length 513;  
Best Local Similarity 29.9%; Pred. No. 4.2e+02;  
RESULT 914  
ID ADP9909 standard; protein; 517 AA.  
DE C. albicans specific gene, CAYGR256W, protein sequence.  
PN W02004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 8; Length 517;  
Best Local Similarity 31.0%; Pred. No. 4.3e+02;  
RESULT 915  
ID ABU45027 standard; protein; 535 AA.  
DE Protein encoded by prokaryotic essential gene #30554.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.5%; Score 63; DB 6; Length 535;  
Best Local Similarity 28.1%; Pred. No. 4.5e+02;  
RESULT 916  
ID ADS21023 standard; protein; 556 AA.  
DE Bacterial polypeptide #10056.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.5%; Score 63; DB 8; Length 556;  
Best Local Similarity 40.0%; Pred. No. 4.7e+02;  
RESULT 917  
ID AAB85851 standard; protein; 900 AA.  
DE Human PMS2 protein.  
PN W0200159092-A2.  
PD 16-AUG-2001.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 12.5%; Score 63; DB 4; Length 900;

Best Local Similarity 26.3%; Pred. No. 8.9e+02;  
RESULT 918  
ID AAR7909 standard; protein; 931 AA.  
DE Human DNA repair protein hMLH2.  
PN W09520678-A1.  
PD 03-AUG-1995.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.5%; Score 63; DB 2; Length 931;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 919  
ID AAB85852 standard; protein; 932 AA.  
DE Human PMS1 protein.  
PN W0200159092-A2.  
PD 16-AUG-2001.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 12.5%; Score 63; DB 4; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 920  
ID AAG63953 standard; protein; 932 AA.  
DE Amino acid sequence of human mismatch repair protein PMS2.  
PN W0200162945-A1.  
PD 30-AUG-2001.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
PA (NICO/) NICOLAIDES N C.  
PA (SASS/) SASS P M.  
PA (GRAS/) GRASSO L.  
PA (VOGE/) VOGELSTEIN B.  
PA (KINZ/) KINZLER K W.  
Query Match 12.5%; Score 63; DB 4; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 921  
ID AAG63954 standard; protein; 932 AA.  
DE Amino acid sequence of human mismatch repair protein PMS1.  
PN W0200162945-A1.  
PD 30-AUG-2001.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
PA (NICO/) NICOLAIDES N C.  
PA (SASS/) SASS P M.  
PA (GRAS/) GRASSO L.  
PA (VOGE/) VOGELSTEIN B.  
PA (KINZ/) KINZLER K W.  
Query Match 12.5%; Score 63; DB 4; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 922  
ID AAU98776 standard; protein; 932 AA.  
DE Human post meiotic segregation increased, PMS1, protein.  
PN W0200238750-A1.  
PD 16-MAY-2002.  
PA (MORP-) MORPHOTEK INC.  
Query Match 12.5%; Score 63; DB 5; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 923  
ID AAE24357 standard; protein; 932 AA.  
DE Human mismatch repair protein, PMS1.  
PN W0200237967-A1.  
PD 16-MAY-2002.  
PA (MORP-) MORPHOTEK INC.  
Query Match 12.5%; Score 63; DB 5; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 924  
ID AAO18553 standard; protein; 932 AA.  
DE Human mismatch repair protein PMS1.  
PN W0200254856-A1.  
PD 18-JUL-2002.  
PA (MORP-) MORPHOTEK INC.  
Query Match 12.5%; Score 63; DB 5; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 925  
ID AAE28277 standard; protein; 932 AA.  
DE Human MLH2 protein.  
PN US6416984-B1.  
PD 09-JUL-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.

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Query Match
Best Local Similarity 12.5%; Score 63; DB 5; Length 932;
PA (KLIN/) MORPHOTEK INC.
RESULT 926
ID AAE24684 standard; protein; 932 AA.
DE Human PMS1 protein.
PN WO20024049-A1.
PD 23-MAY-2002.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 5; Length 932;
RESULT 927
ID ABU07972 standard; protein; 932 AA.
DE Human PMS1 protein.
PN WO2003012130-A1.
PD 13-FEB-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 6; Length 932;
RESULT 928
ID ABU07971 standard; protein; 932 AA.
DE Human PMS2 protein.
PN WO2003012130-A1.
PD 13-FEB-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 6; Length 932;
RESULT 929
ID ABU089659 standard; protein; 932 AA.
DE Human PMS2 mismatch repair protein.
PN WO200301937-A2.
PD 17-APR-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 6; Length 932;
RESULT 930
ID ABU089660 standard; protein; 932 AA.
DE Human PMS1 mismatch repair protein.
PN WO200301937-A2.
PD 17-APR-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 6; Length 932;
RESULT 931
ID ABO07415 standard; protein; 932 AA.
DE Human Mult homologue, hMLH2.
PN US2003027177-A1.
PD 06-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 6; Length 932;
RESULT 932
ID AAO27514 standard; protein; 932 AA.
DE Human mismatch repair protein PMS (post meiotic segregation) 2.
PN WO2003062435-A1.
PD 31-JUL-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 6; Length 932;
RESULT 933
ID AAO27515 standard; protein; 932 AA.
DE Human mismatch repair protein PMS (post meiotic segregation) 1.
PN WO2003062435-A1.
PD 31-JUL-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 6; Length 932;
RESULT 934
ID ADA06246 standard; protein; 932 AA.
DE Human mismatch repair, MMR, protein PMS1.
PN US2003068808-A1.
PD 10-APR-2003.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (SASS/) SASS P M.

PA (GRAS/) GRASSO L.
PA (KLIN/) KLINE J B.
Query Match
Best Local Similarity 12.5%; Score 63; DB 7; Length 932;
RESULT 935
ID ADA06244 standard; protein; 932 AA.
DE Human mismatch repair, MMR, protein PMS2.
PN US2003068808-A1.
PD 10-APR-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (KLIN/) KLINE J B.
Query Match
Best Local Similarity 12.5%; Score 63; DB 7; Length 932;
RESULT 936
ID ADC089605 standard; protein; 932 AA.
DE Human PMS2 protein SEQ ID NO:5.
PN WO2003072732-A2.
PD 04-SEP-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 7; Length 932;
RESULT 937
ID ADC089607 standard; protein; 932 AA.
DE Human PMS1 protein SEQ ID NO:7.
PN WO2003072732-A2.
PD 04-SEP-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 7; Length 932;
RESULT 938
ID ADP17892 standard; protein; 932 AA.
DE Human PMS1 protein, a mismatch repair protein.
PN US6576468-B1.
PD 10-JUN-2003.
PA (MORP-) MORPHOTEK INC.
Query Match
Best Local Similarity 12.5%; Score 63; DB 7; Length 932;
RESULT 939
ID ADG62881 standard; protein; 932 AA.
DE Human PMS2 protein.
PN US2003165468-A1.
PD 04-SEP-2003.
PA (GRAS/) GRASSO L.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
Query Match
Best Local Similarity 12.5%; Score 63; DB 7; Length 932;
RESULT 940
ID ADG62882 standard; protein; 932 AA.
DE Human PMS1 protein.
PN US2003165468-A1.
PD 04-SEP-2003.
PA (GRAS/) GRASSO L.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
Query Match
Best Local Similarity 12.5%; Score 63; DB 7; Length 932;
RESULT 941
ID ADH62629 standard; protein; 932 AA.
DE Human mismatch repair protein PMS1.
PN US2003143682-A1.
PD 31-JUL-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
Query Match
Best Local Similarity 12.5%; Score 63; DB 7; Length 932;
RESULT 942
ID ADH60983 standard; protein; 932 AA.
DE Human mismatch repair protein hMLH2.
PN US6610477-B1.
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PD 26-AUG-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 12.5%; Score 63; DB 7; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 943  
ID ADJ68675 standard; protein; 932 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID481.  
PN W02003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 12.5%; Score 63; DB 7; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 944  
ID ADF78840 standard; protein; 932 AA.  
DE Human mismatch repair protein PMS1, cDNA.  
PN US2003186441-A1.  
PD 02-OCT-2003.  
PA (NICO/) NICOLAIDES N C.  
PA (GRAS/) GRASSO L.  
PA (SASS/) SASS P M.  
Query Match 12.5%; Score 63; DB 8; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 945  
ID ADG46767 standard; protein; 932 AA.  
DE Human MMR protein (mismatch protein), PMS1.  
PN US2003091997-A1.  
PD 15-MAY-2003.  
PA (NICO/) NICOLAIDES N C.  
PA (GRAS/) GRASSO L.  
PA (SASS/) SASS P M.  
Query Match 12.5%; Score 63; DB 8; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 946  
ID ADO40066 standard; protein; 932 AA.  
DE Human PMS1 protein.  
PN US6737268-B1.  
PD 18-MAY-2004.  
PA (MORP-) MORPHOTEK INC.  
Query Match 12.5%; Score 63; DB 8; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 947  
ID ADP66682 standard; protein; 932 AA.  
DE Human mismatch repair protein PMS2.  
PN W02004046330-A2.  
PD 03-JUN-2004.  
PA (MORP-) MORPHOTEK INC.  
Query Match 12.5%; Score 63; DB 8; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 948  
ID ADP66680 standard; protein; 932 AA.  
DE Human mismatch repair protein PMS1.  
PN W02004046330-A2.  
PD 03-JUN-2004.  
PA (MORP-) MORPHOTEK INC.  
Query Match 12.5%; Score 63; DB 8; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 949  
ID ADR13883 standard; protein; 932 AA.  
DE Human DNA mismatch repair protein PMS1.  
PN US2004158886-A1.  
PD 12-AUG-2004.  
PA (MORP-) MORPHOTEK INC.  
Query Match 12.5%; Score 63; DB 8; Length 932;  
Best Local Similarity 26.3%; Pred. No. 9.3e+02;  
RESULT 950  
ID ADP31471 standard; protein; 960 AA.  
DE Human secreted protein SEQ ID #2238.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.5%; Score 63; DB 8; Length 960;

Best Local Similarity 35.7%; Pred. No. 9.6e+02;  
RESULT 951  
ID ADP31470 standard; protein; 960 AA.  
DE Human secreted protein SEQ ID #2237.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.5%; Score 63; DB 8; Length 960;  
Best Local Similarity 35.7%; Pred. No. 9.6e+02;  
RESULT 952  
ID ABB60399 standard; protein; 985 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7989.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.5%; Score 63; DB 4; Length 985;  
Best Local Similarity 42.1%; Pred. No. 1e+03;  
RESULT 953  
ID ABB57807 standard; protein; 1007 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 213.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.5%; Score 63; DB 4; Length 1007;  
Best Local Similarity 23.6%; Pred. No. 1e+03;  
RESULT 954  
ID AAG65895 standard; protein; 1062 AA.  
DE Amino acid sequence of GSK gene Id 97078.  
PN W0200172961-A2.  
PD 04-OCT-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 12.5%; Score 63; DB 4; Length 1062;  
Best Local Similarity 27.8%; Pred. No. 1.1e+03;  
RESULT 955  
ID AA017856 standard; protein; 1062 AA.  
DE Pysin domain containing protein NALP2/PY7-hs.  
PN W0200240668-A2.  
PD 23-MAY-2002.  
PA (APOT-) APOTTECH RES & DEV LTD.  
Query Match 12.5%; Score 63; DB 5; Length 1062;  
Best Local Similarity 27.8%; Pred. No. 1.1e+03;  
RESULT 956  
ID ADM25903 standard; protein; 1299 AA.  
DE Hyperthermophile Methanopyrus kandleri protein #509.  
PN W02003076575-A2.  
PD 18-SEP-2003.  
PA (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALV/) MALYKH A.  
Query Match 12.5%; Score 63; DB 7; Length 1299;  
Best Local Similarity 28.4%; Pred. No. 1.4e+03;  
RESULT 957  
ID AAY53970 standard; protein; 1857 AA.  
DE Human peripheral benzodiazepine receptor associated protein-1.  
PN W09960117-A2.  
PD 25-NOV-1999.  
PA (SNFI ) SANOFI-SYNTHELABO.  
Query Match 12.5%; Score 63; DB 3; Length 1857;  
Best Local Similarity 28.8%; Pred. No. 2.3e+03;  
RESULT 958  
ID ADK40938 standard; protein; 3913 AA.  
DE Novel human kinase protein #45.  
PN W02003057841-A2.  
PD 17-JUL-2003.  
PA (GRIG/) GRIGORIIEV I V.  
PA (SUDA/) SUDARSANAM S.  
Query Match 12.5%; Score 63; DB 7; Length 3913;  
Best Local Similarity 26.2%; Pred. No. 6.1e+03;  
RESULT 959  
ID ADR18659 standard; protein; 3913 AA.  
DE Kinase 51594 1 hCT33056 1, SEQ ID 52.  
PN W02004069154-A2.  
PD 19-AUG-2004.

Query Match	12.5%;	Score 62.5;	DB 7;	Length 289;
Best Local Similarity	23.9%;	Pred. No. 2.3e+02;		
RESULT 969				
ID AAE01780 standard; protein; 302 AA.				
DE Human gene 11 encoded secreted protein HMBPE57, SEQ ID NO:101.				
PN WO200114627-A1.				
PD 17-MAY-2001.				
PA (HUMA-) HUMAN GENOME SCI INC.				
Query Match	12.5%;	Score 62.5;	DB 4;	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 970				
ID ABG64161 standard; protein; 302 AA.				
DE Human albumin fusion protein #836.				
PN WO200177137-A1.				
PD 18-OCT-2001.				
PA (HUMA-) HUMAN GENOME SCI INC.				
Query Match	12.5%;	Score 62.5;	DB 5;	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 971				
ID ADA57295 standard; protein; 302 AA.				
DE Human secreted protein #578.				
PN WO2002102994-A2.				
PD 27-DEC-2002.				
PA (HUMA-) HUMAN GENOME SCI INC.				
Query Match	12.5%;	Score 62.5;	DB 6;	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 972				
ID ADA41174 standard; protein; 302 AA.				
DE Human secreted protein.				
PN WO2002102993-A2.				
PD 27-DEC-2002.				
PA (HUMA-) HUMAN GENOME SCI INC.				
Query Match	12.5%;	Score 62.5;	DB 6;	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 973				
ID ADL77426 standard; protein; 302 AA.				
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 908.				
PN US2004010134-A1.				
PD 15-JAN-2004.				
PA (ROSE/) ROSEN C A.				
PA (HASE/) HASELTINE W A.				
Query Match	12.5%;	Score 62.5;	DB 8;	Length 302;
Best Local Similarity	41.9%;	Pred. No. 2.4e+02;		
RESULT 974				
ID AAG65717 standard; protein; 361 AA.				
DE A. gossypii Ag008 gene product.				
PN US6291665-B1.				
PD 18-SEP-2001.				
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.				
Query Match	12.5%;	Score 62.5;	DB 4;	Length 361;
Best Local Similarity	34.5%;	Pred. No. 3e+02;		
RESULT 975				
ID ADS15031 standard; protein; 401 AA.				
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 586				
PN WO2004083385-A2.				
PD 30-SEP-2004.				
PA (IOWA ) UNIV IOWA RES FOUND.				
Query Match	12.5%;	Score 62.5;	DB 8;	Length 401;
Best Local Similarity	31.0%;	Pred. No. 3.5e+02;		
RESULT 976				
ID AAG44543 standard; protein; 426 AA.				
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55809.				
PN EPI0133405-A2.				
PD 06-SEP-2000.				
Query Match	12.5%;	Score 62.5;	DB 3;	Length 426;
Best Local Similarity	29.5%;	Pred. No. 3.8e+02;		
RESULT 977				
ID ABB91634 standard; protein; 426 AA.				
DE Herbicidially active polypeptide SEQ ID NO 845.				
PN WO2002012010-A2.				
PD 07-FEB-2002.				
PA (PARP ) PARVER IC				



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Best Local Similarity 29.5%; Pred. No. 3.8e+02;
RESULT 978
ID ABU26371 standard; protein; 445 AA.
DE Protein encoded by Prokaryotic essential gene #11898.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 62.5; DB 6; Length 445;
Best Local Similarity 26.2%; Pred. No. 4e+02;
RESULT 979
ID ABU3109 standard; protein; 471 AA.
DE Protein encoded by Prokaryotic essential gene #18636.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 12.5%; Score 62.5; DB 6; Length 471;
Best Local Similarity 29.7%; Pred. No. 4.3e+02;
RESULT 980
ID ABB71148 standard; protein; 505 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40236.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (BEKE-) PE CORP NY.
Query Match 12.5%; Score 62.5; DB 4; Length 505;
Best Local Similarity 28.8%; Pred. No. 4.7e+02;
RESULT 981
ID ADS27978 standard; protein; 511 AA.
DE Bacterial polypeptide #17011.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 62.5; DB 8; Length 511;
Best Local Similarity 28.3%; Pred. No. 4.8e+02;
RESULT 982
ID ABB57291 standard; protein; 560 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:819.
PN W0200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 12.5%; Score 62.5; DB 5; Length 560;
Best Local Similarity 29.6%; Pred. No. 5.4e+02;
RESULT 983
ID ADO80490 standard; protein; 573 AA.
DE Deinococcus radiodurans mety protein.
PN DE10239082-A1.
PD 04-MAR-2004.
PA (BADI-) BASF AG.
Query Match 12.5%; Score 62.5; DB 8; Length 573;
Best Local Similarity 32.9%; Pred. No. 5.6e+02;
RESULT 984
ID ADN17889 standard; protein; 573 AA.
DE Bacterial polypeptide #542.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 62.5; DB 8; Length 573;
Best Local Similarity 32.9%; Pred. No. 5.6e+02;
RESULT 985
ID ADM99207 standard; protein; 596 AA.
DE Environmentally sourced protease protein Segid 90.
PN W02004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 12.5%; Score 62.5; DB 8; Length 596;
Best Local Similarity 29.5%; Pred. No. 5.9e+02;

Best Local Similarity 29.5%; Pred. No. 5.9e+02;
RESULT 986
ID ADN18270 standard; protein; 601 AA.
DE Bacterial polypeptide #923.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 62.5; DB 8; Length 601;
Best Local Similarity 28.7%; Pred. No. 5.9e+02;
RESULT 987
ID ADG31175 standard; protein; 615 AA.
DE Fruit fly cpo protein.
PN W02003092715-A2.
PD 13-NOV-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 12.5%; Score 62.5; DB 7; Length 615;
Best Local Similarity 28.8%; Pred. No. 6.1e+02;
RESULT 988
ID ADS14849 standard; protein; 618 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 404.
PN W02004083385-A2.
PD 30-SEP-2004.
PA (IOWA-) UNIV IOWA RES FOUND.
Query Match 12.5%; Score 62.5; DB 8; Length 618;
Best Local Similarity 27.8%; Pred. No. 6.1e+02;
RESULT 989
ID AAE18906 standard; protein; 643 AA.
DE Human PAS domain protein (PASDP-1).
PN W0200210200-A2.
PD 07-FEB-2002.
PA (INCYTE-) INCYTE GENOMICS INC.
Query Match 12.5%; Score 62.5; DB 5; Length 643;
Best Local Similarity 50.0%; Pred. No. 6.5e+02;
RESULT 990
ID AAU62829 standard; protein; 652 AA.
DE Propionibacterium acnes immunogenic protein #23725.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.5%; Score 62.5; DB 4; Length 652;
Best Local Similarity 29.2%; Pred. No. 6.6e+02;
RESULT 991
ID AAM59348 standard; protein; 652 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #24024.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.5%; Score 62.5; DB 6; Length 652;
Best Local Similarity 29.2%; Pred. No. 6.6e+02;
RESULT 992
ID AAM65103 standard; protein; 652 AA.
DE Propionibacterium acnes immunogenic polypeptide #29779.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.5%; Score 62.5; DB 6; Length 652;
Best Local Similarity 29.2%; Pred. No. 6.6e+02;
RESULT 993
ID AAM69757 standard; protein; 802 AA.
DE Acetobacter xylinum bcsb gene product.
PN W09839455-A1.
PD 11-SEP-1998.
PA (BIOP-) BIO-POLYMER RES CO LTD.
Query Match 12.5%; Score 62.5; DB 2; Length 802;
Best Local Similarity 26.4%; Pred. No. 8.7e+02;
RESULT 994
ID AA018572 standard; protein; 802 AA.
DE Rat transcriptional regulatory factor.
PN W0200253735-A1.
PD 11-JUL-2002.
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PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 995  
ID AAO18571 standard; protein; 802 AA.  
DE Murine transcriptional regulatory factor.  
PN WO200253735-A1.  
PD 11-JUL-2002.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 996  
ID AAO18570 standard; protein; 802 AA.  
DE Human transcriptional regulatory factor.  
PN WO200253735-A1.  
PD 11-JUL-2002.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 997  
ID AAO18254 standard; protein; 802 AA.  
DE Murine basic helix-loop-helix BHLH-PAS protein.  
PN WO200253729-A1.  
PD 11-JUL-2002.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 998  
ID AAO18255 standard; protein; 802 AA.  
DE Rat basic helix-loop-helix BHLH-PAS protein.  
PN WO200253729-A1.  
PD 11-JUL-2002.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 999  
ID AAO18253 standard; protein; 802 AA.  
DE Human basic helix-loop-helix BHLH-PAS protein.  
PN WO200253729-A1.  
PD 11-JUL-2002.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1000  
ID ABB81802 standard; protein; 802 AA.  
DE Rat transcriptional regulator.  
PN WO200253736-A1.  
PD 11-JUL-2002.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1001  
ID ABB81800 standard; protein; 802 AA.  
DE Human transcriptional regulator.  
PN WO200253736-A1.  
PD 11-JUL-2002.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1002  
ID ABB81801 standard; protein; 802 AA.  
DE Mouse transcriptional regulator.  
PN WO200253736-A1.  
PD 11-JUL-2002.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 12.5%; Score 62.5; DB 5; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1003  
ID ADD31213 standard; protein; 802 AA.  
DE Variant of rat K11 polypeptide.  
PN US2003190653-A1.  
PD 09-OCT-2003.  
PA (SHAW/) SHAWLOO M.

PA (GONZ/) GONZALEZ-ZULUETA M.  
Query Match 12.5%; Score 62.5; DB 7; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1004  
ID ADD31203 standard; protein; 802 AA.  
DE Human K11 polypeptide.  
PN US2003190653-A1.  
PD 09-OCT-2003.  
PA (SHAW/) SHAWLOO M.  
PA (GONZ/) GONZALEZ-ZULUETA M.  
PA (WIEL/) WIELOCH T.  
Query Match 12.5%; Score 62.5; DB 7; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1005  
ID ADD31201 standard; protein; 802 AA.  
DE Rat K11 polypeptide.  
PN US2003190653-A1.  
PD 09-OCT-2003.  
PA (SHAW/) SHAWLOO M.  
PA (GONZ/) GONZALEZ-ZULUETA M.  
PA (WIEL/) WIELOCH T.  
Query Match 12.5%; Score 62.5; DB 7; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1006  
ID ADM04925 standard; protein; 802 AA.  
DE Human protein of the invention SEQ ID NO:3610.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) REAS ASSOC BIOTECHNOLOGY.  
Query Match 12.5%; Score 62.5; DB 7; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1007  
ID ADJ17241 standard; protein; 802 AA.  
DE Human nucleic-acid associated protein NNAIP-30 SEQ ID NO:30.  
PN WO2004011604-A2.  
PD 05-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.5%; Score 62.5; DB 8; Length 802;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;  
RESULT 1008  
ID ABO62421 standard; protein; 922 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8938.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.5%; Score 62.5; DB 7; Length 922;  
Best Local Similarity 29.6%; Pred. No. 1e+03;  
RESULT 1009  
ID ADE08640 standard; protein; 967 AA.  
DE Novel protein (useful for identifying genetic disorders) #795.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.5%; Score 62.5; DB 7; Length 967;  
Best Local Similarity 31.1%; Pred. No. 1.1e+03;  
RESULT 1010  
ID ABB69643 standard; protein; 970 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35721.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PERE-) PER CORP NY.  
Query Match 12.5%; Score 62.5; DB 4; Length 970;  
Best Local Similarity 33.3%; Pred. No. 1.1e+03;  
RESULT 1011  
ID AAB23249 standard; protein; 999 AA.  
DE Streptomyces collinus Ansd/Ansk protein.  
PN WO20005304-A2.  
PD 21-SEP-2000.  
PA (UTVI-) UNIV VIRGINIA COMMONWEALTH.  
Query Match 12.5%; Score 62.5; DB 3; Length 999;  
Best Local Similarity 29.3%; Pred. No. 1.2e+03;  
RESULT 1012

ID ADC13549 standard; protein; 1149 AA.  
DE Human NOVX protein, SEQ ID No 28.  
PN WO2003004617-A2.  
PD 16-JUN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.5%; Score 62.5; DB 7; Length 1149;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
RESULT 1013  
ID ABB62191 standard; protein; 1224 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 13365.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.5%; Score 62.5; DB 4; Length 1224;  
Best Local Similarity 27.6%; Pred. No. 1.5e+03;  
RESULT 1014  
ID ABO75059 standard; protein; 1626 AA.  
DE Pseudomonas aeruginosa polypeptide #7234.  
PN US651795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.5%; Score 62.5; DB 7; Length 1626;  
Best Local Similarity 25.3%; Pred. No. 2.2e+03;  
RESULT 1015  
ID AAU04484 standard; protein; 1873 AA.  
DE Human PD-ARP-binding cassette (PD-ABC) protein form #2.  
PN WO200153490-A1.  
PD 26-JUL-2001.  
PA (WARN) WARNER LAMBERT CO.  
Query Match 12.5%; Score 62.5; DB 4; Length 1873;  
Best Local Similarity 41.9%; Pred. No. 2.6e+03;  
RESULT 1016  
ID ABU08465 standard; protein; 1993 AA.  
DE Amino acid sequence for human ABCA7 splice variant #2.  
PN WO2003010315-A1.  
PD 06-FEB-2003.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
PA (KAZU-) KAZUSA DNA RES INST FOUND.  
Query Match 12.5%; Score 62.5; DB 6; Length 1993;  
Best Local Similarity 41.9%; Pred. No. 2.9e+03;  
RESULT 1017  
ID ADP55322 standard; protein; 2000 AA.  
DE Human PRO protein sequence SEQ ID NO:1298.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 12.5%; Score 62.5; DB 8; Length 2000;  
Best Local Similarity 41.9%; Pred. No. 2.9e+03;  
RESULT 1018  
ID ABU08464 standard; protein; 2008 AA.  
DE Amino acid sequence for human ABCA7 splice variant #1.  
PN WO2003010315-A1.  
PD 06-FEB-2003.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
PA (KAZU-) KAZUSA DNA RES INST FOUND.  
Query Match 12.5%; Score 62.5; DB 6; Length 2008;  
Best Local Similarity 41.9%; Pred. No. 2.9e+03;  
RESULT 1019  
ID ABU54629 standard; protein; 2059 AA.  
DE Human NOVX polypeptide #88.  
PN WO200281498-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.5%; Score 62.5; DB 6; Length 2059;  
Best Local Similarity 41.9%; Pred. No. 3e+03;  
RESULT 1020  
ID ABG20760 standard; protein; 2120 AA.  
DE Novel human diagnostic protein #20751.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.5%; Score 62.5; DB 4; Length 2120;  
Best Local Similarity 26.6%; Pred. No. 3.1e+03;

RESULT 1021  
ID AAU04483 standard; protein; 2146 AA.  
DE Human PD-ARP-binding cassette (PD-ABC) protein form #1.  
PN WO200153490-A1.  
PD 26-JUL-2001.  
PA (WARN) WARNER LAMBERT CO.  
Query Match 12.5%; Score 62.5; DB 4; Length 2146;  
Best Local Similarity 41.9%; Pred. No. 3.2e+03;  
RESULT 1022  
ID ABP52096 standard; protein; 2146 AA.  
DE Homo sapiens ABC transporter ABCA7 protein SEQ ID NO:48.  
PN EP1217066-A1.  
PD 26-JUN-2002.  
PA (UYGE-) UNIV GENT.  
Query Match 12.5%; Score 62.5; DB 5; Length 2146;  
Best Local Similarity 41.9%; Pred. No. 3.2e+03;  
RESULT 1023  
ID ABU08466 standard; protein; 2146 AA.  
DE Human ABCA-SSN protein.  
PN WO2003010315-A1.  
PD 06-FEB-2003.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
PA (KAZU-) KAZUSA DNA RES INST FOUND.  
Query Match 12.5%; Score 62.5; DB 6; Length 2146;  
Best Local Similarity 41.9%; Pred. No. 3.2e+03;  
RESULT 1024  
ID ABG72696 standard; protein; 2146 AA.  
DE Human ARP-binding cassette transporter-like protein, ABCL.  
PN US2002127647-A1.  
PD 12-SEP-2002.  
PA (SHUT/) SHUTTER J.  
PA (ULIA/) ULIAS L.  
Query Match 12.5%; Score 62.5; DB 6; Length 2146;  
Best Local Similarity 41.9%; Pred. No. 3.2e+03;  
RESULT 1025  
ID AAO14210 standard; protein; 2180 AA.  
DE Human transporter and ion channel TRICH-27.  
PN WO200204520-A2.  
PD 17-JUN-2002.  
PA (INCT-) INCTE GENOMICS INC.  
Query Match 12.5%; Score 62.5; DB 5; Length 2180;  
Best Local Similarity 41.9%; Pred. No. 3.2e+03;  
RESULT 1026  
ID ABB81459 standard; protein; 2541 AA.  
DE Human Talin protein SEQ ID NO:3.  
PN US6372492-B1.  
PD 16-APR-2002.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 12.5%; Score 62.5; DB 5; Length 2541;  
Best Local Similarity 24.3%; Pred. No. 3.9e+03;  
RESULT 1027  
ID ADG90450 standard; protein; 2541 AA.  
DE Human talin.  
PN WO200268446-A1.  
PD 06-SEP-2002.  
PA (ISIS-) ISIS PHARM INC.  
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.  
Query Match 12.5%; Score 62.5; DB 5; Length 2541;  
Best Local Similarity 24.3%; Pred. No. 3.9e+03;  
RESULT 1028  
ID ABR47614 standard; protein; 2541 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:470.  
PN WO2003004989-A2.  
PD 16-JUN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 12.5%; Score 62.5; DB 6; Length 2541;  
Best Local Similarity 24.3%; Pred. No. 3.9e+03;  
RESULT 1029  
ID ADP85745 standard; protein; 2541 AA.  
DE Human Talin protein.  
PN US2004110705-A1.  
PD 10-JUN-2004.  
PA (BENN/) BENNETT C F.

PA (COMS/) COMSERT L M.  
 Query Match 12.5%; Score 62.5; DB 8; Length 2541;  
 Best Local Similarity 24.3%; Pred. No. 3.9e+03;  
 RESULT 1030  
 ID AAM56448 standard; protein; 2723 AA.  
 DE Fragment Hgu1775 of a new Hepatitis virus g protein.  
 PN UPI0108685-A.  
 PD 28-APR-1998.  
 PA (BMLB-) BML KK.  
 Query Match 12.5%; Score 62.5; DB 2; Length 2723;  
 Best Local Similarity 27.1%; Pred. No. 4.3e+03;  
 RESULT 1031  
 ID AAM27227 standard; protein; 2861 AA.  
 DE Human TRIO phosphoprotein.  
 PN W09735979-A1.  
 PD 02-OCT-1997.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 Query Match 12.5%; Score 62.5; DB 2; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1032  
 ID ABG17024 standard; protein; 2861 AA.  
 DE Novel human diagnostic protein #17015.  
 PN W0200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 12.5%; Score 62.5; DB 4; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1033  
 ID AAG68192 standard; protein; 2861 AA.  
 DE GTPase protein SEQ ID NO:108.  
 PN W0200177327-A1.  
 PD 18-OCT-2001.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 12.5%; Score 62.5; DB 4; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1034  
 ID ABR41116 standard; protein; 2861 AA.  
 DE Human GTPase Gene TRIO protein product.  
 PN W0200292764-A2.  
 PD 21-NOV-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 12.5%; Score 62.5; DB 6; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1035  
 ID ABU70968 standard; protein; 2861 AA.  
 DE Human adipocyte Selected Interacting domain, SID, #599.  
 PN W0200286122-A2.  
 PD 31-OCT-2002.  
 PA (HYBR-) HYBRIGENICS.  
 Query Match 12.5%; Score 62.5; DB 6; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1036  
 ID ADB98736 standard; protein; 2861 AA.  
 DE Human GTPase.  
 PN W0200292000-A2.  
 PD 21-NOV-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 12.5%; Score 62.5; DB 7; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1037  
 ID ADE82532 standard; protein; 2861 AA.  
 DE Human protein sequence related to the invention #22.  
 PN W0200292015-A2.  
 PD 21-NOV-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 12.5%; Score 62.5; DB 7; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1038  
 ID ADD89085 standard; protein; 2861 AA.  
 DE TAT288.

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PN W02003057160-A2.  
 PD 17-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.5%; Score 62.5; DB 7; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1039  
 ID ADG14306 standard; protein; 2861 AA.  
 DE Human TRIO, SEQ ID 8.  
 PN W02003074007-A2.  
 PD 12-SEP-2003.  
 PA (RIGE-) RIGEL PHARM INC.  
 Query Match 12.5%; Score 62.5; DB 7; Length 2861;  
 Best Local Similarity 26.6%; Pred. No. 4.6e+03;  
 RESULT 1040  
 ID ADH39702 standard; protein; 3295 AA.  
 DE Streptomyces rochei ORF33 protein SEQ ID NO:33.  
 PN W02004001039-A1.  
 PD 31-DEC-2003.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Query Match 12.5%; Score 62.5; DB 8; Length 3295;  
 Best Local Similarity 29.9%; Pred. No. 5.6e+03;  
 RESULT 1041  
 ID AAB42036 standard; protein; 98 AA.  
 DE Human ORFX ORF1800 polypeptide sequence SEQ ID NO:3600.  
 PN W0200058473-A2.  
 PD 05-OCT-2000.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 12.4%; Score 62; DB 3; Length 98;  
 Best Local Similarity 28.0%; Pred. No. 62;  
 RESULT 1042  
 ID AAM18090 standard; protein; 111 AA.  
 DE Peptide #4524 encoded by probe for measuring cervical gene expression.  
 PN W0200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 12.4%; Score 62; DB 4; Length 111;  
 Best Local Similarity 31.2%; Pred. No. 73;  
 RESULT 1043  
 ID ABB37124 standard; peptide; 111 AA.  
 DE Peptide #4630 encoded by human foetal liver single exon probe.  
 PN W0200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 12.4%; Score 62; DB 4; Length 111;  
 Best Local Similarity 31.2%; Pred. No. 73;  
 RESULT 1044  
 ID AAM30600 standard; protein; 111 AA.  
 DE Peptide #4637 encoded by probe for measuring placental gene expression.  
 PN W0200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 12.4%; Score 62; DB 4; Length 111;  
 Best Local Similarity 31.2%; Pred. No. 73;  
 RESULT 1045  
 ID ABB31885 standard; peptide; 111 AA.  
 DE Peptide #4536 encoded by breast cell single exon nucleic acid probe.  
 PN W0200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 12.4%; Score 62; DB 4; Length 111;  
 Best Local Similarity 31.2%; Pred. No. 73;  
 RESULT 1046  
 ID ABB22436 standard; protein; 111 AA.  
 DE Protein #4435 encoded by probe for measuring heart cell gene expression.  
 PN W0200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 12.4%; Score 62; DB 4; Length 111;  
 Best Local Similarity 31.2%; Pred. No. 73;  
 RESULT 1047  
 ID AAM70262 standard; protein; 111 AA.  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30568.  
 PN W0200157276-A2.

PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 12.4%; Score 62; DB 4; Length 111;  
Best Local Similarity 31.2%; Pred. No. 73;  
RESULT 1048  
ID AAM57845 standard; protein; 111 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29950.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 12.4%; Score 62; DB 4; Length 111;  
Best Local Similarity 31.2%; Pred. No. 73;  
RESULT 1049  
ID ABG51959 standard; peptide; 111 AA.  
DE Human liver peptide, SEQ ID No 30607.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 12.4%; Score 62; DB 4; Length 111;  
Best Local Similarity 31.2%; Pred. No. 73;  
RESULT 1050  
ID AAM05724 standard; protein; 111 AA.  
DE Peptide #4406 encoded by probe for measuring breast gene expression.  
PN W0200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 12.4%; Score 62; DB 4; Length 111;  
Best Local Similarity 31.2%; Pred. No. 73;  
RESULT 1051  
ID ABG39904 standard; peptide; 111 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29569.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 12.4%; Score 62; DB 5; Length 111;  
Best Local Similarity 31.2%; Pred. No. 73;  
RESULT 1052  
ID AAY19666 standard; protein; 123 AA.  
DE SEQ ID NO 384 from W09922243.  
PN W09922243-A1.  
PD 06-MAY-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.4%; Score 62; DB 2; Length 123;  
Best Local Similarity 28.6%; Pred. No. 84;  
RESULT 1053  
ID AAG90290 standard; protein; 128 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4044.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOM-) KYOMA HAKKO KOGYO KK.  
Query Match 12.4%; Score 62; DB 4; Length 128;  
Best Local Similarity 30.9%; Pred. No. 88;  
RESULT 1054  
ID ABG73369 standard; protein; 280 AA.  
DE Murine ischaemia activated protein (IAP).  
PN US2002160495-A1.  
PD 31-OCT-2002.  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
Query Match 12.4%; Score 62; DB 6; Length 280;  
Best Local Similarity 25.6%; Pred. No. 2.5e+02;  
RESULT 1055  
ID AAE20090 standard; protein; 289 AA.  
DE Lactobacillus rhamnosus serine dehydratase alpha subunit (sdha).  
PN W0200212506-A1.  
PD 14-FEB-2002.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 12.4%; Score 62; DB 5; Length 289;  
Best Local Similarity 32.8%; Pred. No. 2.6e+02;  
RESULT 1056  
ID ABO82283 standard; protein; 312 AA.  
DE Pseudomonas aeruginosa polypeptide #14458.  
PN US6551795-B1.

PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.4%; Score 62; DB 7; Length 312;  
Best Local Similarity 30.3%; Pred. No. 2.8e+02;  
RESULT 1057  
ID ABU3983 standard; protein; 322 AA.  
DE Protein encoded by Prokaryotic essential gene #19510.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.4%; Score 62; DB 6; Length 322;  
Best Local Similarity 28.9%; Pred. No. 3e+02;  
RESULT 1058  
ID ABO70710 standard; protein; 336 AA.  
DE Pseudomonas aeruginosa polypeptide #2885.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.4%; Score 62; DB 7; Length 336;  
Best Local Similarity 26.8%; Pred. No. 3.1e+02;  
RESULT 1059  
ID AEO78853 standard; protein; 372 AA.  
DE Pseudomonas aeruginosa polypeptide #11028.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.4%; Score 62; DB 7; Length 372;  
Best Local Similarity 26.3%; Pred. No. 3.6e+02;  
RESULT 1060  
ID ABB58579 standard; protein; 393 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2529.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 12.4%; Score 62; DB 4; Length 393;  
Best Local Similarity 25.9%; Pred. No. 3.9e+02;  
RESULT 1061  
ID ADS21653 standard; protein; 393 AA.  
DE Bacterial polypeptide #10686.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.4%; Score 62; DB 8; Length 393;  
Best Local Similarity 34.5%; Pred. No. 3.9e+02;  
RESULT 1062  
ID ABO60011 standard; protein; 408 AA.  
DE Human genome derived single exon protein #6245.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENNY/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 12.4%; Score 62; DB 8; Length 408;  
Best Local Similarity 25.3%; Pred. No. 4.1e+02;  
RESULT 1063  
ID ABO71750 standard; protein; 444 AA.  
DE Pseudomonas aeruginosa polypeptide #3925.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.4%; Score 62; DB 7; Length 444;  
Best Local Similarity 27.3%; Pred. No. 4.5e+02;  
RESULT 1064  
ID ABO74128 standard; protein; 468 AA.  
DE Pseudomonas aeruginosa polypeptide #6303.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.4%; Score 62; DB 7; Length 468;

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Best Local Similarity 27.6%; Pred. No. 4.9e+02;
RESULT 1065
ID ABU49789 standard; protein; 474 AA.
DE Human NOV14c protein.
PN WO200272757-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 28.8%; Pred. No. 4.9e+02;
RESULT 1066
ID AB063015 standard; protein; 484 AA.
DE Klebsiella pneumoniae polypeptide seqid 9532.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 25.5%; Pred. No. 5.1e+02;
RESULT 1067
ID ABO63222 standard; protein; 528 AA.
DE Klebsiella pneumoniae polypeptide seqid 9739.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 29.5%; Pred. No. 5.7e+02;
RESULT 1068
ID ADG47934 standard; protein; 549 AA.
DE Beta-vulgaris-like sugar transport protein #1.
PN US2002199217-A1.
PD 26-DEC-2002.
PA (HELE/) HELENTJARIUS T G.
Query Match
Best Local Similarity 22.7%; Pred. No. 6e+02;
RESULT 1069
ID ADS24035 standard; protein; 549 AA.
DE Bacterial polypeptide #13068.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 27.3%; Pred. No. 6e+02;
RESULT 1070
ID ABU41401 standard; protein; 559 AA.
DE Protein encoded by Prokaryotic essential gene #26928;
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 28.6%; Pred. No. 6.1e+02;
RESULT 1071
ID ABB65575 standard; protein; 574 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23517.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 32.8%; Pred. No. 6.3e+02;
RESULT 1072
ID ADQ03088 standard; protein; 574 AA.
DE P. aeruginosa virulence gene, VIR18, protein.
PN US2004122212-A1.
PD 24-JUN-2004.
PA (COSS/) COSSON P.
PA (KOHL/) KOHLER T.
PA (BENG/) BENGHEZAI M.
PA (MARC/) MARCHETTI A.
PA (DELD/) DELDEN C V.
Query Match
Best Local Similarity 27.3%; Pred. No. 6.3e+02;
RESULT 1073
ID ABU65064 standard; protein; 616 AA.
DE Human NOV14c protein.
PN WO200272757-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02;
RESULT 1074
ID ABU65063 standard; protein; 616 AA.
DE Human NOV14b protein.
PN WO200272757-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02;
RESULT 1075
ID ADK51048 standard; protein; 616 AA.
DE Human NOV18A protein sequence SeqID68.
PN WO2003083046-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02;
RESULT 1076
ID ADH42447 standard; protein; 616 AA.
DE Novel human protein NOV67d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02;
RESULT 1077
ID ADN61777 standard; protein; 616 AA.
DE Human novel protein NOV14b.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOV S G.
PA (TAUP/) TAUFIER R J.
PA (PENA/) PENA C E A.
PA (LILL/) LI L.
PA (ZERR/) ZERRHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (JIMW/) JI W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KERU/) KERUDA R.
PA (PART/) PARTURAJAN M.
PA (GANG/) GANGOLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEV V T.
PA (FERN/) FERNANDES B R.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR V M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATT/) CATBERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match
Best Local Similarity 22.9%; Pred. No. 7e+02;
RESULT 1078
ID ADN61779 standard; protein; 616 AA.
DE Human novel protein NOV14c.
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PN US2004043382-A1.  
PD 04-MAR-2004.  
PA (PADI/) PADIGARU M.  
PA (SPYT/) SPYTEK K A.  
PA (SHEN/) SHENOY S G.  
PA (TAUP/) TAUPIER R J.  
PA (PENA/) PENA C E A.  
PA (LILL/) LI L.  
PA (ZERN/) ZERHUSEN B D.  
PA (GUSE/) GUSEV V Y.  
PA (UTIM/) JT W.  
PA (GORM/) GORMAN L.  
PA (MILL/) MILLER C E.  
PA (KEKU/) KEKUDA R.  
PA (PATT/) PATTURAJAN M.  
PA (GANG/) GANGOLI E A.  
PA (VERN/) VERNET C A M.  
PA (GUOX/) GUO X S.  
PA (TCHE/) TCHERNEV V T.  
PA (FERN/) FERNANDES E R.  
PA (CASW/) CASWAN S J.  
PA (MALY/) MALYANKAR U M.  
PA (GERL/) GERLACH V.  
PA (LITY/) LITY Y.  
PA (ANDE/) ANDERSON D W.  
PA (SPAD/) SPADERNA S K.  
PA (CATT/) CATTERON E.  
PA (LEIT/) LEITE M W.  
PA (ZHON/) ZHONG H.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEPLLEY D M.  
PA (RIEG/) RIEGER D K.  
PA (BURG/) BURGESS C B.  
Query Match 12.4%; Score 62; DB 8; Length 616;  
Best Local Similarity 22.9%; Pred. No. 7e+02;  
RESULT 1079  
ID ADS96436 standard; protein; 637 AA.  
DE Drosophila melanogaster protein, SEQ ID 57.  
PN MO200403999-A2.  
PD 13-MAY-2004.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 12.4%; Score 62; DB 8; Length 637;  
Best Local Similarity 32.0%; Pred. No. 7.3e+02;  
RESULT 1080  
ID ADS27839 standard; protein; 643 AA.  
DE Bacterial polypeptide #16872.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.4%; Score 62; DB 8; Length 643;  
Best Local Similarity 28.0%; Pred. No. 7.4e+02;  
RESULT 1081  
ID ADC00466 standard; protein; 645 AA.  
DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 511.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Query Match 12.4%; Score 62; DB 7; Length 645;  
Best Local Similarity 22.7%; Pred. No. 7.4e+02;  
RESULT 1082  
ID ADI45319 standard; protein; 649 AA.  
DE Rice isoprenoid biosynthesis-associated protein #125.  
PN US2004010815-A1.  
PD 15-JAN-2004.  
PA (LANG/) LANGE B M.  
PA (GHAS/) GHASSEMIAN M.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUC/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICKE D.  
PA (ZHUT/) ZHU T.  
Query Match 12.4%; Score 62; DB 8; Length 649;  
Best Local Similarity 31.5%; Pred. No. 7.5e+02;  
RESULT 1083  
ID ADF74751 standard; protein; 671 AA.  
DE Murine dnaform 41412 protein, an ATP binding cassette (SeqID 30).  
PN MO2003091435-A1.  
PD 06-NOV-2003.  
PA (RIKE ) RIKEN KK.  
PA (DNMF-) DNAMFORM KK.  
PA (MITU ) MITSUBISHI CHEM CORP.  
Query Match 12.4%; Score 62; DB 7; Length 671;  
Best Local Similarity 39.5%; Pred. No. 7.8e+02;  
RESULT 1084  
ID ABB62230 standard; protein; 883 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 13482.  
PN MO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.4%; Score 62; DB 4; Length 883;  
Best Local Similarity 25.4%; Pred. No. 1.1e+03;  
RESULT 1085  
ID AAB42926 standard; protein; 903 AA.  
DE Human ORFX ORF2690 polypeptide sequence SEQ ID NO:5380.  
PN MO200058473-A2.  
PD 05-OCT-2000.  
PA (CUPA-) CUPAGEN CORP.  
Query Match 12.4%; Score 62; DB 3; Length 903;  
Best Local Similarity 30.3%; Pred. No. 1.2e+03;  
RESULT 1086  
ID ADF69021 standard; protein; 903 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID827.  
PN MO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 12.4%; Score 62; DB 7; Length 903;  
Best Local Similarity 30.3%; Pred. No. 1.2e+03;  
RESULT 1087  
ID ABB97506 standard; protein; 966 AA.  
DE Novel human protein SEQ ID NO: 774.  
PN MO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.4%; Score 62; DB 5; Length 966;  
Best Local Similarity 25.3%; Pred. No. 1.3e+03;  
RESULT 1088  
ID ADJ70349 standard; protein; 966 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID2155.  
PN MO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 12.4%; Score 62; DB 7; Length 966;  
Best Local Similarity 25.3%; Pred. No. 1.3e+03;  
RESULT 1089  
ID ABU41551 standard; protein; 1215 AA.  
DE Protein encoded by Prokaryotic essential gene #27078.  
PN MO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.4%; Score 62; DB 6; Length 1215;  
Best Local Similarity 35.7%; Pred. No. 1.7e+03;  
RESULT 1090  
ID ADF74752 standard; protein; 1250 AA.  
DE Murine dnaform 43395 protein, an ATP binding cassette (SeqID 31).  
PN MO2003091435-A1.

PD 06-NOV-2003.  
PA (RIKE ) RIKEN KK.  
PA (DNAF-) DNAFORM KK.  
PA (MITU ) MITSUBISHI CHEM CORP.  
Query Match  
Best Local Similarity 12.4%; Score 62; DB 7; Length 1250;  
RESULT 1091  
ID ADH15715 standard; protein; 1652 AA.  
DE C. elegans neuromuscular junction GABA receptor complex subunit #1.  
PN US2003065144-A1.  
PD 03-APR-2003.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match  
Best Local Similarity 12.4%; Score 62; DB 6; Length 1652;  
RESULT 1092  
ID AAB76532 standard; protein; 1874 AA.  
DE Corynebacterium glutamicum MCT protein SEQ ID NO:46.  
PN WO200100805-A2.  
PD 04-JUN-2001.  
PA (BADI ) BASF AG.  
Query Match  
Best Local Similarity 12.4%; Score 62; DB 4; Length 1874;  
RESULT 1093  
ID AAG90680 standard; protein; 2969 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4434.  
PN EP108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match  
Best Local Similarity 12.4%; Score 62; DB 4; Length 2969;  
RESULT 1094  
ID ADL65607 standard; protein; 2969 AA.  
DE C. glutamicum membrane transport and synthesis-associated protein #90.  
PN DE10154179-A1.  
PD 08-MAY-2003.  
PA (BADI ) BASF AG.  
Query Match  
Best Local Similarity 12.4%; Score 62; DB 7; Length 2969;  
RESULT 1095  
ID ABP34033 standard; protein; 96 AA.  
DE Human dehydrogenase-like ORF3006 protein, SEQ ID NO:6012.  
PN WO200190386-A2.  
PD 29-NOV-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 5; Length 96;  
RESULT 1096  
ID AAY06407 standard; protein; 105 AA.  
DE Human secreted protein nF87\_1.  
PN WO9935252-A2.  
PD 15-JUL-1999.  
PA (GEMY ) GENETICS INST INC.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 2; Length 105;  
RESULT 1097  
ID AAT39018 standard; protein; 105 AA.  
DE Human secreted protein nF87\_1.  
PN WO200175068-A2.  
PD 11-OCT-2001.  
PA (GEMY ) GENETICS INST INC.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 4; Length 105;  
RESULT 1098  
ID ABB55727 standard; protein; 105 AA.  
DE Human polypeptide SEQ ID NO 60.  
PN US2001039335-A1.  
PD 08-NOV-2001.  
PA (JACO) JACOBS K.  
PA (MCCO) MCCOY J M.  
PA (LAVA) LAVALLIE E R.  
PA (COLL) COLLINS-RACIE L A.  
PA (EVAN) EVANS C.  
PA (MERB) MERBERG D.  
  
PA (TREA) TREACY M.  
PA (AGOS) AGOSTINO M J.  
PA (STEL) STEININGER R J.  
PA (SPAU) SPAULDING V.  
PA (WONG) WONG G G.  
PA (CLAR) CLARK H.  
PA (FECH) FECHTEL K.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 5; Length 105;  
RESULT 1099  
ID AAY12408 standard; protein; 115 AA.  
DE Human 5' EST secreted protein SEQ ID NO:439.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 2; Length 115;  
RESULT 1100  
ID ADI49821 standard; protein; 124 AA.  
DE O11-associated gene related protein #1321.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR) LAURIE C C.  
PA (RAVA) RAVANELLO M.  
PA (SAVA) SAVAGE T.  
PA (LEDE) LEDERER J R.  
PA (ROGE) ROGERS J A.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 124;  
RESULT 1101  
ID AAY12410 standard; protein; 130 AA.  
DE Human 5' EST secreted protein SEQ ID NO:441.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 2; Length 130;  
RESULT 1102  
ID ADE28306 standard; protein; 217 AA.  
DE Human KRP protein - SEQ ID 17.  
PN WO2003080805-A2.  
PD 02-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 217;  
RESULT 1103  
ID ABU41469 standard; protein; 223 AA.  
DE Protein encoded by Prokaryotic essential gene #26996.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 6; Length 223;  
RESULT 1104  
ID ADS21979 standard; protein; 256 AA.  
DE Bacterial polypeptide #11012.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 256;  
RESULT 1105  
ID ADG74661 standard; protein; 282 AA.  
DE Human kinase and phosphatase protein (KPP) #18.  
PN WO2003091419-A2.  
PD 06-NOV-2003.  
PA (INCY-) INCYTE CORP.  
PA (LEES-) LEE S Y.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 7; Length 282;



Best Local Similarity 32.0%; Pred. No. 2.8e+02;  
RESULT 1106  
ID AUI35598 standard; protein; 306 AA.  
DE Haemophilus influenzae cellular proliferation protein #239.  
PN W0200170955-A2.  
PD 27-SEP-2001.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.3%; Score 61.5; DB 4; Length 306;  
Best Local Similarity 31.6%; Pred. No. 3.2e+02;  
RESULT 1107  
ID ABP56999 standard; protein; 306 AA.  
DE Haemophilus influenzae D-Ala-D-Ala ligase enzyme SEQ ID NO:5.  
PN W02003002063-A2.  
PD 09-JAN-2003.  
PA (ESSE-) ESSENTIAL THERAPEUTICS INC.  
PA (PLIV ) PLIVA DD ZAGREB.  
Query Match 12.3%; Score 61.5; DB 6; Length 306;  
Best Local Similarity 31.6%; Pred. No. 3.2e+02;  
RESULT 1108  
ID ABU0500 standard; protein; 306 AA.  
DE Protein encoded by Prokaryotic essential gene #16027.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.3%; Score 61.5; DB 6; Length 306;  
Best Local Similarity 31.6%; Pred. No. 3.2e+02;  
RESULT 1109  
ID ABG29367 standard; protein; 309 AA.  
DE Novel human diagnostic protein #29358.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 12.3%; Score 61.5; DB 4; Length 309;  
Best Local Similarity 30.6%; Pred. No. 3.2e+02;  
RESULT 1110  
ID AAB03955 standard; protein; 344 AA.  
DE Human mesenchymal stem cell polypeptide.  
PN W0200059933-A2.  
PD 12-OCT-2000.  
PA (OSIR-) OSIRIS THERAPEUTICS INC.  
Query Match 12.3%; Score 61.5; DB 3; Length 344;  
Best Local Similarity 32.0%; Pred. No. 3.7e+02;  
RESULT 1111  
ID AAB93360 standard; protein; 344 AA.  
DE Human protein sequence SEQ ID NO:12497.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELT-) HELIX RES INST.  
Query Match 12.3%; Score 61.5; DB 4; Length 344;  
Best Local Similarity 32.0%; Pred. No. 3.7e+02;  
RESULT 1112  
ID ABB89632 standard; protein; 344 AA.  
DE Human polypeptide SEQ ID NO 2008.  
PN W0200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.3%; Score 61.5; DB 5; Length 344;  
Best Local Similarity 32.0%; Pred. No. 3.7e+02;  
RESULT 1113  
ID ADJ69569 standard; protein; 344 AA.  
DE Human heat mitochondrial protein as a therapeutic target SegID1375.  
PN W02003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 12.3%; Score 61.5; DB 7; Length 344;  
Best Local Similarity 32.0%; Pred. No. 3.7e+02;  
RESULT 1114  
ID ADS42410 standard; protein; 344 AA.  
DE Bacterial polypeptide #20840.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.3%; Score 61.5; DB 8; Length 344;  
Best Local Similarity 29.1%; Pred. No. 3.7e+02;  
RESULT 1115  
ID ABU18838 standard; protein; 350 AA.  
DE Protein encoded by Prokaryotic essential gene #4365.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.3%; Score 61.5; DB 6; Length 350;  
Best Local Similarity 30.8%; Pred. No. 3.8e+02;  
RESULT 1116  
ID AUI30935 standard; protein; 361 AA.  
DE Novel human secreted protein #1426.  
PN W0200179449-A2.  
PD 25-OCT-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 12.3%; Score 61.5; DB 4; Length 361;  
Best Local Similarity 25.6%; Pred. No. 3.9e+02;  
RESULT 1117  
ID ABB10101 standard; protein; 367 AA.  
DE Human homeobox protein NKx6.1 amino acid sequence.  
PN W0200218545-A1.  
PD 07-MAR-2002.  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
Query Match 12.3%; Score 61.5; DB 5; Length 367;  
Best Local Similarity 28.9%; Pred. No. 4e+02;  
RESULT 1118  
ID ABG70892 standard; protein; 367 AA.  
DE Human NKX-6.1 protein.  
PN US643667-B1.  
PD 20-AUG-2002.  
PA (REGC ) UNIV CALIFORNIA.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 12.3%; Score 61.5; DB 5; Length 367;  
Best Local Similarity 28.9%; Pred. No. 4e+02;  
RESULT 1119  
ID ADQ09851 standard; protein; 367 AA.  
DE Human NK-2 class homeobox protein, NKx6.1.  
PN US2004132679-A1.  
PD 08-JUL-2004.  
PA (BAYO ) BAYLOR COLLEGE MEDICINE.  
Query Match 12.3%; Score 61.5; DB 8; Length 367;  
Best Local Similarity 28.9%; Pred. No. 4e+02;  
RESULT 1120  
ID AAU45721 standard; protein; 369 AA.  
DE Propionibacterium acnes immunogenic protein #6617.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 12.3%; Score 61.5; DB 4; Length 369;  
Best Local Similarity 27.4%; Pred. No. 4e+02;  
RESULT 1121  
ID ABM42240 standard; protein; 369 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6916.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 12.3%; Score 61.5; DB 6; Length 369;  
Best Local Similarity 27.4%; Pred. No. 4e+02;  
RESULT 1122  
ID ADN25671 standard; protein; 378 AA.  
DE Bacterial polypeptide #8324.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.

Query Match 12.3%; Score 61.5; DB 8; Length 378;  
Best Local Similarity 30.6%; Pred. No. 4.2e+02;  
RESULT 1123  
ID ABB82801 standard; protein; 384 AA.  
DE A. radiobacter Opda polypeptide mutant Opda2.  
PN W0200292803-A1.  
PD 21-NOV-2002.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 12.3%; Score 61.5; DB 6; Length 384;  
Best Local Similarity 32.9%; Pred. No. 4.3e+02;  
RESULT 1124  
ID ABB82798 standard; protein; 384 AA.  
DE A. radiobacter Opda polypeptide.  
PN W0200292803-A1.  
PD 21-NOV-2002.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 12.3%; Score 61.5; DB 6; Length 384;  
Best Local Similarity 32.9%; Pred. No. 4.3e+02;  
RESULT 1125  
ID ABB82800 standard; protein; 384 AA.  
DE A. radiobacter Opda polypeptide mutant Opda1.  
PN W0200292803-A1.  
PD 21-NOV-2002.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 12.3%; Score 61.5; DB 6; Length 384;  
Best Local Similarity 32.9%; Pred. No. 4.3e+02;  
RESULT 1126  
ID ADJ45734 standard; protein; 384 AA.  
DE Agrobacterium radiobacter Opda protein SEQ ID NO:30.  
PN W02004011492-A1.  
PD 05-FEB-2004.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 12.3%; Score 61.5; DB 8; Length 384;  
Best Local Similarity 32.9%; Pred. No. 4.3e+02;  
RESULT 1127  
ID ADN22118 standard; protein; 389 AA.  
DE Bacterial polypeptide #4771.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 12.3%; Score 61.5; DB 8; Length 389;  
Best Local Similarity 27.0%; Pred. No. 4.3e+02;  
RESULT 1128  
ID ADN24878 standard; protein; 392 AA.  
DE Bacterial polypeptide #7531.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 12.3%; Score 61.5; DB 8; Length 392;  
Best Local Similarity 27.0%; Pred. No. 4.4e+02;  
RESULT 1129  
ID AD623141 standard; protein; 422 AA.  
DE Bacterial polypeptide #12174.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 12.3%; Score 61.5; DB 8; Length 422;  
Best Local Similarity 29.3%; Pred. No. 4.8e+02;  
RESULT 1130  
ID ADN19902 standard; protein; 428 AA.  
DE Bacterial polypeptide #2555.

PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 12.3%; Score 61.5; DB 8; Length 428;  
Best Local Similarity 24.5%; Pred. No. 4.9e+02;  
RESULT 1131  
ID ABU25929 standard; protein; 431 AA.  
DE Protein encoded by Prokaryotic essential gene #11456.  
PN W0200077183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.3%; Score 61.5; DB 6; Length 431;  
Best Local Similarity 26.7%; Pred. No. 5e+02;  
RESULT 1132  
ID AAM12400 standard; protein; 433 AA.  
DE A. chrysoeum O-acetylhomoserine sulphydrylase protein.  
PN JF08336391-A.  
PD 24-DEC-1996.  
PA (ASAH) ASAH KASEI KOGYO KK.  
Query Match 12.3%; Score 61.5; DB 2; Length 433;  
Best Local Similarity 28.0%; Pred. No. 5e+02;  
RESULT 1133  
ID AAG81144 standard; protein; 441 AA.  
DE Mycobacterium tuberculosis potential drug target protein SEQ ID 195.  
PN W0200135317-A1.  
PD 17-MAY-2001.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 12.3%; Score 61.5; DB 4; Length 441;  
Best Local Similarity 24.5%; Pred. No. 5.1e+02;  
RESULT 1134  
ID ABP57503 standard; protein; 441 AA.  
DE Mycobacterium tuberculosis protein SEQ ID NO:135.  
PN W0200300721-A2.  
PD 03-JAN-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 12.3%; Score 61.5; DB 6; Length 441;  
Best Local Similarity 24.5%; Pred. No. 5.1e+02;  
RESULT 1135  
ID ABU24297 standard; protein; 447 AA.  
DE Protein encoded by Prokaryotic essential gene #9824.  
PN W020027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.3%; Score 61.5; DB 6; Length 447;  
Best Local Similarity 28.4%; Pred. No. 5.2e+02;  
RESULT 1136  
ID ABO79444 standard; protein; 447 AA.  
DE Pseudomonas aeruginosa polypeptide #11619.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.3%; Score 61.5; DB 7; Length 447;  
Best Local Similarity 25.6%; Pred. No. 5.2e+02;  
RESULT 1137  
ID AD139278 standard; protein; 476 AA.  
DE S. hygroscopicus geldanamycin gene cluster-encoded protein, SEQ ID:120.  
PN W02003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID) REID R C.  
Query Match 12.3%; Score 61.5; DB 8; Length 476;  
Best Local Similarity 31.6%; Pred. No. 5.6e+02;  
RESULT 1138  
ID ABO62871 standard; protein; 578 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9388.  
PN US610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.3%; Score 61.5; DB 7; Length 578;

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Best Local Similarity 23.8%; Pred. No. 7.3e+02;
RESULT 1139
ID ADN18902 standard; protein; 587 AA.
DE Bacterial polypeptide #1555.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.3%; Score 61.5; DB 8; Length 587;
Best Local Similarity 27.5%; Pred. No. 7.4e+02;
RESULT 1140
ID ADJ87349 standard; protein; 630 AA.
DE DNA replication and pathogenesis associated protein RXA00157.
PN DE10154246-A1.
PD 08-MAY-2003.
PA (BADI ) BASF AG.
Query Match 12.3%; Score 61.5; DB 7; Length 630;
Best Local Similarity 27.1%; Pred. No. 8.2e+02;
RESULT 1141
ID ABU21547 standard; protein; 704 AA.
DE Protein encoded by Prokaryotic essential gene #7074.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 704;
Best Local Similarity 27.9%; Pred. No. 9.5e+02;
RESULT 1142
ID ABG25695 standard; protein; 705 AA.
DE Novel human diagnostic protein #25686.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 61.5; DB 4; Length 705;
Best Local Similarity 28.2%; Pred. No. 9.5e+02;
RESULT 1143
ID AAM93207 standard; protein; 739 AA.
DE Human polypeptide, SEQ ID NO: 2601.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INSTR.
Query Match 12.3%; Score 61.5; DB 4; Length 739;
Best Local Similarity 31.1%; Pred. No. 1e+03;
RESULT 1144
ID ADL30568 standard; protein; 739 AA.
DE Human protein encoded by a full length CDNA clone segid 2601.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.3%; Score 61.5; DB 8; Length 739;
Best Local Similarity 31.1%; Pred. No. 1e+03;
RESULT 1145
ID AAB43831 standard; protein; 766 AA.
DE Human cancer associated protein sequence SEQ ID NO:1276.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.3%; Score 61.5; DB 3; Length 766;
Best Local Similarity 31.1%; Pred. No. 1.1e+03;
RESULT 1146
ID ABP41543 standard; protein; 766 AA.
DE Human ovarian antigen HPCY73, SEQ ID NO:2675.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.3%; Score 61.5; DB 5; Length 766;
Best Local Similarity 31.1%; Pred. No. 1.1e+03;
RESULT 1147
ID ABU38459 standard; protein; 820 AA.
DE Protein encoded by Prokaryotic essential gene #23986.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 61.5; DB 6; Length 820;
Best Local Similarity 37.3%; Pred. No. 1.2e+03;
RESULT 1148
ID ABM82561 standard; protein; 966 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:2810.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.3%; Score 61.5; DB 8; Length 966;
Best Local Similarity 27.3%; Pred. No. 1.4e+03;
RESULT 1149
ID ABB70304 standard; protein; 984 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37704.
PN WO200172042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 12.3%; Score 61.5; DB 4; Length 984;
Best Local Similarity 33.9%; Pred. No. 1.5e+03;
RESULT 1150
ID ABM82559 standard; protein; 1008 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2808.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.3%; Score 61.5; DB 8; Length 1008;
Best Local Similarity 27.3%; Pred. No. 1.5e+03;
RESULT 1151
ID AAB93169 standard; protein; 1014 AA.
DE Human protein sequence SEQ ID NO:12102.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INSTR.
Query Match 12.3%; Score 61.5; DB 4; Length 1014;
Best Local Similarity 27.3%; Pred. No. 1.5e+03;
RESULT 1152
ID ABM82563 standard; protein; 1041 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2812.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.3%; Score 61.5; DB 8; Length 1041;
Best Local Similarity 27.3%; Pred. No. 1.6e+03;
RESULT 1153
ID ADA05674 standard; protein; 1054 AA.
DE Human NOV6a protein SEQ ID NO:34.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.3%; Score 61.5; DB 6; Length 1054;
Best Local Similarity 27.3%; Pred. No. 1.6e+03;
RESULT 1154
ID ADN62839 standard; protein; 1054 AA.
DE Human NOV6a.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KERUDA R.
PA (JUTJ/) JU J.
PA (LILL/) LI L.
PA (GUOK/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELER/) ELIERMAN K.
PA (MALV/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERNUSSEN B D.
PA (ANDE/) ANDERSON D W.
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PA (ZHON/) ZHONG M.  
PA (CAT/) CATTERTON E.  
PA (JIMW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENNA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIRP/) DIRIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1054;  
RESULT 1155  
ID ADM63232 standard; protein; 1054 AA.  
DE Human NOV6a variant.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYN/) PEYMAN J A.  
PA (KERU/) KERUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTUPAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERR/) ZERRHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CAT/) CATTERTON E.  
PA (JIMW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENNA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIRP/) DIRIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1054;  
RESULT 1156  
ID AWM82562 standard; protein; 1076 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2811.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1076;  
RESULT 1157  
ID AAE14346 standard; protein; 1108 AA.  
DE Human protease PRPS-11 protein.  
PN WO200183775-A2.

PD 08-NOV-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 5; Length 1108;  
RESULT 1158  
ID AWM82560 standard; protein; 1121 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2809.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1121;  
RESULT 1159  
ID AWM82558 standard; protein; 1128 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2807.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1128;  
RESULT 1160  
ID AD116339 standard; protein; 1145 AA.  
DE Human protein modification and maintenance molecule (PMM) protein #24.  
PN WO2003100016-A2.  
PD 04-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1145;  
RESULT 1161  
ID AD116340 standard; protein; 1165 AA.  
DE Human protein modification and maintenance molecule (PMM) protein #25.  
PN WO2003100016-A2.  
PD 04-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 8; Length 1165;  
RESULT 1162  
ID ABJ26652 standard; protein; 1236 AA.  
DE Human protein modification + maintenance molecule protein SEQ ID No 6.  
PN WO200300844-A2.  
PD 03-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 6; Length 1236;  
RESULT 1163  
ID ABJ26649 standard; protein; 1256 AA.  
DE Human protein modification + maintenance molecule protein SEQ ID No 3.  
PN WO200300844-A2.  
PD 03-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 6; Length 1256;  
RESULT 1164  
ID AAU68534 standard; protein; 1324 AA.  
DE Human novel cytokine encoded by cDNA 790CIP2C\_5 #1.  
PN WO200175093-A1.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 4; Length 1324;  
RESULT 1165  
ID AAU68535 standard; protein; 1346 AA.  
DE Human novel cytokine encoded by cDNA 790CIP2C\_6 #1.  
PN WO200175093-A1.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.3%; Score 61.5; DB 4; Length 1346;  
RESULT 1166  
ID ABG15667 standard; protein; 1444 AA.  
DE Novel human diagnostic protein #15658.  
PN WO200175067-A2.  
PD 11-OCT-2001.

PA (HYSE-) HYSEO INC.  
Query Match 12.3%; Score 61.5; DB 4; Length 1444;  
Best Local Similarity 26.8%; Pred. No. 2.4e+03;  
RESULT 1167  
ID ABU35729 standard; protein; 2103 AA.  
DE Protein encoded by Prokaryotic essential gene #21256.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.3%; Score 61.5; DB 6; Length 2103;  
Best Local Similarity 27.5%; Pred. No. 4e+03;  
RESULT 1168  
ID AAB23751 standard; protein; 4881 AA.  
DE S. avermitilis avermectin aglycon synthase protein SEQ ID NO:5.  
PN WO200050605-A1.  
PD 31-AUG-2000.  
PA (KITA) KITASATO INST.  
Query Match 12.3%; Score 61.5; DB 3; Length 4881;  
Best Local Similarity 28.3%; Pred. No. 1.2e+04;  
RESULT 1169  
ID AAG65266 standard; protein; 4881 AA.  
DE Streptomyces avermitilis protein SEQ ID NO: 6.  
PN WO200162939-A1.  
PD 30-AUG-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Query Match 12.3%; Score 61.5; DB 4; Length 4881;  
Best Local Similarity 28.3%; Pred. No. 1.2e+04;  
RESULT 1170  
ID ABO75855 standard; protein; 98 AA.  
DE Pseudomonas aeruginosa polypeptide #8030.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.2%; Score 61; DB 7; Length 98;  
Best Local Similarity 29.3%; Pred. No. 80;  
RESULT 1171  
ID ABP56643 standard; protein; 142 AA.  
DE Chimpanzee C68 adenovirus hexon-associated protein PIX SEQ ID NO:8.  
PN WO2003000851-A2.  
PD 03-JAN-2003.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 12.2%; Score 61; DB 6; Length 142;  
Best Local Similarity 31.1%; Pred. No. 1.3e+02;  
RESULT 1172  
ID ABU09748 standard; protein; 199 AA.  
DE Mouse interleukin 11 (IL-11).  
PN US2003008343-A1.  
PD 09-JAN-2003.  
PA (TIMA) TIMANS J C.  
PA (PFLA) PFLANZ S K.  
PA (KAST/) KASTELEIN R A.  
PA (BAZA/) BAZAN J F.  
Query Match 12.2%; Score 61; DB 6; Length 199;  
Best Local Similarity 29.5%; Pred. No. 2e+02;  
RESULT 1173  
ID ABB09165 standard; protein; 212 AA.  
DE Methylomonas KHG/KDPG aldolase SEQ ID NO:10.  
PN WO20020796-A2.  
PD 14-MAR-2002.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 12.2%; Score 61; DB 5; Length 212;  
Best Local Similarity 29.5%; Pred. No. 2.2e+02;  
RESULT 1174  
ID AAE22300 standard; protein; 212 AA.  
DE Methylomonas 16a sp. KHG/KDPG aldolase enzyme.  
PN WO200218617-A2.  
PD 07-MAR-2002.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 12.2%; Score 61; DB 5; Length 212;  
Best Local Similarity 29.5%; Pred. No. 2.2e+02;  
RESULT 1175  
ID ABG61560 standard; protein; 212 AA.  
DE High growth mechanotrophic bacterial strain polypeptide #10.  
PN WO200220728-A2.  
PD 14-MAR-2002.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 12.2%; Score 61; DB 5; Length 212;  
Best Local Similarity 29.5%; Pred. No. 2.2e+02;  
RESULT 1176  
ID ABM67390 standard; protein; 233 AA.  
DE Photorhabdus luminescens protein sequence #487.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 12.2%; Score 61; DB 6; Length 233;  
Best Local Similarity 24.3%; Pred. No. 2.5e+02;  
RESULT 1177  
ID ABO78539 standard; protein; 236 AA.  
DE Pseudomonas aeruginosa polypeptide #10714.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.2%; Score 61; DB 7; Length 236;  
Best Local Similarity 24.8%; Pred. No. 2.6e+02;  
RESULT 1178  
ID ADN26268 standard; protein; 256 AA.  
DE Bacterial polypeptide #8921.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.2%; Score 61; DB 8; Length 256;  
Best Local Similarity 25.0%; Pred. No. 2.8e+02;  
RESULT 1179  
ID ADJ98209 standard; protein; 269 AA.  
DE Rice phytyl kinase protein.  
PN WO2004013312-A2.  
PD 12-FEB-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match 12.2%; Score 61; DB 8; Length 269;  
Best Local Similarity 28.4%; Pred. No. 3e+02;  
RESULT 1180  
ID ABO84568 standard; protein; 296 AA.  
DE Mouse cancer-associated protein MPl6-049.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 12.2%; Score 61; DB 8; Length 296;  
Best Local Similarity 25.9%; Pred. No. 3.4e+02;  
RESULT 1181  
ID ADJ98208 standard; protein; 314 AA.  
DE Rice phytyl kinase protein.  
PN WO2004013312-A2.  
PD 12-FEB-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match 12.2%; Score 61; DB 8; Length 314;  
Best Local Similarity 28.4%; Pred. No. 3.7e+02;  
RESULT 1182  
ID ABU39775 standard; protein; 329 AA.  
DE Protein encoded by Prokaryotic essential gene #25302.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.2%; Score 61; DB 6; Length 329;  
Best Local Similarity 26.2%; Pred. No. 4e+02;  
RESULT 1183  
ID ABU36699 standard; protein; 343 AA.  
DE Protein encoded by Prokaryotic essential gene #22226.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.

Query Match 12.2%; Score 61; DB 6; Length 343;  
Best Local Similarity 23.9%; Pred. No. 4.2e+02;  
RESULT 1184  
ID ABO63783 standard; protein; 374 AA.  
DE Klebsiella pneumoniae polypeptide seqid 10300.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.2%; Score 61; DB 7; Length 374;  
Best Local Similarity 38.5%; Pred. No. 4.7e+02;  
RESULT 1185  
ID ADN22787 standard; protein; 390 AA.  
DE Bacterial polypeptide #5440.  
PN US200323675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.2%; Score 61; DB 8; Length 390;  
Best Local Similarity 30.6%; Pred. No. 4.9e+02;  
RESULT 1186  
ID ABR82131 standard; protein; 417 AA.  
DE Bacterial P450 enzyme SEQ ID NO:26.  
PN WO2003052050-A2.  
PD 26-JUN-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 12.2%; Score 61; DB 6; Length 417;  
Best Local Similarity 34.3%; Pred. No. 5.4e+02;  
RESULT 1187  
ID AAY81741 standard; protein; 419 AA.  
DE Streptococcus pneumoniae protein sequence ID47.  
PN WO200006738-A2.  
PD 10-FEB-2000.  
PA (MCR-) MICROBIAL TECHNIQS LTD.  
Query Match 12.2%; Score 61; DB 3; Length 419;  
Best Local Similarity 29.4%; Pred. No. 5.4e+02;  
RESULT 1188  
ID ABU01175 standard; protein; 419 AA.  
DE S. pneumoniae type 4 strain protein from coding region #748.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 12.2%; Score 61; DB 6; Length 419;  
Best Local Similarity 29.4%; Pred. No. 5.4e+02;  
RESULT 1189  
ID ADX46237 standard; protein; 419 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 2752.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.2%; Score 61; DB 8; Length 419;  
Best Local Similarity 29.4%; Pred. No. 5.4e+02;  
RESULT 1190  
ID AD95141 standard; protein; 425 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 3776.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.2%; Score 61; DB 8; Length 425;  
Best Local Similarity 29.4%; Pred. No. 5.5e+02;  
RESULT 1191  
ID ABP66308 standard; protein; 430 AA.  
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:1052.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST-) SOC PROD NESTLE SA.  
Query Match 12.2%; Score 61; DB 5; Length 430;  
Best Local Similarity 29.4%; Pred. No. 5.6e+02;  
RESULT 1192  
ID AAM57832 standard; protein; 435 AA.

DE C1cm protein.  
PN EP83909-A1.  
PD 06-MAY-1998.  
PA (UYGR-) RIJXSUNIV GRONINGEN.  
Query Match 12.2%; Score 61; DB 2; Length 435;  
Best Local Similarity 22.9%; Pred. No. 5.7e+02;  
RESULT 1193  
ID AAU44346 standard; protein; 455 AA.  
DE Propionibacterium acnes immunogenic protein #5242.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 12.2%; Score 61; DB 4; Length 455;  
Best Local Similarity 32.8%; Pred. No. 6.1e+02;  
RESULT 1194  
ID ABM40865 standard; protein; 455 AA.  
DE Propionibacterium acnes immunogenic polypeptide #5541.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 12.2%; Score 61; DB 6; Length 455;  
Best Local Similarity 32.8%; Pred. No. 6.1e+02;  
RESULT 1195  
ID ABB71149 standard; protein; 473 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40239.  
PN WO200177042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 12.2%; Score 61; DB 4; Length 473;  
Best Local Similarity 28.3%; Pred. No. 6.4e+02;  
RESULT 1196  
ID ABU22761 standard; protein; 474 AA.  
DE Protein encoded by Prokaryotic essential gene #8288.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELTRA-) ELITRA PHARM INC.  
Query Match 12.2%; Score 61; DB 6; Length 474;  
Best Local Similarity 32.3%; Pred. No. 6.4e+02;  
RESULT 1197  
ID ABP65910 standard; protein; 500 AA.  
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:654.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST-) SOC PROD NESTLE SA.  
Query Match 12.2%; Score 61; DB 5; Length 500;  
Best Local Similarity 24.7%; Pred. No. 6.9e+02;  
RESULT 1198  
ID ADC13196 standard; protein; 505 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1478.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.2%; Score 61; DB 7; Length 505;  
Best Local Similarity 31.6%; Pred. No. 7e+02;  
RESULT 1199  
ID ABG15005 standard; protein; 510 AA.  
DE Novel human diagnostic protein #14996.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.2%; Score 61; DB 4; Length 510;  
Best Local Similarity 31.6%; Pred. No. 7e+02;  
RESULT 1200  
ID ABU11797 standard; protein; 519 AA.  
DE Human MDPY polypeptide SEQ ID 744.  
PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 12.2%; Score 61; DB 6; Length 519;  
Best Local Similarity 31.6%; Pred. No. 7.2e+02;  
RESULT 1201  
ID AAU07370 standard; protein; 524 AA.  
DE G protein-coupled receptor.

PN WO200162924-A2.  
PD 30-AUG-2001.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 12.2%; Score 61; DB 4; Length 524;  
Best Local Similarity 34.8%; Pred. No. 7.3e+02;  
RESULT 1202  
ID ABB06166 standard; protein; 528 AA.  
DE Human liver with hepatitis related protein SEQ ID NO:12.  
PN WO200200874-A1.  
PD 03-JAN-2002.  
PA (AJIN) AJINOMOTO CO INC.  
Query Match 12.2%; Score 61; DB 5; Length 528;  
Best Local Similarity 31.6%; Pred. No. 7.4e+02;  
RESULT 1203  
ID ABB67264 standard; protein; 545 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28584.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.2%; Score 61; DB 4; Length 545;  
Best Local Similarity 32.0%; Pred. No. 7.7e+02;  
RESULT 1204  
ID ABB58578 standard; protein; 545 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2526.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.2%; Score 61; DB 4; Length 545;  
Best Local Similarity 32.0%; Pred. No. 7.7e+02;  
RESULT 1205  
ID ADC08307 standard; protein; 549 AA.  
DE Rice protein sequence Seq ID612 related to grain filling.  
PN WO2003000905-A2.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 12.2%; Score 61; DB 7; Length 549;  
Best Local Similarity 25.3%; Pred. No. 7.8e+02;  
RESULT 1206  
ID ADC07912 standard; protein; 549 AA.  
DE Rice protein sequence Seq ID178 related to grain filling.  
PN WO2003000905-A2.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 12.2%; Score 61; DB 7; Length 549;  
Best Local Similarity 25.3%; Pred. No. 7.8e+02;  
RESULT 1207  
ID ADN63051 standard; protein; 568 AA.  
DE Human NOV55D.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT) SMITHSON G.  
PA (MILL) MILLET I.  
PA (PEYM) PEYMAN J A.  
PA (KEKU) KEKUDA R.  
PA (JUJ) JU J.  
PA (LILL) LI L.  
PA (GUOX) GUO X.  
PA (PAT) PATTURAJAN M.  
PA (SPYT) SPYTEK K A.  
PA (EDIN) EDINGER S R.  
PA (ELLE) ELLERMAN K.  
PA (MALY) MALYANKAR U M.  
PA (ORTT) ORT T.  
PA (GORM) GORMAN L.  
PA (ZERR) ZERRHUSEN B D.  
PA (ANDE) ANDERSON D W.  
PA (ZHON) ZHONG M.  
PA (CAT) CATERTON E.  
PA (JIW) JI W.  
PA (MILL) MILLER C E.  
PA (RAST) RASTELLI L.  
PA (STON) STONE D J.  
PA (PENA) PENA C E A.

PA (SHEN) SHENOY S G.  
PA (SHIM) SHIMKETS R A.  
PA (ROTH) ROTHENBERG M E.  
PA (LEAC) LEACH M D.  
PA (AGEE) AGEER M L.  
PA (BERG) BERGHS C.  
PA (DIP) DIPPEO V A.  
PA (EISE) EISEN A.  
PA (GANG) GANGOLLI E A.  
PA (RIEG) RIEGER D K.  
PA (SPAD) SPADERNA S K.  
Query Match 12.2%; Score 61; DB 8; Length 568;  
Best Local Similarity 20.0%; Pred. No. 8.1e+02;  
RESULT 1208  
ID ADO42971 standard; protein; 579 AA.  
DE Murine fatty acid amide hydrolase (FAAH), SEQ ID NO:4.  
PN WO2004037371-A2.  
PD 06-MAY-2004.  
PA (JANC) JANSSEN PHARM NV.  
Query Match 12.2%; Score 61; DB 8; Length 579;  
Best Local Similarity 29.2%; Pred. No. 8.3e+02;  
RESULT 1209  
ID AAW57782 standard; protein; 581 AA.  
DE Mouse fatty acid amide hydrolase.  
PN WO9820119-A1.  
PD 14-MAY-1998.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 12.2%; Score 61; DB 2; Length 581;  
Best Local Similarity 29.2%; Pred. No. 8.4e+02;  
RESULT 1210  
ID ABU38916 standard; protein; 582 AA.  
DE Protein encoded by Prokaryotic essential gene #24443.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT) ELITRA PHARM INC.  
Query Match 12.2%; Score 61; DB 6; Length 582;  
Best Local Similarity 26.8%; Pred. No. 8.4e+02;  
RESULT 1211  
ID ABO70115 standard; protein; 588 AA.  
DE Pseudomonas aeruginosa polypeptide #2290.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO) GENOME THERAPEUTICS CORP.  
Query Match 12.2%; Score 61; DB 7; Length 588;  
Best Local Similarity 26.8%; Pred. No. 8.5e+02;  
RESULT 1212  
ID ADP31467 standard; protein; 618 AA.  
DE Human secreted protein SEQ ID #2234.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.2%; Score 61; DB 8; Length 618;  
Best Local Similarity 40.0%; Pred. No. 9.1e+02;  
RESULT 1213  
ID ADP31466 standard; protein; 618 AA.  
DE Human secreted protein SEQ ID #2233.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.2%; Score 61; DB 8; Length 618;  
Best Local Similarity 40.0%; Pred. No. 9.1e+02;  
RESULT 1214  
ID ADS30153 standard; protein; 620 AA.  
DE Bacterial polypeptide #19186.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 12.2%; Score 61; DB 8; Length 620;  
Best Local Similarity 27.1%; Pred. No. 9.1e+02;

RESULT 1215  
ID ABB66879 standard; protein; 637 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 27429.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.2%; Score 61; DB 4; Length 637;  
Best Local Similarity 32.0%; Pred. No. 9.4e+02;  
RESULT 1216  
ID ADJ98211 standard; protein; 657 AA.  
DE Rice phycol kinase protein.  
PN WO2004013312-A2.  
PD 12-FEB-2004.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Query Match 12.2%; Score 61; DB 8; Length 657;  
Best Local Similarity 28.4%; Pred. No. 9.8e+02;  
RESULT 1217  
ID AAY37620 standard; protein; 658 AA.  
DE Protein involved in transcription, translation and/or maturation.  
PN WO9928475-A2.  
PD 10-JUN-1999.  
PA (GSEST ) GENSEST.  
Query Match 12.2%; Score 61; DB 2; Length 658;  
Best Local Similarity 27.9%; Pred. No. 9.8e+02;  
RESULT 1218  
ID ABB61294 standard; protein; 693 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 10674.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.2%; Score 61; DB 4; Length 693;  
Best Local Similarity 39.0%; Pred. No. 1.1e+03;  
RESULT 1219  
ID ABO69796 standard; protein; 707 AA.  
DE Pseudomonas aeruginosa polypeptide #1971.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.2%; Score 61; DB 7; Length 707;  
Best Local Similarity 35.3%; Pred. No. 1.1e+03;  
RESULT 1220  
ID ABU19429 standard; protein; 769 AA.  
DE Protein encoded by prokaryotic essential gene #4956.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.2%; Score 61; DB 6; Length 769;  
Best Local Similarity 31.8%; Pred. No. 1.2e+03;  
RESULT 1221  
ID AAR45001 standard; protein; 802 AA.  
DE Cellulose synthase operon, gene B product.  
PN US5268274-A.  
PD 07-DEC-1993.  
PA (CETU ) CETUS CORP.  
Query Match 12.2%; Score 61; DB 2; Length 802;  
Best Local Similarity 25.8%; Pred. No. 1.3e+03;  
RESULT 1222  
ID ADJ98210 standard; protein; 803 AA.  
DE Rice phycol kinase protein.  
PN WO2004013312-A2.  
PD 12-FEB-2004.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Query Match 12.2%; Score 61; DB 8; Length 803;  
Best Local Similarity 28.4%; Pred. No. 1.3e+03;  
RESULT 1223  
ID ADS42575 standard; protein; 873 AA.  
DE Bacterial polypeptide #21005.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.  
Query Match 12.2%; Score 61; DB 8; Length 873;  
Best Local Similarity 27.5%; Pred. No. 1.4e+03;  
RESULT 1224  
ID AAB6456 standard; protein; 920 AA.  
DE Protein encoded by Mycobacterium tuberculosis mmpL7 (RV2942) gene.  
PN WO200102555-A1.  
PD 11-JAN-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 12.2%; Score 61; DB 4; Length 920;  
Best Local Similarity 28.0%; Pred. No. 1.5e+03;  
RESULT 1225  
ID ABR55195 standard; protein; 920 AA.  
DE Nucleotide sequence of gene down-regulated during nutrient starvation.  
PN WO2003035681-A2.  
PD 01-MAY-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 12.2%; Score 61; DB 6; Length 920;  
Best Local Similarity 28.0%; Pred. No. 1.5e+03;  
RESULT 1226  
ID ABO68019 standard; protein; 927 AA.  
DE Pseudomonas aeruginosa polypeptide #194.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.2%; Score 61; DB 7; Length 927;  
Best Local Similarity 25.7%; Pred. No. 1.5e+03;  
RESULT 1227  
ID ADJ80167 standard; protein; 1006 AA.  
DE Novel human nucleic acid-associated protein #43.  
PN WO2003038052-A2.  
PD 08-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 12.2%; Score 61; DB 7; Length 1006;  
Best Local Similarity 28.7%; Pred. No. 1.7e+03;  
RESULT 1228  
ID ABE64908 standard; protein; 1044 AA.  
DE Human protein SEQ ID 568.  
PN WO200259260-A2.  
PD 01-AUG-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.2%; Score 61; DB 5; Length 1044;  
Best Local Similarity 28.7%; Pred. No. 1.8e+03;  
RESULT 1229  
ID ABB61832 standard; protein; 1086 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12288.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.2%; Score 61; DB 4; Length 1086;  
Best Local Similarity 33.9%; Pred. No. 1.9e+03;  
RESULT 1230  
ID ADS96730 standard; protein; 1086 AA.  
DE Drosophila melanogaster protein, SEQ ID 351.  
PN WO200403999-A2.  
PD 13-MAY-2004.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 12.2%; Score 61; DB 8; Length 1086;  
Best Local Similarity 33.9%; Pred. No. 1.9e+03;  
RESULT 1231  
ID ADB64795 standard; protein; 1166 AA.  
DE Human protein encoded by clone NTONG20053630.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.2%; Score 61; DB 7; Length 1166;  
Best Local Similarity 28.7%; Pred. No. 2.1e+03;  
RESULT 1232  
ID ADG42630 standard; protein; 1531 AA.  
DE Mouse SLIT1.  
PN US2003204052-A1.  
PD 30-OCT-2003.



PA (HERR/) HERRMANN J L.  
PA (RAST/) RASTFELI L.  
PA (SHIM/) SHIMKETS R A.  
Query Match 12.2%; Score 61; DB 7; Length 1531;  
Best Local Similarity 27.7%; Pred. No. 3e+03;  
RESULT 1233  
ID AAM18305 standard; protein; 1565 AA.  
DE Photorhabdus luminescens insect toxin Tccb.  
PN MO9717432-A1.  
PD 15-MAY-1997.  
PA (WISC) WISCONSIN ALUMNI RES FOUND.  
Query Match 12.2%; Score 61; DB 2; Length 1565;  
Best Local Similarity 35.1%; Pred. No. 3.1e+03;  
RESULT 1234  
ID ABG97432 standard; protein; 1977 AA.  
DE S. carzinostaticus FKSE protein.  
PN CA2387401-A1.  
PD 04-SEP-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 12.2%; Score 61; DB 5; Length 1977;  
Best Local Similarity 30.2%; Pred. No. 4.2e+03;  
RESULT 1235  
ID ADM45916 standard; protein; 3696 AA.  
DE S. mycarofaciens mddecamycin polyketide synthetase ORF3 protein.  
PN JP2004049100-A.  
PD 19-FEB-2004.  
PA (MEIT) MEITI SEIKA KAISHA LTD.  
Query Match 12.2%; Score 61; DB 8; Length 3696;  
Best Local Similarity 27.6%; Pred. No. 9.5e+03;  
RESULT 1236  
ID ADP31425 standard; protein; 8976 AA.  
DE Human secreted protein SEQ ID #2192.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.2%; Score 61; DB 8; Length 8976;  
Best Local Similarity 38.5%; Pred. No. 3e+04;  
RESULT 1237  
ID ADP31494 standard; protein; 9195 AA.  
DE Human secreted protein SEQ ID #2261.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.2%; Score 61; DB 8; Length 9195;  
Best Local Similarity 38.5%; Pred. No. 3.1e+04;  
RESULT 1238  
ID ABB62457 standard; protein; 138 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 14163.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.1%; Score 60.5; DB 4; Length 138;  
Best Local Similarity 23.3%; Pred. No. 1.4e+02;  
RESULT 1239  
ID AAG50109 standard; protein; 144 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63463.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (PEKE) PE CORP NY.  
Query Match 12.1%; Score 60.5; DB 3; Length 144;  
Best Local Similarity 28.0%; Pred. No. 1.5e+02;  
RESULT 1240  
ID AAG07169 standard; protein; 144 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4219.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (PEKE) PE CORP NY.  
Query Match 12.1%; Score 60.5; DB 3; Length 144;  
Best Local Similarity 28.0%; Pred. No. 1.5e+02;  
RESULT 1241  
ID AAG05467 standard; protein; 144 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1883.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (PEKE) PE CORP NY.  
Query Match 12.1%; Score 60.5; DB 3; Length 144;

Best Local Similarity 28.0%; Pred. No. 1.5e+02;  
RESULT 1242  
ID AAG48112 standard; protein; 144 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60724.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (PEKE) PE CORP NY.  
Query Match 12.1%; Score 60.5; DB 3; Length 144;  
Best Local Similarity 28.0%; Pred. No. 1.5e+02;  
RESULT 1243  
ID ABP99217 standard; protein; 159 AA.  
DE Orthosomycin biosynthetic polypeptide SEQ ID NO 21.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 12.1%; Score 60.5; DB 6; Length 159;  
Best Local Similarity 25.3%; Pred. No. 1.7e+02;  
RESULT 1244  
ID ABU15772 standard; protein; 192 AA.  
DE Protein encoded by Prokaryotic essential gene #1299.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 6; Length 192;  
Best Local Similarity 29.3%; Pred. No. 2.2e+02;  
RESULT 1245  
ID AAG07168 standard; protein; 196 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4218.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 3; Length 196;  
Best Local Similarity 28.0%; Pred. No. 2.3e+02;  
RESULT 1246  
ID AAG05466 standard; protein; 196 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1882.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 3; Length 196;  
Best Local Similarity 28.0%; Pred. No. 2.3e+02;  
RESULT 1247  
ID AAG50108 standard; protein; 196 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63462.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 3; Length 196;  
Best Local Similarity 28.0%; Pred. No. 2.3e+02;  
RESULT 1248  
ID AAG48111 standard; protein; 196 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60723.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 3; Length 196;  
Best Local Similarity 28.0%; Pred. No. 2.3e+02;  
RESULT 1249  
ID AAG50107 standard; protein; 209 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63461.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 3; Length 209;  
Best Local Similarity 28.0%; Pred. No. 2.5e+02;  
RESULT 1250  
ID AAG05465 standard; protein; 209 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1881.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 3; Length 209;  
Best Local Similarity 28.0%; Pred. No. 2.5e+02;  
RESULT 1251  
ID AAG07167 standard; protein; 209 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4217.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 3; Length 209;  
Best Local Similarity 28.0%; Pred. No. 2.5e+02;

RESULT 1252  
 ID AAG4810 standard; protein; 209 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 60722.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 3; Length 209;  
 RESULT 1253  
 ID ABU44901 standard; protein; 249 AA.  
 DE Protein encoded by Prokaryotic essential gene #30428.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 6; Length 249;  
 RESULT 1254  
 ID ABB54446 standard; protein; 297 AA.  
 DE Lactococcus lactis protein ylec.  
 PN FR2807446-A1.  
 PD 12-OCT-2001.  
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 5; Length 297;  
 RESULT 1255  
 ID ABU24698 standard; protein; 301 AA.  
 DE Protein encoded by Prokaryotic essential gene #10225.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 6; Length 301;  
 RESULT 1256  
 ID AAB76785 standard; protein; 304 AA.  
 DE Corynebacterium glutamicum MCT protein SEQ ID NO:552.  
 PN WO200100805-A2.  
 PD 04-JAN-2001.  
 PA (BADT) BASF AG.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 4; Length 304;  
 RESULT 1257  
 ID ADR08655 standard; protein; 304 AA.  
 DE Human protein useful for creating neurological disease Seq 2161.  
 PN EPI447413-A2.  
 PD 18-AUG-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 8; Length 304;  
 RESULT 1258  
 ID AAG92285 standard; protein; 309 AA.  
 DE C glutamicum protein fragment SEQ ID NO: 6039.  
 PN EPI108790-A2.  
 PD 20-JUN-2001.  
 PA (KJOW) KYOWA HAKKO KOGYO KK.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 4; Length 309;  
 RESULT 1259  
 ID ABU47526 standard; protein; 312 AA.  
 DE Protein encoded by Prokaryotic essential gene #33053.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 6; Length 312;  
 RESULT 1260  
 ID ADR43268 standard; protein; 325 AA.  
 DE IPT-like structural protein #337.  
 PN WO200407442-A2.  
 PD 02-SEP-2004.  
 PA (MONS) MONSANTO TECHNOLOGY LLC.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 8; Length 325;  
 RESULT 1261  
 ID ABU26210 standard; protein; 340 AA.

DE Protein encoded by Prokaryotic essential gene #11737.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 6; Length 340;  
 RESULT 1262  
 ID AAW72102 standard; protein; 341 AA.  
 DE HSV-2 strain SBS Contig ID 10 ORF#8 protein.  
 PN WO9820016-A1.  
 PD 14-MAY-1998.  
 PA (SMRK) SMITHKLINE BEECHAM CORP.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 2; Length 341;  
 RESULT 1263  
 ID AAG52435 standard; protein; 341 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 66652.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 3; Length 341;  
 RESULT 1264  
 ID ADO29667 standard; protein; 341 AA.  
 DE Mouse GPCR TBXA2R. SEQ ID NO:769.  
 PN WO2004060000-A2.  
 PD 13-MAY-2004.  
 PA (PRIM-) PRIMAL INC.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 8; Length 341;  
 RESULT 1265  
 ID AAW72015 standard; protein; 345 AA.  
 DE HSV-2 strain SBS Contig ID 102 ORF#1 protein.  
 PN WO9820016-A1.  
 PD 14-MAY-1998.  
 PA (SMRK) SMITHKLINE BEECHAM CORP.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 2; Length 345;  
 RESULT 1266  
 ID AAB26052 standard; protein; 352 AA.  
 DE Streptococcus polypeptide SEQ ID NO 1280.  
 PN WO200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 5; Length 352;  
 RESULT 1267  
 ID AABM65262 standard; protein; 354 AA.  
 DE Mouse protein sequence MCP7634.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 7; Length 354;  
 RESULT 1268  
 ID ADR67011 standard; protein; 354 AA.  
 DE Mouse cancer associated protein sequence SEQ ID NO:57.  
 PN WO2004074321-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 8; Length 354;  
 RESULT 1269  
 ID ADP30505 standard; protein; 357 AA.  
 DE Human secreted protein SEQ ID #1272.  
 PN WO2004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match  
 Best Local Similarity 12.1%; Score 60.5; DB 8; Length 357;  
 RESULT 1270  
 ID ABU47532 standard; protein; 367 AA.  
 DE Protein encoded by Prokaryotic essential gene #33059.

PN W0200277183-A2.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 6; Length 367;  
Best Local Similarity 24.5%; Pred. No. 5.2e+02;  
RESULT 1271  
ID ABU46966 standard; protein; 367 AA.  
DE Protein encoded by Prokaryotic essential gene #32493.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 6; Length 367;  
Best Local Similarity 24.5%; Pred. No. 5.2e+02;  
RESULT 1272  
ID AAG64284 standard; protein; 382 AA.  
DE Rice gibberellin 2-beta-hydroxylase.  
PN W0200148215-A1.  
PD 05-JUL-2001.  
PA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.  
PA (RIKE) RIKEN KK.  
Query Match 12.1%; Score 60.5; DB 4; Length 382;  
Best Local Similarity 27.2%; Pred. No. 5.5e+02;  
RESULT 1273  
ID ADK00083 standard; protein; 382 AA.  
DE Rice gibberellin 2-oxidase, OSG2ox1.  
PN US2004060080-A1.  
PD 25-MAR-2004.  
PA (NAG-) NAT INST AGROBIOLOGICAL SCI.  
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.  
Query Match 12.1%; Score 60.5; DB 8; Length 382;  
Best Local Similarity 27.2%; Pred. No. 5.5e+02;  
RESULT 1274  
ID AAM41928 standard; protein; 383 AA.  
DE Human polypeptide seq ID NO 6859.  
PN W020015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 60.5; DB 4; Length 383;  
Best Local Similarity 30.6%; Pred. No. 5.5e+02;  
RESULT 1275  
ID ABO63274 standard; protein; 391 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9791.  
PN US610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.1%; Score 60.5; DB 7; Length 391;  
Best Local Similarity 30.4%; Pred. No. 5.7e+02;  
RESULT 1276  
ID ABU36811 standard; protein; 401 AA.  
DE Protein encoded by Prokaryotic essential gene #22338.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 6; Length 401;  
Best Local Similarity 35.4%; Pred. No. 5.8e+02;  
RESULT 1277  
ID ABR42482 standard; protein; 402 AA.  
DE Coumermycin A1 biosynthetic glycosyltransferase.  
PN W02003014352-A2.  
PD 20-FEB-2003.  
PA (UYTU-) UNIV TUEBINGEN.  
Query Match 12.1%; Score 60.5; DB 6; Length 402;  
Best Local Similarity 26.8%; Pred. No. 5.9e+02;  
RESULT 1278  
ID ABU34528 standard; protein; 412 AA.  
DE Protein encoded by Prokaryotic essential gene #20055.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 6; Length 412;  
Best Local Similarity 35.4%; Pred. No. 6.1e+02;  
RESULT 1279  
ID AAM72232 standard; protein; 414 AA.

DE HSV-2 strain SBS Contig ID 15 ORF#46b protein.  
PN W09820016-A1.  
PD 14-MAY-1998.  
PA (SMIR) SMITHKLINE BEECHAM CORP.  
Query Match 12.1%; Score 60.5; DB 2; Length 414;  
Best Local Similarity 31.8%; Pred. No. 6.1e+02;  
RESULT 1280  
ID ADQ96058 standard; protein; 415 AA.  
DE T cell activation associated protein #118.  
PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 12.1%; Score 60.5; DB 8; Length 415;  
Best Local Similarity 33.6%; Pred. No. 6.1e+02;  
RESULT 1281  
ID ADQ96060 standard; protein; 415 AA.  
DE T cell activation associated protein #119.  
PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 12.1%; Score 60.5; DB 8; Length 415;  
Best Local Similarity 33.6%; Pred. No. 6.1e+02;  
RESULT 1282  
ID ABO76672 standard; protein; 420 AA.  
DE Pseudomonas aeruginosa polypeptide #8847.  
PN US651795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.1%; Score 60.5; DB 7; Length 420;  
Best Local Similarity 39.0%; Pred. No. 6.2e+02;  
RESULT 1283  
ID ABG32423 standard; protein; 448 AA.  
DE Human secreted protein #1.  
PN W0200264626-A2.  
PD 22-AUG-2002.  
PA (PEKE) PE CORP NY.  
Query Match 12.1%; Score 60.5; DB 5; Length 448;  
Best Local Similarity 31.7%; Pred. No. 6.8e+02;  
RESULT 1284  
ID ABU40066 standard; protein; 458 AA.  
DE Protein encoded by Prokaryotic essential gene #25593.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.1%; Score 60.5; DB 6; Length 458;  
Best Local Similarity 29.0%; Pred. No. 7e+02;  
RESULT 1285  
ID AAM72231 standard; protein; 462 AA.  
DE HSV-2 strain SBS Contig ID 15 ORF#46a protein.  
PN W09820016-A1.  
PD 14-MAY-1998.  
PA (SMIR) SMITHKLINE BEECHAM CORP.  
Query Match 12.1%; Score 60.5; DB 2; Length 462;  
Best Local Similarity 31.8%; Pred. No. 7e+02;  
RESULT 1286  
ID ADN21440 standard; protein; 470 AA.  
DE Bacterial polypeptide #4093.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.1%; Score 60.5; DB 8; Length 470;  
Best Local Similarity 32.0%; Pred. No. 7.2e+02;  
RESULT 1287  
ID AAM40142 standard; protein; 476 AA.  
DE Human polypeptide seq ID NO 3287.  
PN W020015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 60.5; DB 4; Length 476;

Best Local Similarity 30.6%; Pred. No. 7.3e+02;  
RESULT 1288  
ID ADQ96066 standard; protein; 499 AA.  
DE T cell activation associated protein #122.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH1 KASEI PHARMA CORP.  
Query Match 12.1%; Score 60.5; DB 8; Length 499;  
Best Local Similarity 33.6%; Pred. No. 7.8e+02;  
RESULT 1289  
ID ADQ96064 standard; protein; 499 AA.  
DE T cell activation associated protein #121.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH1 KASEI PHARMA CORP.  
Query Match 12.1%; Score 60.5; DB 8; Length 499;  
Best Local Similarity 33.6%; Pred. No. 7.8e+02;  
RESULT 1290  
ID ADU48347 standard; protein; 515 AA.  
DE Maize c11-associated gene protein #6.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDERBAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 12.1%; Score 60.5; DB 8; Length 515;  
Best Local Similarity 27.1%; Pred. No. 8.1e+02;  
RESULT 1291  
ID AAM85864 standard; protein; 535 AA.  
DE Mouse protein sequence mcp8121.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 12.1%; Score 60.5; DB 7; Length 535;  
Best Local Similarity 25.0%; Pred. No. 8.5e+02;  
RESULT 1292  
ID AAB67476 standard; protein; 538 AA.  
DE Amino acid sequence of a Mumps virus protein.  
PN WO200109309-A2.  
PD 08-FEB-2001.  
PA (AMHP) AMERICAN HOME PROD CORP.  
Query Match 12.1%; Score 60.5; DB 4; Length 538;  
Best Local Similarity 22.1%; Pred. No. 8.6e+02;  
RESULT 1293  
ID AAM70178 standard; protein; 542 AA.  
DE Photorhabdus luminescens protein sequence #3275.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 12.1%; Score 60.5; DB 6; Length 542;  
Best Local Similarity 22.4%; Pred. No. 8.7e+02;  
RESULT 1294  
ID ADR95242 standard; protein; 574 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 3877.  
PN US8600744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.1%; Score 60.5; DB 8; Length 574;  
Best Local Similarity 25.4%; Pred. No. 9.4e+02;  
RESULT 1295  
ID AAB28684 standard; protein; 577 AA.  
DE Streptococcus polypeptide SEQ ID NO 6544.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 12.1%; Score 60.5; DB 5; Length 577;  
Best Local Similarity 23.7%; Pred. No. 9.4e+02;  
RESULT 1296  
ID AAB93779 standard; protein; 595 AA.

DE Human protein sequence SEQ ID NO:13509.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 12.1%; Score 60.5; DB 4; Length 595;  
Best Local Similarity 29.6%; Pred. No. 9.8e+02;  
RESULT 1297  
ID AAG91443 standard; protein; 600 AA.  
DE C glutamicum protein fragment SEQ ID NO: 5197.  
PN EP108790-A2.  
PD 20-JUN-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Query Match 12.1%; Score 60.5; DB 4; Length 600;  
Best Local Similarity 27.8%; Pred. No. 9.9e+02;  
RESULT 1298  
ID ADH87898 standard; protein; 601 AA.  
DE Enterococcus faecalis polypeptide #2378.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 12.1%; Score 60.5; DB 7; Length 601;  
Best Local Similarity 21.2%; Pred. No. 9.9e+02;  
RESULT 1299  
ID ABO44210 standard; protein; 617 AA.  
DE Novel human diagnostic protein #4201.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 60.5; DB 4; Length 617;  
Best Local Similarity 30.6%; Pred. No. 1e+03;  
RESULT 1300  
ID AAY01402 standard; protein; 621 AA.  
DE Secreted protein encoded by gene 20 clone HGCA662.  
PN WO99030990-A1.  
PD 28-JAN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.1%; Score 60.5; DB 2; Length 621;  
Best Local Similarity 33.6%; Pred. No. 1e+03;  
RESULT 1301  
ID ABO23308 standard; protein; 621 AA.  
DE Human secreted protein #20.  
PN US200305045-A1.  
PD 13-MAR-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (YOIN/) YOUNG P E.  
PA (GREB/) GREENE J M.  
PA (NIJU/) NI J.  
PA (FENG/) FENG P.  
PA (FLOR/) FLORENCE K A.  
PA (HUJU/) HU J.  
PA (FERR/) FERRITE A M.  
PA (YUGG/) YU G.  
PA (DUAN/) DUAN R D.  
PA (JANA/) JANAT F.  
Query Match 12.1%; Score 60.5; DB 7; Length 621;  
Best Local Similarity 33.6%; Pred. No. 1e+03;  
RESULT 1302  
ID ADQ96062 standard; protein; 621 AA.  
DE T cell activation associated protein #120.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH1 KASEI PHARMA CORP.  
Query Match 12.1%; Score 60.5; DB 8; Length 621;  
Best Local Similarity 33.6%; Pred. No. 1e+03;  
RESULT 1303  
ID AAB60616 standard; protein; 774 AA.  
DE Cephalosporin C acylase.  
PN JP61152286-A.  
PD 10-JUL-1986.  
PA (ASAH) ASAH1 CHEM IND CO LTD.  
Query Match 12.1%; Score 60.5; DB 1; Length 774;

Best Local Similarity 32.1%; Pred. No. 1.4e+03;  
RESULT 1304  
ID ADP30506 standard; protein; 774 AA.  
DE Human secreted protein SEQ ID #1273.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.1%; Score 60.5; DB 8; Length 774;  
Best Local Similarity 36.4%; Pred. No. 1.4e+03;  
RESULT 1305  
ID ABB54868 standard; protein; 867 AA.  
DE Lactococcus lactis protein clpB.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 12.1%; Score 60.5; DB 5; Length 867;  
Best Local Similarity 23.9%; Pred. No. 1.6e+03;  
RESULT 1306  
ID ADS29415 standard; protein; 867 AA.  
DE Bacterial polypeptide #18448.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SIAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.1%; Score 60.5; DB 8; Length 867;  
Best Local Similarity 23.9%; Pred. No. 1.6e+03;  
RESULT 1307  
ID ABB62035 standard; protein; 950 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12897.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 12.1%; Score 60.5; DB 4; Length 950;  
Best Local Similarity 32.9%; Pred. No. 1.8e+03;  
RESULT 1308  
ID ABB07645 standard; protein; 1114 AA.  
DE Novel human diagnostic protein #7636.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 60.5; DB 4; Length 1114;  
Best Local Similarity 26.1%; Pred. No. 2.2e+03;  
RESULT 1309  
ID ABO83693 standard; protein; 1118 AA.  
DE Pseudomonas aeruginosa polypeptide #15868.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENC-) GENOME THERAPEUTICS CORP.  
Query Match 12.1%; Score 60.5; DB 7; Length 1118;  
Best Local Similarity 37.3%; Pred. No. 2.3e+03;  
RESULT 1310  
ID ADJ70257 standard; protein; 1191 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID2063.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 12.1%; Score 60.5; DB 7; Length 1191;  
Best Local Similarity 30.6%; Pred. No. 2.4e+03;  
RESULT 1311  
ID ADDE7541 standard; protein; 1606 AA.  
DE Human ly1484p protein SEQ ID NO:18.  
PN WO2003062401-A2.  
PD 31-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 12.1%; Score 60.5; DB 7; Length 1606;  
Best Local Similarity 25.4%; Pred. No. 3.6e+03;  
RESULT 1312  
ID ADL05773 standard; protein; 2142 AA.  
DE M. catarrhalis protein #1539.

PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENC-) GENOME THERAPEUTICS CORP.  
Query Match 12.1%; Score 60.5; DB 8; Length 2142;  
Best Local Similarity 27.2%; Pred. No. 5.3e+03;  
RESULT 1313  
ID AAU30691 standard; protein; 107 AA.  
DE Novel human secreted protein #1182.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.0%; Score 60; DB 4; Length 107;  
Best Local Similarity 28.2%; Pred. No. 1.2e+02;  
RESULT 1314  
ID AAW72908 standard; protein; 130 AA.  
DE Mycobacterium tuberculosis antigen CPPI6.  
PN WO9844119-A1.  
PD 08-OCT-1998.  
PA (STAT-) STATENS SERUM INST.  
Query Match 12.0%; Score 60; DB 2; Length 130;  
Best Local Similarity 27.7%; Pred. No. 1.5e+02;  
RESULT 1315  
ID AAY21925 standard; protein; 130 AA.  
DE Amino acid sequence of antigen CPPI6.  
PN WO924577-A1.  
PD 20-MAY-1999.  
PA (STAT-) STATENS SERUM INST.  
Query Match 12.0%; Score 60; DB 2; Length 130;  
Best Local Similarity 27.7%; Pred. No. 1.5e+02;  
RESULT 1316  
ID AAM50746 standard; protein; 130 AA.  
DE Mycobacterium tuberculosis immunodominant Mtb protein RplL.  
PN WO200204018-A2.  
PD 17-JAN-2002.  
PA (COLS-) UNIV COLORADO STATE RES FOUND.  
Query Match 12.0%; Score 60; DB 5; Length 130;  
Best Local Similarity 27.7%; Pred. No. 1.5e+02;  
RESULT 1317  
ID ABU34454 standard; protein; 130 AA.  
DE Protein encoded by Prokaryotic essential gene #19981.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 130;  
Best Local Similarity 27.7%; Pred. No. 1.5e+02;  
RESULT 1318  
ID ABU36489 standard; protein; 130 AA.  
DE Protein encoded by Prokaryotic essential gene #22016.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 130;  
Best Local Similarity 27.7%; Pred. No. 1.5e+02;  
RESULT 1319  
ID ADE63753 standard; protein; 157 AA.  
DE Rat Protein CAA42203, SEQ ID NO 9697.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO-) GEN HOSPITAL CORP.  
PA (PARB-) BAYER AG.  
Query Match 12.0%; Score 60; DB 7; Length 157;  
Best Local Similarity 36.2%; Pred. No. 1.9e+02;  
RESULT 1320  
ID ADCE8215 standard; protein; 179 AA.  
DE Ribosomal protein similar to FCWP1 #431.  
PN US6573361-B1.  
PD 03-JUN-2003.  
PA (MONS-) MONSANTO TECHNOLOGY LLC.  
Query Match 12.0%; Score 60; DB 7; Length 179;  
Best Local Similarity 33.3%; Pred. No. 2.3e+02;  
RESULT 1321  
ID ABO00479 standard; protein; 196 AA.  
DE Novel human polypeptide #66.

PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 196;  
RESULT 1322  
ID ABU020750 standard; protein; 206 AA.  
DE Protein encoded by Prokaryotic essential gene #6277.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 206;  
RESULT 1323  
ID AB083684 standard; protein; 208 AA.  
DE Pseudomonas aeruginosa polypeptide #15859.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 208;  
RESULT 1324  
ID ADS23376 standard; protein; 209 AA.  
DE Bacterial polypeptide #12409.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 8; Length 209;  
RESULT 1325  
ID ABP29761 standard; protein; 230 AA.  
DE Streptococcus polypeptide SEQ ID NO 8698.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 5; Length 230;  
RESULT 1326  
ID ABG96327 standard; protein; 232 AA.  
DE Human ovarian cancer marker M444.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 5; Length 232;  
RESULT 1327  
ID ABP26904 standard; protein; 238 AA.  
DE Streptococcus polypeptide SEQ ID NO 2984.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 5; Length 238;  
RESULT 1328  
ID ABU22030 standard; protein; 240 AA.  
DE Protein encoded by Prokaryotic essential gene #7557.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 240;  
RESULT 1329  
ID AB09051 standard; protein; 263 AA.  
DE Thermus caldophilus GK24 cosmid clone 3 related protein SEQ ID NO:3.  
PN KR2001019888-A.  
PD 15-MAR-2001.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 263;  
RESULT 1330  
ID AB067879 standard; protein; 264 AA.  
DE Pseudomonas aeruginosa polypeptide #54.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 264;  
RESULT 1331  
ID ADN26129 standard; protein; 270 AA.  
DE Bacterial polypeptide #8782.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 8; Length 270;  
RESULT 1332  
ID AAU91157 standard; protein; 273 AA.  
DE Treponema pallidum penicillinase Kinase Coax.  
PN WO200216601-A2.  
PD 28-FEB-2002.  
PA (OMNI-) OMNIGENE BIOPRODUCTS INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 5; Length 273;  
RESULT 1333  
ID AB836116 standard; peptide; 307 AA.  
DE Peptide #3622 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;  
RESULT 1334  
ID AAM29607 standard; protein; 307 AA.  
DE Peptide #3644 encoded by probe for measuring placental gene expression.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;  
RESULT 1335  
ID AB830928 standard; peptide; 307 AA.  
DE Peptide #3579 encoded by breast cell single exon nucleic acid probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;  
RESULT 1336  
ID AB821504 standard; protein; 307 AA.  
DE Protein #3503 encoded by probe for measuring heart cell gene expression.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;  
RESULT 1337  
ID AAM69287 standard; protein; 307 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29593.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 307;  
RESULT 1338  
ID AAM56899 standard; protein; 307 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29004.

PN WO200157275-A2.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 12.0%; Score 60; DB 4; Length 307;  
Best Local Similarity 43.6%; Pred. No. 4.7e+02;  
RESULT 1339  
ID ABG38901 standard; peptide; 307 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28566.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 12.0%; Score 60; DB 5; Length 307;  
Best Local Similarity 43.6%; Pred. No. 4.7e+02;  
RESULT 1340  
ID AAM39798 standard; protein; 308 AA.  
DE Human polypeptide SEQ ID NO 2943.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.0%; Score 60; DB 4; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1341  
ID AAE25381 standard; protein; 308 AA.  
DE Human NZMS-5 protein.  
PN WO200246385-A2.  
PD 13-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 12.0%; Score 60; DB 5; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1342  
ID AAE21813 standard; protein; 308 AA.  
DE Human 46873 asparaginase.  
PN US2002038014-A1.  
PD 28-MAR-2002.  
PA (MEYE/) MEYERS R A.  
Query Match 12.0%; Score 60; DB 5; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1343  
ID AAE37617 standard; protein; 308 AA.  
DE Human 25943 (glycosylasparaginase) protein.  
PN WO2003038113-A2.  
PD 08-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1344  
ID AAE29747 standard; protein; 308 AA.  
DE Novel human asparaginase (NHA) protein.  
PN WO200277219-A1.  
PD 03-OCT-2002.  
PA (LEXT-) LEXICON GENETICS INC.  
Query Match 12.0%; Score 60; DB 6; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1345  
ID ADB64580 standard; protein; 308 AA.  
DE Human protein encoded by clone KIDNE20083620.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELT-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.0%; Score 60; DB 7; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1346  
ID ADB64015 standard; protein; 308 AA.  
DE Human protein encoded by clone BRAMY20125360.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELT-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.0%; Score 60; DB 7; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1347  
ID ADC26179 standard; protein; 308 AA.

DE Human NOV2a protein.  
PN WO2003004687-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 7; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1348  
ID ADC26185 standard; protein; 308 AA.  
DE Human NOV2d protein.  
PN WO2003004687-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 7; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1349  
ID ADC26183 standard; protein; 308 AA.  
DE Human NOV2c protein.  
PN WO2003004687-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 7; Length 308;  
Best Local Similarity 28.0%; Pred. No. 4.7e+02;  
RESULT 1350  
ID ADC26189 standard; protein; 312 AA.  
DE Human NOV2f protein.  
PN WO2003004687-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 7; Length 312;  
Best Local Similarity 28.0%; Pred. No. 4.8e+02;  
RESULT 1351  
ID ADC26191 standard; protein; 312 AA.  
DE Human NOV2g protein.  
PN WO2003004687-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 7; Length 312;  
Best Local Similarity 28.0%; Pred. No. 4.8e+02;  
RESULT 1352  
ID ADO30431 standard; protein; 313 AA.  
DE Mouse GPCR OR212, SEQ ID NO:1534.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 12.0%; Score 60; DB 8; Length 313;  
Best Local Similarity 34.3%; Pred. No. 4.8e+02;  
RESULT 1353  
ID ADC26187 standard; protein; 314 AA.  
DE Human NOV2e protein.  
PN WO2003004687-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 7; Length 314;  
Best Local Similarity 28.0%; Pred. No. 4.8e+02;  
RESULT 1354  
ID AUI38294 standard; protein; 321 AA.  
DE Salmonella typhi cellular proliferation protein #185.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 4; Length 321;  
Best Local Similarity 26.1%; Pred. No. 5e+02;  
RESULT 1355  
ID AAG39429 standard; protein; 321 AA.  
DE Escherichia coli protein sequence SEQ ID NO:477.  
PN WO200148209-A2.  
PD 05-JUL-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 4; Length 321;  
Best Local Similarity 27.0%; Pred. No. 5e+02;  
RESULT 1356  
ID ABP41427 standard; protein; 321 AA.  
DE Human ovarian antigen HRP5H76, SEQ ID NO:2559.

PN W0200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 5; Length 321;  
RESULT 1357  
ID ABO44809 standard; protein; 321 AA.  
DE Protein encoded by Prokaryotic essential gene #30336.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 321;  
RESULT 1358  
ID ABO48212 standard; protein; 321 AA.  
DE Protein encoded by Prokaryotic essential gene #33739.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 321;  
RESULT 1359  
ID ABO44841 standard; protein; 321 AA.  
DE Protein encoded by Prokaryotic essential gene #368.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 321;  
RESULT 1360  
ID ABO47031 standard; protein; 321 AA.  
DE Protein encoded by Prokaryotic essential gene #32558.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 321;  
RESULT 1361  
ID ABO72294 standard; protein; 331 AA.  
DE Pseudomonas aeruginosa polypeptide #4469.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 331;  
RESULT 1362  
ID ABB52481 standard; protein; 336 AA.  
DE Escherichia coli polypeptide SEQ ID NO 305.  
PN W0200166572-A2.  
PD 13-SEP-2001.  
PA (INRM) INSERM NAT SANTE & RECH MEDICALE.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 336;  
RESULT 1363  
ID ABO63632 standard; protein; 337 AA.  
DE Klebsiella pneumoniae polypeptide seqid 10149.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 337;  
RESULT 1364  
ID ABG28657 standard; protein; 342 AA.  
DE Novel human diagnostic protein #28648.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 342;  
RESULT 1365  
ID AAY38901 standard; protein; 343 AA.  
DE Neisseria gonorrhoeae antigen encoded by partial ORF125.  
PN W09924578-A2.

PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 2; Length 343;  
RESULT 1366  
ID AAM41584 standard; protein; 346 AA.  
DE Human polypeptide SEQ ID NO 6515.  
PN W020015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 346;  
RESULT 1367  
ID AAM98317 standard; protein; 350 AA.  
DE H. pylori GHP0 1024 protein.  
PN W09843478-A1.  
PD 08-OCT-1998.  
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 2; Length 350;  
RESULT 1368  
ID ABG24784 standard; protein; 369 AA.  
DE Novel human diagnostic protein #24775.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 369;  
RESULT 1369  
ID ABR52878 standard; protein; 371 AA.  
DE Protein sequence #SEQ ID 621.  
PN EPI258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 371;  
RESULT 1370  
ID ADK62082 standard; protein; 371 AA.  
DE Disease treating protein complex-derived protein #167.  
PN EPI38608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 371;  
RESULT 1371  
ID ADS43667 standard; protein; 371 AA.  
DE Bacterial polypeptide #22097.  
PN US200323675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 8; Length 371;  
RESULT 1372  
ID ABO49108 standard; protein; 372 AA.  
DE Protein encoded by Prokaryotic essential gene #34635.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 372;  
RESULT 1373  
ID ADA33213 standard; protein; 381 AA.  
DE Acinetobacter baumannii protein #374.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 381;  
RESULT 1374  
ID AAY38901 standard; protein; 343 AA.  
DE Neisseria gonorrhoeae antigen encoded by partial ORF125.  
PN W09924578-A2.



RESULT 1374  
ID ABP77627 standard; protein; 392 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 1784.  
PN W0200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 12.0%; Score 60; DB 6; Length 392;  
Best Local Similarity 29.6%; Pred. No. 6.5e+02;  
RESULT 1375  
ID AAM51351 standard; protein; 402 AA.  
DE P. velutina lectin protein sequence.  
PN W09816825-A1.  
PD 23-APR-1998.  
PA (SEGG) SEIRGAKU CORP.  
Query Match 12.0%; Score 60; DB 2; Length 402;  
Best Local Similarity 28.2%; Pred. No. 6.7e+02;  
RESULT 1376  
ID ADP31390 standard; protein; 402 AA.  
DE Human secreted protein SEQ ID #2157.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.0%; Score 60; DB 8; Length 402;  
Best Local Similarity 36.0%; Pred. No. 6.7e+02;  
RESULT 1377  
ID AAY38902 standard; protein; 408 AA.  
DE Neisseria gonorrhoeae antigen encoded by ORF125.  
PN W0924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.  
Query Match 12.0%; Score 60; DB 2; Length 408;  
Best Local Similarity 32.6%; Pred. No. 6.8e+02;  
RESULT 1378  
ID ADC26181 standard; protein; 426 AA.  
DE Human NOV2b protein.  
PN W02003004687-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 7; Length 426;  
Best Local Similarity 28.0%; Pred. No. 7.2e+02;  
RESULT 1379  
ID ABO72701 standard; protein; 435 AA.  
DE Pseudomonas aeruginosa polypeptide #4876.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.0%; Score 60; DB 7; Length 435;  
Best Local Similarity 31.1%; Pred. No. 7.4e+02;  
RESULT 1380  
ID ABB06896 standard; protein; 438 AA.  
DE Micromonospora carbonacea evernimicin locus protein ORF 16.  
PN W0200155180-A2.  
PD 02-AUG-2001.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
PA (FARNET/) FARNET C.  
Query Match 12.0%; Score 60; DB 4; Length 438;  
Best Local Similarity 25.6%; Pred. No. 7.5e+02;  
RESULT 1381  
ID ABP99230 standard; protein; 438 AA.  
DE Orthosomycin biosynthetic polypeptide SEQ ID NO 47.  
PN W0200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 12.0%; Score 60; DB 6; Length 438;  
Best Local Similarity 25.6%; Pred. No. 7.5e+02;  
RESULT 1382  
ID ABU39628 standard; protein; 450 AA.  
DE Protein encoded by Prokaryotic essential gene #25155.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 450;  
Best Local Similarity 30.7%; Pred. No. 7.7e+02;

RESULT 1383  
ID ABU22956 standard; protein; 453 AA.  
DE Protein encoded by Prokaryotic essential gene #8483.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 453;  
Best Local Similarity 26.8%; Pred. No. 7.8e+02;  
RESULT 1384  
ID AAY75758 standard; protein; 466 AA.  
DE Neisseria meningitidis ORF 989 protein sequence SEQ ID NO:2988.  
PN W09597280-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 12.0%; Score 60; DB 3; Length 466;  
Best Local Similarity 26.2%; Pred. No. 8.1e+02;  
RESULT 1385  
ID ABO72512 standard; protein; 467 AA.  
DE Pseudomonas aeruginosa polypeptide #4687.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.0%; Score 60; DB 7; Length 467;  
Best Local Similarity 28.6%; Pred. No. 8.1e+02;  
RESULT 1386  
ID ADS23989 standard; protein; 479 AA.  
DE Bacterial polypeptide #13022.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.0%; Score 60; DB 8; Length 479;  
Best Local Similarity 26.7%; Pred. No. 8.4e+02;  
RESULT 1387  
ID ABU15177 standard; protein; 485 AA.  
DE Protein encoded by Prokaryotic essential gene #704.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 485;  
Best Local Similarity 29.0%; Pred. No. 8.5e+02;  
RESULT 1388  
ID ADS22830 standard; protein; 485 AA.  
DE Bacterial polypeptide #11863.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.0%; Score 60; DB 8; Length 485;  
Best Local Similarity 26.0%; Pred. No. 8.5e+02;  
RESULT 1389  
ID ABU35862 standard; protein; 490 AA.  
DE Protein encoded by Prokaryotic essential gene #21389.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 490;  
Best Local Similarity 23.6%; Pred. No. 8.7e+02;  
RESULT 1390  
ID ABU21209 standard; protein; 496 AA.  
DE Protein encoded by Prokaryotic essential gene #6736.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 496;  
Best Local Similarity 31.6%; Pred. No. 8.8e+02;

RESULT 1391  
ID ADP30474 standard; protein; 498 AA.  
DE Human secreted protein SEQ ID #1241.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.0%; Score 60; DB 8; Length 498;  
Best Local Similarity 36.0%; Pred. No. 8.8e+02;  
RESULT 1392  
ID ABG28672 standard; protein; 506 AA.  
DE Novel human diagnostic protein #28663.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.0%; Score 60; DB 4; Length 506;  
Best Local Similarity 27.8%; Pred. No. 9e+02;  
RESULT 1393  
ID ABU19802 standard; protein; 507 AA.  
DE Protein encoded by Prokaryotic essential gene #5329.  
PN WO200271183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 507;  
Best Local Similarity 25.5%; Pred. No. 9.1e+02;  
RESULT 1394  
ID ABG94648 standard; protein; 511 AA.  
DE Human NOV10b protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 5; Length 511;  
Best Local Similarity 26.2%; Pred. No. 9.1e+02;  
RESULT 1395  
ID ABB61121 standard; protein; 516 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 10155.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 12.0%; Score 60; DB 4; Length 516;  
Best Local Similarity 25.2%; Pred. No. 9.3e+02;  
RESULT 1396  
ID ABU15345 standard; protein; 530 AA.  
DE Protein encoded by Prokaryotic essential gene #872.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 530;  
Best Local Similarity 26.9%; Pred. No. 9.6e+02;  
RESULT 1397  
ID ABO71163 standard; protein; 549 AA.  
DE Pseudomonas aeruginosa polypeptide #3338.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 12.0%; Score 60; DB 7; Length 549;  
Best Local Similarity 23.0%; Pred. No. 1e+03;  
RESULT 1398  
ID ABB76947 standard; protein; 554 AA.  
DE Acidocella sp. phytease.  
PN WO200238774-A2.  
PD 16-MAY-2002.  
PA (AVER-) AVENTIS ANIMAL NUTRITION SA.  
Query Match 12.0%; Score 60; DB 5; Length 554;  
Best Local Similarity 30.0%; Pred. No. 1e+03;  
RESULT 1399  
ID ADN25815 standard; protein; 554 AA.  
DE Bacterial polypeptide #8468.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.

PA (GOLD-) GOLDMAN B S.  
Query Match 12.0%; Score 60; DB 8; Length 554;  
Best Local Similarity 27.8%; Pred. No. 1e+03;  
RESULT 1400  
ID AAB38766 standard; protein; 587 AA.  
DE Rat 69624 protein sodium sulphate symporter domain.  
PN US002193582-A1.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 12.0%; Score 60; DB 7; Length 587;  
Best Local Similarity 36.2%; Pred. No. 1.1e+03;  
RESULT 1401  
ID ADP55467 standard; protein; 592 AA.  
DE Human novel polypeptide #31.  
PN JP2003245081-A.  
PD 02-SEP-2003.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
Query Match 12.0%; Score 60; DB 7; Length 592;  
Best Local Similarity 26.8%; Pred. No. 1.1e+03;  
RESULT 1402  
ID AAR05589 standard; protein; 638 AA.  
DE Acetylhydroxy acid synthetase (AHAS) from maize C3 genome.  
PN EP360750-A.  
PD 28-MAR-1990.  
PA (CIBA-) CIBA GEIGY AG.  
Query Match 12.0%; Score 60; DB 2; Length 638;  
Best Local Similarity 23.0%; Pred. No. 1.2e+03;  
RESULT 1403  
ID AAB42426 standard; protein; 652 AA.  
DE Human ORFX ORF2190 polypeptide sequence SEQ ID NO:4380.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 3; Length 652;  
Best Local Similarity 26.6%; Pred. No. 1.3e+03;  
RESULT 1404  
ID ADS26132 standard; protein; 652 AA.  
DE Bacterial polypeptide #15165.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match 12.0%; Score 60; DB 8; Length 652;  
Best Local Similarity 23.6%; Pred. No. 1.3e+03;  
RESULT 1405  
ID ADS25855 standard; protein; 652 AA.  
DE Bacterial polypeptide #14688.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match 12.0%; Score 60; DB 8; Length 652;  
Best Local Similarity 23.6%; Pred. No. 1.3e+03;  
RESULT 1406  
ID ADS25373 standard; protein; 655 AA.  
DE Bacterial polypeptide #14406.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match 12.0%; Score 60; DB 8; Length 655;  
Best Local Similarity 23.6%; Pred. No. 1.3e+03;  
RESULT 1407  
ID ADS22602 standard; protein; 656 AA.

DE Bacterial polypeptide #11635.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.0%; Score 60; DB 8; Length 656;  
Best Local Similarity 23.6%; Pred. No. 1.3e+03;  
RESULT 1408  
ID ABB62255 standard; protein; 680 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 13557.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.0%; Score 60; DB 4; Length 680;  
Best Local Similarity 32.8%; Pred. No. 1.3e+03;  
RESULT 1409  
ID ABU23341 standard; protein; 706 AA.  
DE Protein encoded by Prokaryotic essential gene #7868.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 12.0%; Score 60; DB 6; Length 706;  
Best Local Similarity 28.4%; Pred. No. 1.4e+03;  
RESULT 1410  
ID AAO14204 standard; protein; 707 AA.  
DE Human transporter and ion channel TRICH-21.  
PN WO200204520-A2.  
PD 17-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 12.0%; Score 60; DB 5; Length 707;  
Best Local Similarity 29.5%; Pred. No. 1.4e+03;  
RESULT 1411  
ID ADD25157 standard; protein; 707 AA.  
DE Fertility restorer protein #16.  
PN WO2003006622-A2.  
PD 23-JAN-2003.  
PA (UYMC-) UNIV MCGILL.  
PA (DNAL-) DNA LANDMARKS INC.  
Query Match 12.0%; Score 60; DB 7; Length 707;  
Best Local Similarity 26.3%; Pred. No. 1.4e+03;  
RESULT 1412  
ID ADN61172 standard; protein; 707 AA.  
DE Radish nuclear fertility restorer Rfo protein SEQ ID NO:31.  
PN WO2004006655-A2.  
PD 22-JAN-2004.  
PA (UYMC-) UNIV MCGILL.  
PA (DNAL-) DNA LANDMARKS INC.  
PA (BADI ) BASF PLANT SCI GMBH.  
Query Match 12.0%; Score 60; DB 8; Length 707;  
Best Local Similarity 26.3%; Pred. No. 1.4e+03;  
RESULT 1413  
ID AD116618 standard; protein; 708 AA.  
DE Human NOVX protein to treat human pathological conditions SeqId154.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 5; Length 708;  
Best Local Similarity 29.5%; Pred. No. 1.4e+03;  
RESULT 1414  
ID ADN42272 standard; protein; 708 AA.  
DE Human novel proteinNOV 41a.  
PN US2004033493-A1.  
PD 19-FEB-2004.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (ZERR/) ZERHUSEN B D.  
PA (PATI/) PATTURAJAN M.  
PA (SHIM/) SHIMKETS R A.  
PA (LIL/) LI L.  
PA (GANG/) GANGOLLI E A.

PA (PADI/) PADIGARU M.  
PA (ANDE/) ANDERSON D W.  
PA (RAST/) RASTELI L.  
PA (MILL/) MILLER C E.  
PA (GERL/) GERLACH V.  
PA (TAUP/) TAUPIER R J.  
PA (GUSE/) GUSEV V Y.  
PA (COLM/) COLMAN S D.  
PA (WOLE/) WOLENC A R.  
PA (PEN/) PENNA C E A.  
PA (FURT/) FURTA K.  
Query Match 12.0%; Score 60; DB 8; Length 708;  
Best Local Similarity 29.5%; Pred. No. 1.4e+03;  
RESULT 1415  
ID AUB5408 standard; protein; 717 AA.  
DE Human protein NOV6.  
PN WO200210216-A2.  
PD 07-FEB-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 5; Length 717;  
Best Local Similarity 29.5%; Pred. No. 1.4e+03;  
RESULT 1416  
ID AAY43379 standard; protein; 722 AA.  
DE M. catarrhalis strain 3 tbp2 protein.  
PN WO952947-A2.  
PD 21-OCT-1999.  
PA (CONN-) CONNAUGHT LAB LTD.  
Query Match 12.0%; Score 60; DB 2; Length 722;  
Best Local Similarity 34.8%; Pred. No. 1.4e+03;  
RESULT 1417  
ID ABB67181 standard; protein; 747 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28335.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.0%; Score 60; DB 4; Length 747;  
Best Local Similarity 30.1%; Pred. No. 1.5e+03;  
RESULT 1418  
ID AD116620 standard; protein; 761 AA.  
DE Human NOVX protein to treat human pathological conditions SeqId156.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.0%; Score 60; DB 5; Length 761;  
Best Local Similarity 29.5%; Pred. No. 1.5e+03;  
RESULT 1419  
ID ADN42274 standard; protein; 761 AA.  
DE Human novel proteinNOV 41b.  
PN US2004033493-A1.  
PD 19-FEB-2004.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (ZERR/) ZERHUSEN B D.  
PA (PATI/) PATTURAJAN M.  
PA (SHIM/) SHIMKETS R A.  
PA (LIL/) LI L.  
PA (GANG/) GANGOLLI E A.  
PA (PADI/) PADIGARU M.  
PA (ANDE/) ANDERSON D W.  
PA (RAST/) RASTELI L.  
PA (MILL/) MILLER C E.  
PA (GERL/) GERLACH V.  
PA (TAUP/) TAUPIER R J.  
PA (GUSE/) GUSEV V Y.  
PA (COLM/) COLMAN S D.  
PA (WOLE/) WOLENC A R.  
PA (PEN/) PENNA C E A.  
PA (FURT/) FURTA K.

PA (GROS/) GROSSE W. M.  
PA (ALSO/) ALSOBROOK J. P.  
PA (LEPL/) LEPEL D. M.  
PA (RIEG/) RIEGER D. K.  
PA (BURG/) BURGESS C. E.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 8; Length 761;  
RESULT 1420  
ID ADC31519 standard; protein; 771 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1601.  
PN W02003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 771;  
RESULT 1421  
ID ADC31078 standard; protein; 776 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1160.  
PN W02003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 776;  
RESULT 1422  
ID AD065222 standard; protein; 776 AA.  
DE Novel human protein sequence #195.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 8; Length 776;  
RESULT 1423  
ID AB02213 standard; protein; 798 AA.  
DE S. pneumoniae type 4 strain protein from coding region #1791.  
PN W0200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 798;  
RESULT 1424  
ID AD081821 standard; protein; 798 AA.  
DE Human Na+/H+ exchange transporter.  
PN W02003062274-A1.  
PD 31-JUL-2003.  
PA (TAKE-) TAKEIDA CHEM IND LTD.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 798;  
RESULT 1425  
ID ADK46589 standard; protein; 798 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 3104.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 8; Length 798;  
RESULT 1426  
ID AAY55803 standard; protein; 804 AA.  
DE S. pneumoniae prfA polypeptide.  
PN W09961453-A2.  
PD 02-DEC-1999.  
PA (SMIK-) SMITHKLINE BEECHAM CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 3; Length 804;  
RESULT 1427  
ID ADK95849 standard; protein; 804 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 4484.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 8; Length 804;  
RESULT 1428

ID ABR52748 standard; protein; 825 AA.  
DE Protein sequence #SEQ ID 361.  
PN EPI258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 825;  
RESULT 1429  
ID ADK62052 standard; protein; 825 AA.  
DE Disease treating protein complex-derived protein #152.  
PN EPI338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 7; Length 825;  
RESULT 1430  
ID ABP73245 standard; protein; 907 AA.  
DE Candida albicans essential protein SEQ ID NO 7082.  
PN W0200253728-A2.  
PD 11-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 5; Length 907;  
RESULT 1431  
ID ABB58283 standard; protein; 935 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 1641.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 935;  
RESULT 1432  
ID ADI46109 standard; protein; 1031 AA.  
DE Single stranded nucleic acid cleavage method related protein #4.  
PN W0200179481-A2.  
PD 25-OCT-2001.  
PA (DYAX-) DYAX CORP.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 5; Length 1031;  
RESULT 1433  
ID AB039615 standard; protein; 1035 AA.  
DE Protein encoded by Prokaryotic essential gene #25142.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 6; Length 1035;  
RESULT 1434  
ID ABB57993 standard; protein; 1054 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 771.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 4; Length 1054;  
RESULT 1435  
ID ADP31430 standard; protein; 1110 AA.  
DE Human secreted protein SEQ ID #2197.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 12.0%; Score 60; DB 8; Length 1110;  
RESULT 1436  
ID ADN25166 standard; protein; 1174 AA.  
DE Bacterial polypeptide #7819.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G. J.  
PA (SLAT/) SLATER S. C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B. S.

Query Match 12.0%; Score 60; DB 8; Length 1174;  
Best Local Similarity 30.5%; Pred. No. 2.7e+03;  
RESULT 1437  
ID ABB66003 standard; protein; 1184 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24801.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.0%; Score 60; DB 4; Length 1184;  
Best Local Similarity 36.2%; Pred. No. 2.8e+03;  
RESULT 1438  
ID ABG24742 standard; protein; 1205 AA.  
DE Novel human diagnostic protein #24733.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.0%; Score 60; DB 4; Length 1205;  
Best Local Similarity 26.9%; Pred. No. 2.8e+03;  
RESULT 1439  
ID ABG10747 standard; protein; 1205 AA.  
DE Novel human diagnostic protein #10738.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.0%; Score 60; DB 4; Length 1205;  
Best Local Similarity 26.9%; Pred. No. 2.8e+03;  
RESULT 1440  
ID ADD71149 standard; protein; 1577 AA.  
DE Human intracellular signalling molecule INTSIG-38 protein SEQ ID NO:38.  
PN WO2003039348-A2.  
PD 15-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 12.0%; Score 60; DB 7; Length 1577;  
Best Local Similarity 27.4%; Pred. No. 4e+03;  
RESULT 1441  
ID ADQ91704 standard; protein; 1657 AA.  
DE Polyketide synthase ORF13 protein, SEQ ID 27.  
PN WO2004065401-A1.  
PD 05-ANG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 12.0%; Score 60; DB 8; Length 1657;  
Best Local Similarity 26.3%; Pred. No. 4.3e+03;  
RESULT 1442  
ID ABG08232 standard; protein; 1700 AA.  
DE Novel human diagnostic protein #8223.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.0%; Score 60; DB 4; Length 1700;  
Best Local Similarity 30.5%; Pred. No. 4.4e+03;  
RESULT 1443  
ID ADJ70367 standard; protein; 1857 AA.  
DE Human heat mitochondrial protein as a therapeutic target SegID2173.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
Query Match 12.0%; Score 60; DB 7; Length 1857;  
Best Local Similarity 27.4%; Pred. No. 5e+03;  
RESULT 1444  
ID AD019538 standard; protein; 1857 AA.  
DE Human pro polypeptide #234.  
PN WO2004043361-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.0%; Score 60; DB 8; Length 1857;  
Best Local Similarity 27.4%; Pred. No. 5e+03;  
RESULT 1445  
ID ADP30882 standard; protein; 2187 AA.  
DE Human secreted protein SEQ ID #1649.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match 12.0%; Score 60; DB 8; Length 2187;  
Best Local Similarity 39.5%; Pred. No. 6.2e+03;  
RESULT 1446  
ID AAB23832 standard; protein; 2625 AA.  
DE Shewanella sp. SCRC-21406 (FERM BP-5979) ORFα protein SEQ ID NO:3.  
PN JP2000217582-A.  
PD 08-AUG-2000.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (BIOT-) BIOINDUSTRY KYOKAI SH.  
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
Query Match 12.0%; Score 60; DB 3; Length 2625;  
Best Local Similarity 26.7%; Pred. No. 7.9e+03;  
RESULT 1447  
ID AAB18637 standard; protein; 4551 AA.  
DE Amino acid sequence of narbonolide synthase subunit 1 (PICAI).  
PN US6117659-A.  
PD 12-SEP-2000.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 12.0%; Score 60; DB 3; Length 4551;  
Best Local Similarity 29.9%; Pred. No. 1.6e+04;  
RESULT 1448  
ID AAY67201 standard; protein; 4551 AA.  
DE Narbonolide synthase subunit 1 (PICAI) protein sequence.  
PN WO9961599-A2.  
PD 02-DEC-1999.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 12.0%; Score 60; DB 3; Length 4551;  
Best Local Similarity 29.9%; Pred. No. 1.6e+04;  
RESULT 1449  
ID ABG71661 standard; protein; 4551 AA.  
DE S. venezuelae narbonolide synthase subunit 1, PICAI.  
PN WO200297062-A2.  
PD 05-DEC-2002.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 12.0%; Score 60; DB 6; Length 4551;  
Best Local Similarity 29.9%; Pred. No. 1.6e+04;  
RESULT 1450  
ID ADN09400 standard; protein; 4551 AA.  
DE S. venezuelae narbonolide synthase subunit 1 (PICAI).  
PN US6509455-B1.  
PD 21-JAN-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 12.0%; Score 60; DB 6; Length 4551;  
Best Local Similarity 29.9%; Pred. No. 1.6e+04;  
RESULT 1451  
ID ADH53444 standard; protein; 4551 AA.  
DE Streptomyces venezuelae narbonolide synthase subunit 1 protein, PICAI.  
PN US2003162262-A1.  
PD 28-AUG-2003.  
PA (ASHL/) ASHLEY G.  
PA (BETL/) BETLACH M. C.  
PA (BETL/) BETLACH M. C.  
PA (MCDA/) MCDANIEL R.  
PA (TANG/) TANG L.  
Query Match 12.0%; Score 60; DB 7; Length 4551;  
Best Local Similarity 29.9%; Pred. No. 1.6e+04;  
RESULT 1452  
ID AAY77200 standard; protein; 4613 AA.  
DE S. venezuelae pik (macrolide biosynthesis) gene cluster protein #1.  
PN WO200000620-A2.  
PD 06-JAN-2000.  
PA (MINI ) UNIV MINNESOTA.  
Query Match 12.0%; Score 60; DB 3; Length 4613;  
Best Local Similarity 29.9%; Pred. No. 1.7e+04;  
RESULT 1453  
ID AAY77192 standard; protein; 4613 AA.  
DE S. venezuelae macrolide biosynthetic enzyme PikAI, SEQ ID NO:31.  
PN WO200000620-A2.  
PD 06-JAN-2000.  
PA (MINI ) UNIV MINNESOTA.  
Query Match 12.0%; Score 60; DB 3; Length 4613;  
Best Local Similarity 29.9%; Pred. No. 1.7e+04;  
RESULT 1454

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ID ADL91916 standard; protein; 4613 AA.
DE Streptomyces macrolide biosynthetic protein - PIKR2.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER/) SHERMAN D H.
PA (LIUH/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 4613;
RESULT 1455
ID AAW19629 standard; protein; 4630 AA.
DE Streptomyces venezuelae polyketide synthase.
PN WO9722711-A1.
PD 26-JUN-1997.
PA (MINU) UNIV MINNESOTA.
Query Match
Best Local Similarity 12.0%; Score 60; DB 2; Length 4630;
RESULT 1456
ID ADL91934 standard; protein; 11877 AA.
DE Streptomyces venezuelae pik gene cluster protein.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER/) SHERMAN D H.
PA (LIUH/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match
Best Local Similarity 12.0%; Score 60; DB 8; Length 11877;
RESULT 1457
ID AAY77180 standard; protein; 12199 AA.
DE S. venezuelae pik gene cluster-encoded protein, SEQ ID NO:6.
PN WO200000620-A2.
PD 06-JAN-2000.
PA (MINU) UNIV MINNESOTA.
Query Match
Best Local Similarity 12.0%; Score 60; DB 3; Length 12199;
RESULT 1458
ID ABP04991 standard; protein; 77 AA.
DE Human ORFX protein sequence SEQ ID NO:9964.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 5; Length 77;
RESULT 1459
ID AAY04746 standard; protein; 100 AA.
DE Mycobacterium species protein sequence 1#4.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 100;
RESULT 1460
ID ADJ50224 standard; protein; 124 AA.
DE Oil-associated gene related protein #1724.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 8; Length 124;
RESULT 1461
ID ADJ49790 standard; protein; 132 AA.
DE Oil-associated gene related protein #1290.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 136;
RESULT 1462
ID AAY04897 standard; protein; 136 AA.
DE Mycobacterium species protein sequence 28.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 136;
RESULT 1463
ID AAY04754 standard; protein; 136 AA.
DE Mycobacterium species protein sequence 2#3.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 136;
RESULT 1464
ID AAY04750 standard; protein; 136 AA.
DE Mycobacterium species protein sequence 1D.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 136;
RESULT 1465
ID AAB52478 standard; protein; 136 AA.
DE Mycobacterium tuberculosis secreted protein #43.
PN WO200066143-A1.
PD 09-NOV-2000.
PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 136;
RESULT 1466
ID ABG31899 standard; protein; 148 AA.
DE Novel human diagnostic protein #13890.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 148;
RESULT 1467
ID ABG00067 standard; protein; 148 AA.
DE Novel human diagnostic protein #58.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 148;
RESULT 1468
ID ABG02758 standard; protein; 148 AA.
DE Novel human diagnostic protein #2749.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 4; Length 148;
RESULT 1469
ID AAY04751 standard; protein; 165 AA.
DE Mycobacterium species protein sequence 1F.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 11.9%; Score 59.5; DB 2; Length 165;
RESULT 1470
ID ABB67828 standard; protein; 176 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30276.
PN WO200171042-A2.
PD 27-SEP-2001.
```

PA (PEKE ) PE CORP NY.  
Query Match 11.9%; Score 59.5; DB 4; Length 176;  
Best Local Similarity 29.0%; Pred. No. 2.6e+02;  
RESULT 1471  
ID AAY71042 standard; protein; 217 AA.  
DE Streptococcus pyogenes strain SF370 full-length GRAB protein.  
PN WO20026240-A2.  
PD 11-MAY-2000.  
PA (ACTI-) ACTINOVA LTD.  
Query Match 11.9%; Score 59.5; DB 3; Length 217;  
Best Local Similarity 29.9%; Pred. No. 3.4e+02;  
RESULT 1472  
ID ABP31003 standard; protein; 217 AA.  
DE Streptococcus polypeptide SEQ ID NO 9202.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 11.9%; Score 59.5; DB 5; Length 217;  
Best Local Similarity 29.9%; Pred. No. 3.4e+02;  
RESULT 1473  
ID ADR83937 standard; protein; 217 AA.  
DE S. pyogenes hyperimmune system reactive antigen Spy1357.  
PN WO2004078907-A2.  
PD 16-SEP-2004.  
PA (INTE-) INTERCELL AG.  
Query Match 11.9%; Score 59.5; DB 8; Length 217;  
Best Local Similarity 29.9%; Pred. No. 3.4e+02;  
RESULT 1474  
ID AAY73464 standard; protein; 220 AA.  
DE Human secreted protein clone y14\_1 protein sequence SEQ ID NO:150.  
PN WO958642-A2.  
PD 18-NOV-1999.  
PA (GENE-) GENETICS INST INC.  
Query Match 11.9%; Score 59.5; DB 3; Length 220;  
Best Local Similarity 28.6%; Pred. No. 3.4e+02;  
RESULT 1475  
ID ABB76449 standard; protein; 252 AA.  
DE Daf-4 bone morphogenetic protein receptor extracellular domain.  
PN WO200239118-A1.  
PD 16-MAY-2002.  
PA (THRA-) THRASOS INC.  
Query Match 11.9%; Score 59.5; DB 5; Length 252;  
Best Local Similarity 26.7%; Pred. No. 4.1e+02;  
RESULT 1476  
ID ABU33941 standard; protein; 256 AA.  
DE Protein encoded by Prokaryotic essential gene #19468.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.9%; Score 59.5; DB 6; Length 256;  
Best Local Similarity 26.5%; Pred. No. 4.2e+02;  
RESULT 1477  
ID AAY71043 standard; protein; 259 AA.  
DE Streptococcus pyogenes strain KTL9 partial GRAB protein.  
PN WO20026240-A2.  
PD 11-MAY-2000.  
PA (ACTI-) ACTINOVA LTD.  
Query Match 11.9%; Score 59.5; DB 3; Length 259;  
Best Local Similarity 29.9%; Pred. No. 4.3e+02;  
RESULT 1478  
ID ADR43144 standard; protein; 295 AA.  
DE IPT-like structural protein #203.  
PN WO2004074442-A2.  
PD 02-SEP-2004.  
PA (MONS) MONGANNO TECHNOLOGY LLC.  
Query Match 11.9%; Score 59.5; DB 8; Length 295;  
Best Local Similarity 25.4%; Pred. No. 5.1e+02;  
RESULT 1479  
ID ABO61089 standard; protein; 302 AA.  
DE Klebsiella pneumoniae polypeptide seqid 7606.  
PN US610836-B1.  
PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 11.9%; Score 59.5; DB 7; Length 302;  
Best Local Similarity 29.5%; Pred. No. 5.2e+02;  
RESULT 1480  
ID AAR31020 standard; protein; 307 AA.  
DE Grass pollen allergen, KRG 60.  
PN CA2066801-A.  
PD 27-OCT-1992.  
PA (MOHA/) MOHAPATRA S S.  
Query Match 11.9%; Score 59.5; DB 2; Length 307;  
Best Local Similarity 29.3%; Pred. No. 5.3e+02;  
RESULT 1481  
ID AAG72623 standard; protein; 317 AA.  
DE Murine OR-like polypeptide query sequence, SEQ ID NO: 2304.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 11.9%; Score 59.5; DB 4; Length 317;  
Best Local Similarity 34.3%; Pred. No. 5.6e+02;  
RESULT 1482  
ID AAY04747 standard; protein; 320 AA.  
DE Mycobacterium species protein sequence 1A'.  
PN WO9909186-A2.  
PD 25-FEB-1999.  
PA (INSP ) INST PASTEUR.  
Query Match 11.9%; Score 59.5; DB 2; Length 320;  
Best Local Similarity 26.9%; Pred. No. 5.6e+02;  
RESULT 1483  
ID ABU28912 standard; protein; 327 AA.  
DE Protein encoded by Prokaryotic essential gene #14439.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.9%; Score 59.5; DB 6; Length 327;  
Best Local Similarity 23.2%; Pred. No. 5.8e+02;  
RESULT 1484  
ID ADC01360 standard; protein; 327 AA.  
DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 1405.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Query Match 11.9%; Score 59.5; DB 7; Length 327;  
Best Local Similarity 23.2%; Pred. No. 5.8e+02;  
RESULT 1485  
ID ADS27824 standard; protein; 328 AA.  
DE Bacterial polypeptide #16857.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 11.9%; Score 59.5; DB 8; Length 328;  
Best Local Similarity 26.3%; Pred. No. 5.8e+02;  
RESULT 1486  
ID ABR56731 standard; protein; 334 AA.  
DE Human secreted protein SSCP-6 SEQ ID NO:6.  
PN WO2003016506-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.9%; Score 59.5; DB 6; Length 334;  
Best Local Similarity 34.8%; Pred. No. 6e+02;  
RESULT 1487  
ID ADE28661 standard; protein; 334 AA.  
DE Human NOV13a protein - SEQ ID 38.  
PN WO2003040330-A2.  
PD 15-MAY-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 11.9%; Score 59.5; DB 7; Length 334;  
Best Local Similarity 34.8%; Pred. No. 6e+02;  
RESULT 1488

ID ADM93406 standard; protein; 334 AA.  
 DE Human NOVX polypeptide #19.  
 PN US2004067882-A1.  
 PD 08-APR-2004.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (ALVA/) ALVAREZ E. P.  
 PA (ANDE/) ANDERSON D W.  
 PA (BARO/) BARON M.  
 PA (BOLD/) BOLDOG F L.  
 PA (BURG/) BURGESS C E.  
 PA (CASM/) CASMAN S J.  
 PA (CHAP/) CHAPOVAL A.  
 PA (DHAN/) DHANABAL M.  
 PA (EDIT/) EDINGER S R.  
 PA (EISE/) EISEN A.  
 PA (ELLE/) ELLERMAN K.  
 PA (ETTE/) ETTEBERG S.  
 PA (GANG/) GANGOLLI E A.  
 PA (GERL/) GERLACH V.  
 PA (GORM/) GORMAN L.  
 PA (GROS/) GROSSE W M.  
 PA (GUOX/) GUO X.  
 PA (HACK/) HACKETT C.  
 PA (JIMW/) JI W.  
 PA (KEKU/) KERUDA R.  
 PA (KERA/) KHRAMTSOV N V.  
 PA (LEPL/) LEPLLEY D M.  
 PA (LILL/) LI L.  
 PA (MACD/) MACDOUGALL J R.  
 PA (MALY/) MALYANKAR U M.  
 PA (MAZU/) MAZUR A.  
 PA (MCOU/) MCCOENEY K.  
 PA (MEZE/) MEZES P S.  
 PA (MILL/) MILLER C E.  
 PA (MILL/) MILLER I.  
 PA (MISH/) MISHRA V.  
 PA (PADI/) PADIGARU M.  
 PA (PATI/) PATTURAJAN M.  
 PA (PENA/) PENNA C E A.  
 PA (PEYM/) PEYMAN J A.  
 PA (RAST/) RASTELLI L.  
 PA (RIEG/) RIEGER D K.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (SHEN/) SHENOY S G.  
 PA (SHIM/) SHIMKETS R A.  
 PA (SPAD/) SPADERNA S K.  
 PA (STAR/) STARLING G.  
 PA (SPYT/) SPYTEK K A.  
 PA (STON/) STONE D J.  
 PA (TCHE/) TCHERNEV V T.  
 PA (TWOI/) TWOMLOW N.  
 PA (VERN/) VERNET C A M.  
 PA (ZERR/) ZERRHUSEN B D.  
 PA (VOSS/) VOSS E Z.  
 PA (ZHON/) ZHONG M.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 8; Length 334;  
 RESULT 1489  
 ID ADR13777 standard; protein; 336 AA.  
 DE Amidase, SEQ ID 114.  
 PN WO2004069848-A2.  
 PD 19-AUG-2004.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 8; Length 336;  
 RESULT 1490  
 ID AAG52436 standard; protein; 337 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 66653.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 3; Length 337;  
 Query Match 29.3%; Pred. No. 6e+02;

RESULT 1491  
 ID ABB66995 standard; protein; 339 AA.  
 DE Drosophila melanogaster polypeptide seq ID 27777.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 4; Length 339;  
 RESULT 1492  
 ID ABO66983 standard; protein; 352 AA.  
 DE Klebsiella pneumoniae polypeptide seqid 13500.  
 PN US6610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 7; Length 352;  
 RESULT 1493  
 ID ADG22336 standard; protein; 353 AA.  
 DE Cyanophage S-2L encoded protein #81.  
 PN FR8839079-A1.  
 PD 31-OCT-2003.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 8; Length 353;  
 RESULT 1494  
 ID ADQ94412 standard; protein; 367 AA.  
 DE E. coli Aspartate semialdehyde dehydrogenase.  
 PN WO2004058954-A2.  
 PD 15-JUL-2004.  
 PA (AFPI-) AFFINITUM PHARM INC.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 8; Length 367;  
 RESULT 1495  
 ID ADS45159 standard; protein; 367 AA.  
 DE Bacterial polypeptide #23589.  
 PN US200323675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 8; Length 367;  
 RESULT 1496  
 ID AAY41496 standard; protein; 368 AA.  
 DE Fragment of human secreted protein encoded by gene 70.  
 PN WO9947540-A1.  
 PD 23-SEP-1999.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 2; Length 368;  
 RESULT 1497  
 ID ADM76949 standard; protein; 368 AA.  
 DE ATG-ase protein sequence.  
 PN WO2004020643-A2.  
 PD 11-MAR-2004.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 8; Length 368;  
 RESULT 1498  
 ID ADM76946 standard; protein; 368 AA.  
 DE GTP-ase protein sequence.  
 PN WO2004020643-A2.  
 PD 11-MAR-2004.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match  
 Best Local Similarity 11.9%; Score 59.5; DB 8; Length 368;  
 RESULT 1499  
 ID AAY43986 standard; protein; 374 AA.  
 DE Mouse alcohol dehydrogenase #1.



PN US5958784-A.  
PD 28-SEP-1999.  
PA (BENN/) BENNER S A.  
Query Match 11.9%; Score 59.5; DB 2; Length 374;  
Best Local Similarity 29.3%; Pred. No. 6.9e+02;  
RESULT 1500  
ID ABU22527 standard; protein; 380 AA.  
DE Protein encoded by Prokaryotic essential gene #8054.  
PN MO200277183-A2.  
PD 03-OCT-2002  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.9%; Score 59.5; DB 6; Length 380;  
Best Local Similarity 28.0%; Pred. No. 7.1e+02;

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Run on: March 8, 2005, 04:41:24 ; Search time 436 Seconds  
GenCore version 5.1.6  
(without alignments)  
7739.111 Million cell updates/sec

Title: US-09-989-731-407

Perfect score: 570

Sequence: 1 gcgagaccg99cataagaa.....aaaaaaaaaaaaaaaa 570  
IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0  
4390206 segs, 2959870667 residues  
8780412

Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn19806:\*  
2: geneseqn19908:\*  
3: geneseqn20008:\*  
4: geneseqn20018:\*  
5: geneseqn20018:\*  
6: geneseqn20028:\*  
7: geneseqn20038:\*  
8: geneseqn20038:\*  
9: geneseqn20038:\*  
10: geneseqn20038:\*  
11: geneseqn20038:\*  
12: geneseqn20048:\*  
13: geneseqn20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID / AAZ65103	standard;	cdNA;	570 BP.			
DE	Membrane-bound protein	PRO1245	encoding	cdNA.		
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 3;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 2						
ID / AAF44249	standard;	cdNA;	570 BP.			
DE	Human PRO1245 (UNQ629)	nucleotide	sequence	SEQ ID NO:407.		
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 5;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 3						
ID	ACA44431	standard;	cdNA;	570 BP.		
DE	Novel human secreted and transmembrane protein	PRO1245	cdNA.			
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 8;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 4						
ID	ABX80890	standard;	cdNA;	570 BP.		
DE	Human secreted/transmembrane protein	cdNA, #163.				
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 8;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 5						
ID	ACD44399	standard;	cdNA;	570 BP.		
DE	cdNA encoding human	PRO1245	polypeptide.			
PN	US2002127576-A1.					
PD	12-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 8;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				

Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 6						
ID	ABX79570	standard;	cdNA;	570 BP.		
DE	Human secreted/transmembrane protein	cdNA, #163.				
PN	US2002142961-A1.					
PD	03-OCT-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 8;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 7						
ID	ACA93591	standard;	cdNA;	570 BP.		
DE	Novel human secreted and transmembrane protein	PRO1245	cdNA.			
PN	US2003022187-A1.					
PD	30-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 8;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 8						
ID	ABX81273	standard;	DNA;	570 BP.		
DE	Novel human secreted or transmembrane protein	PRO1358	DNA.			
PN	US2003027985-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 8;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 9						
ID	ACA93089	standard;	cdNA;	570 BP.		
DE	Novel human secreted and transmembrane protein	PRO1245	cdNA.			
PN	US2003017476-A1.					
PD	23-JUN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 8;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 10						
ID	ABX17173	standard;	cdNA;	570 BP.		
DE	Human PRO polynucleotide	#127.				
PN	US2002123463-A1.					
PD	05-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 8;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 11						
ID	ACA68028	standard;	cdNA;	570 BP.		
DE	Novel human secreted and transmembrane protein	PRO1245	cdNA.			
PN	US2002177164-A1.					
PD	28-NOV-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 9;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 12						
ID	ACA88477	standard;	cdNA;	570 BP.		
DE	Human secreted and transmembrane polypeptide	PRO1245	cdNA.			
PN	US2002197615-A1.					
PD	26-DEC-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 9;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 13						
ID	ACD81984	standard;	cdNA;	570 BP.		
DE	cdNA encoding human	PRO1245	polypeptide.			
PN	US2003017991-A1.					
PD	23-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 9;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 14						
ID	ADA37918	standard;	cdNA;	570 BP.		
DE	Human cdNA encoding secreted/transmembrane protein	PRO1245.				
PN	US2003008297-A1.					
PD	09-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 570;	DB 9;	Length 570;		
Best Local Similarity	100.0%;	Pred. No. 5.5e-89;				
RESULT 15						
ID	ADA21604	standard;	cdNA;	570 BP.		
DE	Human cdNA encoding secreted/transmembrane polypeptide	PRO1245.				
PN	US2003054404-A1.					

PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 16  
ID ADA10391 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1245.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 17  
ID ADA17935 standard; cDNA; 570 BP.  
DE cDNA encoding human PRO1245 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 18  
ID ADA28043 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 19  
ID ADA94623 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 20  
ID ADA38848 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 21  
ID ADA92969 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 22  
ID ACH65545 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 23  
ID ADA22530 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1245.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 24  
ID ACD39535 standard; cDNA; 570 BP.  
DE Human cDNA encoding PRO1358.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 25  
ID ADA06696 standard; cDNA; 570 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #127.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
PD 100.0%; Pred. No. 5.5e-89;

RESULT 26  
ID ADA39389 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 27  
ID ADB96415 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 9; Length 570;  
RESULT 28  
ID ADC57887 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;  
RESULT 29  
ID ADC55251 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;  
RESULT 30  
ID ADC12118 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;  
RESULT 31  
ID ADC65640 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;  
RESULT 32  
ID ADC07595 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;  
RESULT 33  
ID ADC11585 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;  
RESULT 34  
ID ADC14707 standard; cDNA; 570 BP.  
DE Novel human secreted and transmembrane protein PRO1245 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;  
RESULT 35  
ID ADD08239 standard; cDNA; 570 BP.  
DE Novel human secreted and transmembrane protein PRO1245 cDNA.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 570; DB 10; Length 570;  
RESULT 36  
ID ADC82064 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.

PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 37  
ID ADD07706 standard; cDNA; 570 BP.  
DE Novel human secreted and transmembrane protein PRO1245 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 38  
ID ADC82597 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 39  
ID ADD08777 standard; cDNA; 570 BP.  
DE Novel human secreted and transmembrane protein PRO1245 cDNA.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 40  
ID ADD07026 standard; cDNA; 570 BP.  
DE Novel human secreted and transmembrane protein PRO1245 cDNA.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 41  
ID ADC83273 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 42  
ID ADD55380 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003077553-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 43  
ID ADD56338 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 44  
ID ADD54776 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 45  
ID ADE26930 standard; cDNA; 570 BP.  
DE Novel human secreted and transmembrane protein PRO1245 cDNA.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 46  
ID ADE26397 standard; cDNA; 570 BP.  
DE Novel human secreted and transmembrane protein PRO1245 cDNA.

PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 47  
ID ADF67334 standard; cDNA; 570 BP.  
DE Human PRO1245 nucleotide sequence SEQ ID NO:407.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 48  
ID ADI35588 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 49  
ID ADI00081 standard; cDNA; 570 BP.  
DE Novel human secreted and transmembrane protein PRO1245 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 50  
ID ABX77974 standard; cDNA; 570 BP.  
DE Human PRO polynucleotide #127.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 51  
ID ABX80386 standard; DNA; 570 BP.  
DE Novel human secreted or transmembrane protein PRO1358 DNA.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 52  
ID ACA69292 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 53  
ID ABX90363 standard; cDNA; 570 BP.  
DE Human secreted/transmembrane protein cDNA, #163.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 54  
ID ABX64209 standard; cDNA; 570 BP.  
DE cDNA encoding human PRO1245 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 570; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 55  
ID ADF35533 standard; cDNA; 570 BP.  
DE cDNA encoding human PRO1245 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 570; DB 12; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 56  
ID ADG11783 standard; cDNA; 570 BP.

DE cDNA encoding human PRO1245 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 12; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 57  
ID ADH19653 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 12; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 58  
ID ADH21146 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003228658-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 12; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 59  
ID ADH20186 standard; cDNA; 570 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1245.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 570; DB 12; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5.5e-89;  
RESULT 60  
ID ABK40267 standard; cDNA; 569 BP.  
DE cDNA encoding human PRO1245 polypeptide.  
PN WO200153486-A1.  
PD 26-JUL-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 99.8%; Score 569; DB 6; Length 569;  
Best Local Similarity 100.0%; Pred. No. 8.2e-89;  
RESULT 61  
ID ADJ37308 standard; cDNA; 569 BP.  
DE Human tumour therapy associated PRO1245 cDNA.  
PN US2003211096-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.8%; Score 569; DB 10; Length 569;  
Best Local Similarity 100.0%; Pred. No. 8.2e-89;  
RESULT 62  
ID ADG68232 standard; cDNA; 569 BP.  
DE Human PRO polypeptide cDNA #14.  
PN US2003170228-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.8%; Score 569; DB 12; Length 569;  
Best Local Similarity 100.0%; Pred. No. 8.2e-89;  
RESULT 63  
ID AAZ29723 standard; DNA; 543 BP.  
DE Human lung specific gene lng107.  
PN WO960160-A1.  
PD 25-NOV-1999.  
PA (DIAD-) DIADEXUS LLC.  
Query Match 92.8%; Score 529; DB 3; Length 543;  
Best Local Similarity 100.0%; Pred. No. 6e-82;  
RESULT 64  
ID AAZ98173 standard; cDNA; 543 BP.  
DE Human signal peptide containing protein HSP-65 cDNA SEQ ID NO:199.  
PN WO200006010-A2.  
PD 06-JAN-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 92.8%; Score 529; DB 3; Length 543;  
Best Local Similarity 100.0%; Pred. No. 6e-82;  
RESULT 65  
ID AD39936 standard; cDNA; 561 BP.  
DE Human lung disorder-related cDNA - SEQ ID 6.  
PN US2003124580-A1.

PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 91.8%; Score 523; DB 10; Length 561;  
Best Local Similarity 100.0%; Pred. No. 6.5e-81;  
RESULT 66  
ID AAV54621 standard; cDNA; 519 BP.  
DE LUI05 polypeptide encoding cDNA clone 1327836IH.  
PN WO9833926-A1.  
PD 06-AUG-1998.  
PA (ABB0 ) ABBOTT LAB.  
Query Match 91.1%; Score 519; DB 2; Length 519;  
Best Local Similarity 100.0%; Pred. No. 3.1e-80;  
RESULT 67  
ID AAV54620 standard; cDNA; 562 BP.  
DE LUI05 specific consensus polynucleotide sequence.  
PN WO9833926-A1.  
PD 06-AUG-1998.  
PA (ABB0 ) ABBOTT LAB.  
Query Match 91.0%; Score 518.6; DB 2; Length 562;  
Best Local Similarity 99.8%; Pred. No. 3.7e-80;  
RESULT 68  
ID ADP45231 standard; DNA; 527 BP.  
DE Human lung cancer specific DNA #2.  
PN US2004101876-A1.  
PD 27-MAY-2004.  
PA (MINT/) MINTZ L.  
PA (XIEH/) XIE H.  
PA (DAHA/) DAFARI D.  
PA (LEVA/) LEVANON E.  
PA (FREI/) FREILICH S.  
PA (BECK/) BECK N.  
PA (ZHUW/) ZHU W.  
PA (WASS/) WASSERMAN A.  
PA (HERM/) HERMESH C.  
PA (AZAR/) AZAR I.  
PA (BERN/) BERNSTEIN J.  
PA (SORE/) SOREK R.  
Query Match 90.9%; Score 518; DB 12; Length 527;  
Best Local Similarity 100.0%; Pred. No. 4.7e-80;  
RESULT 69  
ID ADJ75215 standard; DNA; 461 BP.  
DE Marker gene SEQ ID NO:467.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 80.3%; Score 457.8; DB 12; Length 461;  
Best Local Similarity 99.6%; Pred. No. 1e-69;  
RESULT 70  
ID ABT10080 standard; cDNA; 526 BP.  
DE Human breast cancer associated coding sequence SEQ ID NO: 214.  
PN WO200259271-A2.  
PD 01-AUG-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 72.1%; Score 411.2; DB 6; Length 526;  
Best Local Similarity 90.7%; Pred. No. 1e-61;  
RESULT 71  
ID ADI36344 standard; cDNA; 312 BP.  
DE Full-length hIN-1 encoding cDNA, seq id 3.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DNA FARMER CANCER INST INC.  
Query Match 54.2%; Score 308.8; DB 10; Length 312;  
Best Local Similarity 99.4%; Pred. No. 3.8e-44;  
RESULT 72  
ID ABI66623 standard; DNA; 380 BP.  
DE lung cancer related gene sequence SEQ ID NO:4960.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 51.5%; Score 293.4; DB 6; Length 380;  
Best Local Similarity 91.9%; Pred. No. 1.7e-41;  
RESULT 73

ID AD136345 standard; cDNA; 258 BP.  
DE Mature hIN-1 encoding cDNA, seq id 4.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 44.9%; Score 256; DB 10; Length 258;  
Best Local Similarity 100.0%; Pred. No. 4.4e-35;  
RESULT 74  
ID AD136346 standard; cDNA; 252 BP.  
DE Mature hIN-1 encoding cDNA, seq id 23.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 44.2%; Score 252; DB 10; Length 252;  
Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
RESULT 75  
ID AAV54617 standard; cDNA; 244 BP.  
DE LUI05 specific polynucleotide sequence from clone 1327836.  
PN WO9833926-A1.  
PD 06-AUG-1998.  
PA (ABRO ) ABBOTT LAB.  
Query Match 42.4%; Score 241.4; DB 2; Length 244;  
Best Local Similarity 99.2%; Pred. No. 1.4e-32;  
RESULT 76  
ID AAV54618 standard; cDNA; 225 BP.  
DE LUI05 specific polynucleotide sequence from clone 1605935.  
PN WO9833926-A1.  
PD 06-AUG-1998.  
PA (ABRO ) ABBOTT LAB.  
Query Match 39.5%; Score 225; DB 2; Length 225;  
Best Local Similarity 100.0%; Pred. No. 9.3e-30;  
RESULT 77  
ID ACH19647 standard; cDNA; 416 BP.  
DE Human adult lung cDNA #650.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 29.5%; Score 168.4; DB 9; Length 416;  
Best Local Similarity 99.4%; Pred. No. 5.1e-20;  
RESULT 78  
ID AAV54616 standard; cDNA; 190 BP.  
DE LUI05 specific polynucleotide sequence from clone 3353867.  
PN WO9833926-A1.  
PD 06-AUG-1998.  
PA (ABRO ) ABBOTT LAB.  
Query Match 25.3%; Score 144; DB 2; Length 190;  
Best Local Similarity 98.0%; Pred. No. 7.5e-16;  
RESULT 79  
ID ADM83730 standard; DNA; 1794 BP.  
DE Human high in normal-1 (HIN-1) cDNA.  
PN US200318783-A1.  
PD 24-JUL-2003.  
PA (SUKU/) SUKUMAR S.  
PA (EVRO/) EVRON E.  
PA (DOOL/) DOOLEY W C.  
PA (SACC/) SACCCHI N.  
PA (DAVI/) DAVIDSON N.  
PA (PACK/) PACKLER M J.  
Query Match 21.8%; Score 124; DB 11; Length 1794;  
Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
RESULT 80  
ID AA186394 standard; cDNA; 404 BP.  
DE Human polynucleotide seq ID NO 6454.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 20.4%; Score 116; DB 4; Length 404;

Best Local Similarity 88.7%; Pred. No. 5.1e-11;  
RESULT 81  
ID AAV54619 standard; cDNA; 114 BP.  
DE LUI05 specific polynucleotide sequence from clone 811640.  
PN WO9833926-A1.  
PD 06-AUG-1998.  
PA (ABRO ) ABBOTT LAB.  
Query Match 20.0%; Score 114; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1e-10;  
RESULT 82  
ID AD136318 standard; cDNA; 312 BP.  
DE Full-length hIN-1 encoding cDNA, seq id 7.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 19.3%; Score 109.8; DB 10; Length 312;  
Best Local Similarity 66.1%; Pred. No. 5.8e-10;  
RESULT 83  
ID AD136319 standard; cDNA; 255 BP.  
DE Mature hIN-1 encoding cDNA, seq id 8.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 16.2%; Score 92.6; DB 10; Length 255;  
Best Local Similarity 64.2%; Pred. No. 5.1e-07;  
RESULT 84  
ID ABT06542 standard; DNA; 1794 BP.  
DE Human HIN-1 coding sequence.  
PN WO200259347-A2.  
PD 01-AUG-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Query Match 16.0%; Score 91.4; DB 6; Length 1794;  
Best Local Similarity 56.9%; Pred. No. 9.3e-07;  
RESULT 85  
ID AD136320 standard; cDNA; 249 BP.  
DE Mature hIN-1 encoding cDNA, seq id 25.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 15.8%; Score 90; DB 10; Length 249;  
Best Local Similarity 64.5%; Pred. No. 1.4e-06;  
RESULT 86  
ID AD136325 standard; cDNA; 279 BP.  
DE Full-length hIN-1 encoding cDNA, seq id 20.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 15.6%; Score 88.8; DB 10; Length 279;  
Best Local Similarity 63.1%; Pred. No. 2.3e-06;  
RESULT 87  
ID AD136327 standard; cDNA; 249 BP.  
DE Mature hIN-1 encoding cDNA, seq id 26.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 15.3%; Score 87.2; DB 10; Length 249;  
Best Local Similarity 65.5%; Pred. No. 4.3e-06;  
RESULT 88  
ID AD136324 standard; DNA; 551 BP.  
DE hIN-1 promoter sequence, seq id 19.  
PN WO200268673-A2.  
PD 06-SEP-2002.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 13.7%; Score 78; DB 10; Length 551;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
RESULT 89  
ID ADP10592 standard; DNA; 200 BP.

DE Reference mRNA sequences for marker probe #269.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 12.5%; Score 71; DB 12; Length 200;  
RESULT 90  
ID AAX26196 standard; DNA; 1613 BP.  
DE DNA sequence of glycosyltransferase gene.  
PN JP11056373-A.  
PD 02-MAR-1999.  
PA (FURU/) FURUKAWA K.  
Query Match  
Best Local Similarity 12.2%; Score 69.4; DB 2; Length 1613;  
RESULT 91  
ID ACN52874 standard; cDNA; 589 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H4, SEQ:7655.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 12.1%; Score 69; DB 13; Length 589;  
RESULT 92  
ID AAT79634 standard; DNA; 1898 BP.  
DE DNA encoding human ubiquituous nuclear receptor polypeptide.  
PN US5639616-A.  
PD 17-JUN-1997.  
PA (ARCH-) ARCH DEV CORP.  
Query Match  
Best Local Similarity 12.1%; Score 69; DB 2; Length 1898;  
RESULT 93  
ID AB190773 standard; cDNA; 1360 BP.  
DE Human polynucleotide SEQ ID NO 1335.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 12.0%; Score 68.4; DB 6; Length 1360;  
RESULT 94  
ID AB278096 standard; cDNA; 862 BP.  
DE Human breast specific nucleic acid #110.  
PN WO200268645-A2.  
PD 06-SEP-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match  
Best Local Similarity 11.9%; Score 68; DB 6; Length 862;  
RESULT 95  
ID ACN56642 standard; cDNA; 598 BP.  
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-001-Q1-N6-H1, SEQ:11423.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 11.9%; Score 67.6; DB 13; Length 598;  
RESULT 96  
ID AAD05580 standard; cDNA; 2187 BP.  
DE Human secreted protein-encoding gene 2 cDNA clone HRAEH37, SEQ ID NO:12.  
PN WO200134627-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.9%; Score 67.6; DB 4; Length 2187;  
RESULT 97  
ID ACN56129 standard; cDNA; 496 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-C10, SEQ:10910.  
PN US2004123340-A1.  
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 13; Length 496;  
RESULT 98  
ID AAC59305 standard; cDNA; 566 BP.  
DE Human secreted protein cDNA #29.  
PN WO200056753-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 3; Length 566;  
RESULT 99  
ID ADA97967 standard; cDNA; 566 BP.  
DE Human secreted protein cDNA sequence #61.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 8; Length 566;  
RESULT 100  
ID ADA43873 standard; cDNA; 566 BP.  
DE Human secreted protein cDNA SEQ ID 61.  
PN WO2003000865-A2.  
PD 03-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 8; Length 566;  
RESULT 101  
ID ADC20123 standard; DNA; 566 BP.  
DE Human secreted protein coding sequence #62.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 10; Length 566;  
RESULT 102  
ID ADP10581 standard; DNA; 566 BP.  
DE Human secreted protein encoding sequence #34.  
PN WO20029085-A2.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 10; Length 566;  
RESULT 103  
ID ACN52093 standard; cDNA; 579 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-C7, SEQ:6874.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 13; Length 579;  
RESULT 104  
ID ADP14449 standard; DNA; 1460 BP.  
DE Human NF-kappaB pathway-associated gene SeqID450.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 13; Length 1460;  
RESULT 105  
ID AA088760 standard; DNA; 1813 BP.  
DE Human ubiquituous nuclear receptor protein DNA.  
PN WO9513373-A1.  
PD 18-MAY-1995.  
PA (ARCH-) ARCH DEV CORP.  
Query Match  
Best Local Similarity 11.8%; Score 67.4; DB 2; Length 1813;  
RESULT 106



RESULT 106  
ID ACN4862 standard; cDNA; 516 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-027-Q6-N6-H7, SEQ:3643.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.8%; Score 67.2; DB 13; Length 516;  
Best Local Similarity 66.2%; Pred. No. 0.012;  
RESULT 107  
ID ADI62837 standard; cDNA; 733 BP.  
DE Human apoptosis-associated cDNA SEQ ID 280.  
PN WO2003058021-A2.  
PD 17-JUL-2003.  
PA (XANT-) XANTOS BIOMEDICINE AG.  
Query Match 11.8%; Score 67; DB 10; Length 733;  
Best Local Similarity 54.7%; Pred. No. 0.014;  
RESULT 108  
ID ADI62835 standard; cDNA; 733 BP.  
DE Human apoptosis-associated cDNA SEQ ID 278.  
PN WO2003058021-A2.  
PD 17-JUL-2003.  
PA (XANT-) XANTOS BIOMEDICINE AG.  
Query Match 11.8%; Score 67; DB 10; Length 733;  
Best Local Similarity 54.7%; Pred. No. 0.014;  
RESULT 109  
ID AB71910 standard; DNA; 1375 BP.  
DE Human breast cancer / ovarian cancer related coding sequence #17.  
PN WO2003000012-A2.  
PD 03-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.8%; Score 67; DB 10; Length 1375;  
Best Local Similarity 61.3%; Pred. No. 0.014;  
RESULT 110  
ID ABZ82489 standard; cDNA; 805 BP.  
DE Human secreted protein cDNA #SEQ ID 36.  
PN WO200268628-A1.  
PD 06-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.7%; Score 66.8; DB 6; Length 805;  
Best Local Similarity 81.9%; Pred. No. 0.015;  
RESULT 111  
ID ACN49708 standard; cDNA; 554 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-F6, SEQ:4489.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.7%; Score 66.6; DB 13; Length 554;  
Best Local Similarity 67.9%; Pred. No. 0.016;  
RESULT 112  
ID ACN45287 standard; cDNA; 573 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-002-Q1-N6-H7, SEQ:68.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.7%; Score 66.6; DB 13; Length 573;  
Best Local Similarity 71.9%; Pred. No. 0.016;  
RESULT 113  
ID ABK3926 standard; DNA; 9884 BP.  
DE Human DNA for staging of Astrocytomas, complement, #4.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 11.7%; Score 66.6; DB 6; Length 9884;  
Best Local Similarity 71.9%; Pred. No. 0.019;

RESULT 114  
ID ADA20341 standard; DNA; 9884 BP.  
DE Prostate tumour related genomic DNA complement sample #3.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 11.7%; Score 66.6; DB 8; Length 9884;  
Best Local Similarity 71.9%; Pred. No. 0.019;  
RESULT 115  
ID ADA84148 standard; DNA; 9884 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:6.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 11.7%; Score 66.6; DB 8; Length 9884;  
Best Local Similarity 71.9%; Pred. No. 0.019;  
RESULT 116  
ID ACN51610 standard; cDNA; 579 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-B6, SEQ:6391.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.6%; Score 66.4; DB 13; Length 579;  
Best Local Similarity 79.0%; Pred. No. 0.017;  
RESULT 117  
ID ADQ23300 standard; DNA; 1744 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6120.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 11.5%; Score 65.8; DB 12; Length 1744;  
Best Local Similarity 85.9%; Pred. No. 0.023;  
RESULT 118  
ID ABX39555 standard; cDNA; 383 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4720.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 11.5%; Score 65.6; DB 8; Length 383;  
Best Local Similarity 64.5%; Pred. No. 0.023;  
RESULT 119  
ID ADN39690 standard; cDNA; 550 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:662.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 11.5%; Score 65.6; DB 11; Length 550;  
Best Local Similarity 51.5%; Pred. No. 0.023;  
RESULT 120  
ID AA45893 standard; cDNA; 646 BP.  
DE cDNA sequence of a novel gene associated with insulin synthesis.  
PN WO200040722-A2.  
PD 13-JUL-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 11.5%; Score 65.4; DB 3; Length 646;  
Best Local Similarity 63.9%; Pred. No. 0.026;  
RESULT 121  
ID AAD42580 standard; cDNA; 646 BP.  
DE Human cDNA #2 co-expressed with collagenase gene.  
PN US2002077309-A1.  
PD 20-JUN-2002.  
PA (WALK/) WALKER M G.  
PA (VOLK/) VOLKUTH W.  
PA (KLIN/) KLINGLER T M.  
Query Match 11.5%; Score 65.4; DB 6; Length 646;  
Best Local Similarity 63.9%; Pred. No. 0.026;  
RESULT 122

ID ADC06744 standard; cDNA; 1723 BP.  
DE Human inositol hexakisphosphate kinase 1 cDNA.  
PN W02003066087-A2.  
PD 14-AUG-2003.  
PA (DEVE-) DEVELOPGEN ENTWICKLUNGSHIOLOGISC AG.  
Query Match 11.5%; Score 65.4; DB 10; Length 1723;  
Best Local Similarity 75.7%; Pred. No. 0.027;  
RESULT 123  
ID AAF18317 standard; DNA; 1607 BP.  
DE Lung cancer associated polynucleotide sequence SEQ ID 336.  
PN W0200055180-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 65; DB 3; Length 1607;  
Best Local Similarity 85.5%; Pred. No. 0.032;  
RESULT 124  
ID AAS29076 standard; cDNA; 316 BP.  
DE cDNA encoding for human DNA-binding protein #47.  
PN W0200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 5; Length 316;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
RESULT 125  
ID ABS68216 standard; cDNA; 316 BP.  
DE cDNA encoding human DNA-binding protein #47.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 11.4%; Score 64.8; DB 6; Length 316;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
RESULT 126  
ID ADC25210 standard; cDNA; 316 BP.  
DE Human cDNA from extracellular matrix gene 47.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 10; Length 316;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
RESULT 127  
ID AAV59298 standard; cDNA; 326 BP.  
DE Human prostate expression marker cDNA 59289.  
PN W0200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 11.4%; Score 64.8; DB 5; Length 326;  
Best Local Similarity 85.7%; Pred. No. 0.031;  
RESULT 128  
ID AAS35460 standard; cDNA; 362 BP.  
DE Human cardiovascular system antigen cDNA polynucleotide SEQ ID No 345.  
PN W0200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 4; Length 362;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
RESULT 129  
ID AAS29148 standard; cDNA; 362 BP.  
DE cDNA encoding for human DNA-binding protein #119.  
PN W0200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 5; Length 362;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
RESULT 130  
ID ABS68288 standard; cDNA; 362 BP.  
DE cDNA encoding human DNA-binding protein #119.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
Query Match 11.4%; Score 64.8; DB 4; Length 1050;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 131  
ID ADC25282 standard; cDNA; 362 BP.  
DE Human cDNA from extracellular matrix gene 119.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 10; Length 362;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
RESULT 132  
ID ADE45539 standard; cDNA; 362 BP.  
DE Human cardiovascular system related polynucleotide #335.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 13; Length 362;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
RESULT 133  
ID ADU06957 standard; DNA; 362 BP.  
DE Human cardiovascular system associated gene SeqID345.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 13; Length 362;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
RESULT 134  
ID ACN67280 standard; cDNA; 483 BP.  
DE Cotton primed seed EST clone ID: LIB3825-009-Q1-N6-D4, SEQ:2061.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.4%; Score 64.8; DB 13; Length 483;  
Best Local Similarity 72.4%; Pred. No. 0.032;  
RESULT 135  
ID ACN62126 standard; cDNA; 533 BP.  
DE Cotton gynoecium tissue EST clone ID: LIB3829-025-Q6-N6-E11, SEQ:16907.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.4%; Score 64.8; DB 13; Length 533;  
Best Local Similarity 78.0%; Pred. No. 0.032;  
RESULT 136  
ID AAD02075 standard; cDNA; 1043 BP.  
DE cDNA encoding human pituitary hormone, pituitrone.  
PN W0200066778-A1.  
PD 09-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 3; Length 1043;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 137  
ID AAZ98064 standard; cDNA; 1050 BP.  
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:58.  
PN W0200004140-A1.  
PD 27-JAN-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 3; Length 1050;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 138  
ID AAD11677 standard; cDNA; 1050 BP.  
DE Human secreted protein-encoding gene 48 cDNA clone HKGDL36, SEQ ID NO:58.  
PN W0200151504-A1.  
PD 19-JUL-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 4; Length 1050;  
Best Local Similarity 78.0%; Pred. No. 0.033;

RESULT 139  
ID ABK69773 standard; cDNA; 1050 BP.  
DE Human secreted protein gene 48.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 6; Length 1050;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 140  
ID ACC60758 standard; cDNA; 1050 BP.  
DE Human secreted protein coding sequence, SEQ ID 425.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 8; Length 1050;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 141  
ID ABZ71421 standard; cDNA; 1050 BP.  
DE Secreted protein-encoding gene 84 cDNA clone HKGDL36, SEQ ID NO:242.  
PN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 8; Length 1050;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 142  
ID ADB91374 standard; cDNA; 1050 BP.  
DE Human secreted protein cDNA #SEQ ID 320.  
PN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 9; Length 1050;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 143  
ID ADC73869 standard; DNA; 1050 BP.  
DE Human secreted protein-related DNA - SEQ ID 502.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 9; Length 1050;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 144  
ID ACC60491 standard; cDNA; 1052 BP.  
DE Human secreted protein coding sequence, SEQ ID 158.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 8; Length 1052;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 145  
ID ABZ71273 standard; cDNA; 1052 BP.  
DE Human secreted protein-encoding gene 84 cDNA clone HKGDL36, SEQ ID NO:94.  
PN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 8; Length 1052;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 146  
ID ADB91179 standard; cDNA; 1052 BP.  
DE Human secreted protein cDNA #SEQ ID 125.  
PN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 9; Length 1052;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 147  
ID ADC73556 standard; DNA; 1052 BP.  
DE Human secreted protein-related DNA - SEQ ID 189.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 10; Length 1052;  
Best Local Similarity 78.0%; Pred. No. 0.033;  
RESULT 148

ID AAC79804 standard; cDNA; 1390 BP.  
DE Human secreted protein gene 6 SEQ ID NO:16.  
PN WO200058336-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 3; Length 1390;  
Best Local Similarity 78.0%; Pred. No. 0.034;  
RESULT 149  
ID ABI90541 standard; cDNA; 1857 BP.  
DE Human polynucleotide SEQ ID NO 1103.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.4%; Score 64.8; DB 6; Length 1857;  
Best Local Similarity 78.0%; Pred. No. 0.035;  
RESULT 150  
ID ACN46220 standard; cDNA; 121 BP.  
DE Cotton primed seed EST clone ID: LIB3825-016-Q1-K6-H3, SEQ:1001.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.3%; Score 64.6; DB 13; Length 121;  
Best Local Similarity 70.4%; Pred. No. 0.032;  
RESULT 151  
ID ABR97599 standard; cDNA; 503 BP.  
DE Human prostate specific nucleic acid DEX0293\_26.  
PN WO200255735-A2.  
PD 18-JUL-2002.  
PA (DID-) DIADEXUS INC.  
Query Match 11.3%; Score 64.6; DB 6; Length 503;  
Best Local Similarity 65.7%; Pred. No. 0.034;  
RESULT 152  
ID ADI27232 standard; DNA; 1718 BP.  
DE Rat LRP binding family associated DNA.  
PN WO2003106657-A2.  
PD 24-DEC-2003.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Query Match 11.3%; Score 64.6; DB 12; Length 1718;  
Best Local Similarity 80.0%; Pred. No. 0.037;  
RESULT 153  
ID ADI27111 standard; DNA; 1718 BP.  
DE Rat LRP binding family protein DNA #2.  
PN WO2003106657-A2.  
PD 24-DEC-2003.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Query Match 11.3%; Score 64.6; DB 12; Length 1718;  
Best Local Similarity 80.0%; Pred. No. 0.037;  
RESULT 154  
ID AAH33160 standard; cDNA; 253 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:216.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.3%; Score 64.4; DB 4; Length 253;  
Best Local Similarity 71.6%; Pred. No. 0.036;  
RESULT 155  
ID ACC68993 standard; cDNA; 811 BP.  
DE Human neurotransmission-associated protein NTRAN-15 cDNA SEQ ID NO:40.  
PN WO2003025129-A2.  
PD 27-MAR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.3%; Score 64.4; DB 10; Length 811;  
Best Local Similarity 70.5%; Pred. No. 0.038;  
RESULT 156  
ID AAC98220 standard; cDNA; 1798 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:230.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.3%; Score 64.4; DB 3; Length 1798;

Best Local Similarity 71.6%; Pred. No. 0.04;  
RESULT 157  
ID AAL16089 standard; cDNA; 495 BP.  
DE Human breast cancer expressed polynucleotide 8546.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 11.3%; Score 64.2; DB 4; Length 495;  
Best Local Similarity 66.7%; Pred. No. 0.04;  
RESULT 158  
ID ACN47369 standard; cDNA; 539 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-010-Q1-N6-F2, SEQ:2150.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.3%; Score 64.2; DB 13; Length 539;  
Best Local Similarity 71.8%; Pred. No. 0.041;  
RESULT 159  
ID ACN45362 standard; cDNA; 570 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A5, SEQ:143.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.3%; Score 64.2; DB 13; Length 570;  
Best Local Similarity 77.2%; Pred. No. 0.041;  
RESULT 160  
ID ACN6045 standard; DNA; 849 BP.  
DE Breast cancer related marker, seq id 7195.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.3%; Score 64.2; DB 11; Length 849;  
Best Local Similarity 66.7%; Pred. No. 0.042;  
RESULT 161  
ID ACA92436 standard; DNA; 1647 BP.  
DE DNA encoding human PMW-21.  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.3%; Score 64.2; DB 10; Length 1647;  
Best Local Similarity 89.6%; Pred. No. 0.043;  
RESULT 162  
ID AAI90382 standard; cDNA; 440 BP.  
DE Human polynucleotide SEQ ID NO 10442.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEO INC.  
Query Match 11.2%; Score 64; DB 4; Length 440;  
Best Local Similarity 78.5%; Pred. No. 0.043;  
RESULT 163  
ID ABO54884 standard; cDNA; 1339 BP.  
DE Human ovarian antigen HaOS253 cDNA, SEQ ID NO:764.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.2%; Score 64; DB 6; Length 1339;  
Best Local Similarity 73.2%; Pred. No. 0.046;  
RESULT 164  
ID ADP65758 standard; DNA; 1451 BP.  
DE Human Tax interaction protein 1 (TIP-1) DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 11.2%; Score 64; DB 11; Length 1451;  
Best Local Similarity 73.2%; Pred. No. 0.047;  
RESULT 165  
ID ADP65836 standard; DNA; 1451 BP.  
PD 29-MAY-2003.

DE Human Tax interaction protein 1 mRNA, complete cds DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 11.2%; Score 64; DB 11; Length 1451;  
Best Local Similarity 73.2%; Pred. No. 0.047;  
RESULT 166  
ID ADP24212 standard; cDNA; 1451 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:1390.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 11.2%; Score 64; DB 13; Length 1451;  
Best Local Similarity 73.2%; Pred. No. 0.047;  
RESULT 167  
ID ACN5513 standard; cDNA; 235 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-029-Q6-K6-H3, SEQ:9916.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.2%; Score 63.8; DB 13; Length 235;  
Best Local Similarity 55.9%; Pred. No. 0.045;  
RESULT 168  
ID ABV83658 standard; cDNA; 254 BP.  
DE Human breast specific gene SEQ ID NO 101.  
PN WO200266605-A2.  
PD 29-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 11.2%; Score 63.8; DB 6; Length 254;  
Best Local Similarity 67.9%; Pred. No. 0.045;  
RESULT 169  
ID AAK56575 standard; cDNA; 893 BP.  
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:1635.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.2%; Score 63.8; DB 4; Length 893;  
Best Local Similarity 85.5%; Pred. No. 0.049;  
RESULT 170  
ID AA206222 standard; DNA; 1621 BP.  
DE Human secreted protein gene No. 4.  
PN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.2%; Score 63.8; DB 2; Length 1621;  
Best Local Similarity 90.7%; Pred. No. 0.051;  
RESULT 171  
ID AAL16186 standard; cDNA; 449 BP.  
DE Human breast cancer expressed polynucleotide 8643.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 11.2%; Score 63.6; DB 4; Length 449;  
Best Local Similarity 63.4%; Pred. No. 0.051;  
RESULT 172  
ID ACN49090 standard; cDNA; 506 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-029-Q6-N6-A2, SEQ:3871.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.2%; Score 63.6; DB 13; Length 506;  
Best Local Similarity 73.6%; Pred. No. 0.051;  
RESULT 173  
ID ACN6134 standard; DNA; 1023 BP.  
DE Breast cancer related marker, seq id 7284.  
PN US2003099974-A1.  
PD 29-MAY-2003.

PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 63.6; DB 11; Length 1023;  
Best Local Similarity 63.4%; Pred. No. 0.053;  
RESULT 174  
ID AAV63176 standard; cDNA, 1307 BP.  
DE cDNA from clone dxk279\_1 which encodes a secreted protein.  
PN WO9840486-A2.  
PD 17-SEP-1998.  
PA (GENVY) GENETICS INST. INC.  
Query Match 11.2%; Score 63.6; DB 2; Length 1307;  
Best Local Similarity 71.2%; Pred. No. 0.054;  
RESULT 175  
ID AAA00681 standard; cDNA, 251 BP.  
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:672.  
PN WO958675-A2.  
PD 18-NOV-1999.  
PA (CHIR) CHIRON CORP.  
Query Match 11.1%; Score 63.4; DB 3; Length 251;  
Best Local Similarity 74.5%; Pred. No. 0.053;  
RESULT 176  
ID ABL87269 standard; cDNA, 451 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:10247.  
PN WO200193581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 11.1%; Score 63.4; DB 6; Length 451;  
Best Local Similarity 70.2%; Pred. No. 0.055;  
RESULT 177  
ID AAC79968 standard; cDNA, 815 BP.  
DE Human secreted protein encoding cDNA for gene 21.  
PN WO200058357-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.1%; Score 63.4; DB 3; Length 815;  
Best Local Similarity 78.4%; Pred. No. 0.057;  
RESULT 178  
ID AAC76992 standard; cDNA, 1662 BP.  
DE Human ORFX ORF2547 polynucleotide sequence SEQ ID NO:5093.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 11.1%; Score 63.4; DB 3; Length 1662;  
Best Local Similarity 70.2%; Pred. No. 0.06;  
RESULT 179  
ID ABQ74268 standard; cDNA, 6582 BP.  
DE Human 67076 transporter protein encoding cDNA SEQ ID NO:13.  
PN WO200255701-A2.  
PD 18-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.1%; Score 63.4; DB 6; Length 6582;  
Best Local Similarity 91.8%; Pred. No. 0.065;  
RESULT 180  
ID ADD37486 standard; cDNA, 6582 BP.  
DE Human transporter 67076 cDNA #1.  
PN US2003143675-A1.  
PD 31-JUL-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.1%; Score 63.4; DB 10; Length 6582;  
Best Local Similarity 91.8%; Pred. No. 0.065;  
RESULT 181  
ID ADI27965 standard; cDNA, 6582 BP.  
DE Human 67076 cDNA.  
PN US200315891-A1.  
PD 04-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.1%; Score 63.4; DB 12; Length 6582;  
Best Local Similarity 91.8%; Pred. No. 0.065;  
RESULT 182  
ID ABX42770 standard; cDNA, 212 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #7935.  
PN US2002137139-A1.  
PD 26-SEP-2002.

PA (BYAT/) BYATT J. C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W. C.  
Query Match 11.1%; Score 63.2; DB 8; Length 212;  
Best Local Similarity 74.1%; Pred. No. 0.057;  
RESULT 183  
ID AAI90374 standard; cDNA, 429 BP.  
DE Human polynucleotide SEQ ID NO 10434.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.1%; Score 63.2; DB 4; Length 429;  
Best Local Similarity 84.5%; Pred. No. 0.059;  
RESULT 184  
ID ACH21618 standard; cDNA, 430 BP.  
DE Human adult liver cDNA #1230.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R. T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M. C.  
PA (JONE/) JONES L. W.  
Query Match 11.1%; Score 63.2; DB 9; Length 430;  
Best Local Similarity 71.6%; Pred. No. 0.059;  
RESULT 185  
ID AAI84683 standard; cDNA, 437 BP.  
DE Human polynucleotide SEQ ID NO 4743.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.1%; Score 63.2; DB 4; Length 437;  
Best Local Similarity 84.5%; Pred. No. 0.059;  
RESULT 186  
ID ABV55470 standard; cDNA, 474 BP.  
DE Human prostate expression marker cDNA 55461.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 11.1%; Score 63.2; DB 5; Length 474;  
Best Local Similarity 84.5%; Pred. No. 0.06;  
RESULT 187  
ID ACN52740 standard; cDNA, 580 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-017-Q1-N6-H12, SEQ:7521.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (PENG/) PENG P. C. C.  
PA (FINC/) FINCHER K. L.  
PA (ZIEG/) ZIEGLER T. E.  
Query Match 11.1%; Score 63.2; DB 13; Length 580;  
Best Local Similarity 77.0%; Pred. No. 0.061;  
RESULT 188  
ID AAI19087 standard; cDNA, 598 BP.  
DE Human breast cancer expressed polynucleotide 11544.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 11.1%; Score 63.2; DB 4; Length 598;  
Best Local Similarity 71.6%; Pred. No. 0.061;  
RESULT 189  
ID AAF21763 standard; cDNA, 780 BP.  
DE Human breast and ovarian cancer associated antigen gene SEQ ID 150.  
PN WO200055173-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.1%; Score 63.2; DB 3; Length 780;  
Best Local Similarity 84.5%; Pred. No. 0.062;  
RESULT 190  
ID ADS73173 standard; cDNA, 882 BP.  
DE Human kidney tumour specific cDNA, SEQ ID 1770.  
PN US2003109434-A1.

PD 12-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 11.1%; Score 63.2; DB 7; Length 882;  
RESULT 191  
ID ADQ24215 standard; DNA; 1469 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7035.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 11.1%; Score 63.2; DB 12; Length 1469;  
RESULT 192  
ID AAT08077 standard; cDNA; 2365 BP.  
DE Human breast specific coding sequence SEQ ID NO: 23.  
PN WO200266607-A2.  
PD 23-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match  
Best Local Similarity 11.1%; Score 63.2; DB 6; Length 2365;  
RESULT 193  
ID ABV57207 standard; cDNA; 394 BP.  
DE Human prostate expression marker cDNA 57198.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 11.1%; Score 63; DB 5; Length 394;  
RESULT 194  
ID AAD02077 standard; cDNA; 396 BP.  
DE cDNA encoding rat pituitary hormone, pituitrone.  
PN WO200066778-A1.  
PD 09-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.1%; Score 63; DB 3; Length 396;  
RESULT 195  
ID ABV54374 standard; cDNA; 407 BP.  
DE Human prostate expression marker cDNA 54365.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 11.1%; Score 63; DB 5; Length 407;  
RESULT 196  
ID AA184858 standard; cDNA; 451 BP.  
DE Human polynucleotide SEQ ID NO 4918.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 11.1%; Score 63; DB 4; Length 451;  
RESULT 197  
ID ADQ24028 standard; DNA; 747 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6848.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 11.1%; Score 63; DB 12; Length 747;  
RESULT 198  
ID ADM03187 standard; cDNA; 2335 BP.  
DE Human cDNA of the invention SEQ ID NO:1872.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 11.1%; Score 63; DB 11; Length 2335;  
RESULT 199  
ID ABX71310 standard; cDNA; 2042 BP.  
DE Human transmembrane protein cDNA DKFZphutcl\_19f19.  
PN WO200112659-A2.  
PD 22-FEB-2001.

PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match  
Best Local Similarity 11.0%; Score 62.8; DB 5; Length 2042;  
RESULT 200  
ID ABR43731 standard; cDNA; 2292 BP.  
DE DNA encoding novel central nervous system protein #311.  
PN WO200155318-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.0%; Score 62.8; DB 4; Length 2292;  
RESULT 201  
ID AD154118 standard; cDNA; 2292 BP.  
DE cDNA encoding novel human protein seq id 321.  
PN US2004018969-A1.  
PD 29-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 11.0%; Score 62.8; DB 12; Length 2292;  
RESULT 202  
ID ADO23054 standard; DNA; 3650 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5874.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 11.0%; Score 62.8; DB 12; Length 3650;  
RESULT 203  
ID ABV58264 standard; cDNA; 201 BP.  
DE Human prostate expression marker cDNA 58255.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 11.0%; Score 62.6; DB 5; Length 201;  
RESULT 204  
ID ABV60873 standard; cDNA; 338 BP.  
DE Human prostate expression marker cDNA 60864.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 11.0%; Score 62.6; DB 5; Length 338;  
RESULT 205  
ID AA183450 standard; cDNA; 365 BP.  
DE Human polynucleotide SEQ ID NO 3510.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 11.0%; Score 62.6; DB 4; Length 365;  
RESULT 206  
ID AAC78443 standard; cDNA; 386 BP.  
DE Human cancer associated gene sequence SEQ ID NO:837.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 11.0%; Score 62.6; DB 3; Length 386;  
RESULT 207  
ID AA191255 standard; cDNA; 388 BP.  
DE Human polynucleotide SEQ ID NO 11315.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 11.0%; Score 62.6; DB 4; Length 388;  
RESULT 208  
ID AA183044 standard; cDNA; 424 BP.  
DE Human polynucleotide SEQ ID NO 3104.  
PN WO200164835-A2.

PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.0%; Score 62.6; DB 4; Length 424;  
Best Local Similarity 88.3%; Pred. No. 0.075;  
RESULT 209  
ID ADG3117 standard; DNA; 508 BP.  
DE Human DNA differentially expressed in patients with SLE SegID441.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 508;  
Best Local Similarity 70.9%; Pred. No. 0.076;  
RESULT 210  
ID AAD56360 standard; DNA; 543 BP.  
DE Human secreted protein-encoding gene 10 cDNA clone HDWG72, SEQ ID NO:20.  
PN WO2003038038-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.0%; Score 62.6; DB 9; Length 543;  
Best Local Similarity 65.9%; Pred. No. 0.076;  
RESULT 211  
ID ACN46017 standard; cDNA; 543 BP.  
DE Cccton primed seed EST Clone ID: LIB3825-013-Q1-N6-A6, SEQ:798.  
PN US200413340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 11.0%; Score 62.6; DB 13; Length 543;  
Best Local Similarity 70.9%; Pred. No. 0.076;  
RESULT 212  
ID AAC80546 standard; cDNA; 587 BP.  
DE Human secreted protein gene 16 SEQ ID NO:26.  
PN WO200058467-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.0%; Score 62.6; DB 3; Length 587;  
Best Local Similarity 76.2%; Pred. No. 0.077;  
RESULT 213  
ID AAL20298 standard; cDNA; 610 BP.  
DE Human breast cancer expressed polynucleotide 12755.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLERNIUM PREDICTIVE MEDICINE INC.  
Query Match 11.0%; Score 62.6; DB 4; Length 610;  
Best Local Similarity 70.9%; Pred. No. 0.077;  
RESULT 214  
ID AAL02545 standard; cDNA; 818 BP.  
DE Human reproductive system related antigen cDNA SEQ ID NO: 2546.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.0%; Score 62.6; DB 4; Length 818;  
Best Local Similarity 73.3%; Pred. No. 0.078;  
RESULT 215  
ID ADF81418 standard; DNA; 2311 BP.  
DE Leukemia-related DNA sequence #1974.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYUL-) UNIV LUDWIG MAXIMILIANS.  
PA (HARE/) HAPERLACH T.  
PA (SCHO/) SCHUCH C.  
PA (KERN/) KERN W.  
Query Match 11.0%; Score 62.6; DB 10; Length 2311;  
Best Local Similarity 59.1%; Pred. No. 0.083;  
RESULT 216  
ID ACN40655 standard; cDNA; 2311 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326739, SEQ ID NO:5566.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.

Query Match 11.0%; Score 62.6; DB 13; Length 2311;  
Best Local Similarity 59.1%; Pred. No. 0.083;  
RESULT 217  
ID AAT61590 standard; cDNA; 2589 BP.  
DE Human C-ITP1.  
PN WO9706182-A1.  
PD 20-FEB-1997.  
PA (TULA-) TULARIK INC.  
Query Match 11.0%; Score 62.6; DB 2; Length 2589;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 218  
ID ADR89078 standard; DNA; 2589 BP.  
DE IAP cleaving polypeptide encoding DNA.  
PN WO2004072241-A2.  
PD 26-AUG-2004.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Query Match 11.0%; Score 62.6; DB 13; Length 2589;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 219  
ID ADR89077 standard; DNA; 2589 BP.  
DE IAP cleaving polypeptide encoding DNA.  
PN WO2004072241-A2.  
PD 26-AUG-2004.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Query Match 11.0%; Score 62.6; DB 13; Length 2589;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 220  
ID AAS08630 standard; cDNA; 2732 BP.  
DE Human cDNA (DNA148380-2827) encoding a Strae6 homologue, PRO10282.  
PN WO200151635-A2.  
PD 19-JUL-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 4; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 221  
ID ABR33575 standard; cDNA; 2732 BP.  
DE cDNA encoding human PRO protein, Seq ID No 79.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 6; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 222  
ID ABR47278 standard; cDNA; 2732 BP.  
DE cDNA encoding human Strae6 (PRO10282) protein.  
PN WO200218608-A2.  
PD 07-MAR-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 6; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 223  
ID ACA68536 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 8; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 224  
ID ABR44265 standard; cDNA; 2732 BP.  
DE Human PRO10282 cDNA.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 9; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 225  
ID ABR44548 standard; cDNA; 2732 BP.  
DE Human PRO10282 cDNA.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 9; Length 2732;

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Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 226
ID ACD82215 standard; cDNA; 2732 BP.
DE Human secreted/transmembrane polypeptide PRO 10282 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 227
ID ABT43921 standard; cDNA; 2732 BP.
DE Human membrane bound receptor/protein PRO10282 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 228
ID ADB83569 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 229
ID ADB80675 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 230
ID ADB73216 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096568-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 231
ID ADB78298 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 9; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 232
ID ADB84946 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 233
ID ADB78052 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 234
ID ADB87118 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 235
ID ADB84700 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 236
ID ADB83815 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 237
ID ADB72970 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 238
ID ADC36808 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 239
ID ADC21798 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 240
ID ADC49629 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 241
ID ADC49028 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 242
ID ADC49545 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 243
ID ADC47406 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.0%; Score 62.6; DB 10; Length 2732;
Best Local Similarity 88.3%; Pred. No. 0.084;
RESULT 244
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ID ADC47151 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 245  
ID ADC78026 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 246  
ID ADD06261 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 247  
ID ADC77780 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 248  
ID ADD50743 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 249  
ID ADD50989 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 250  
ID ADD50470 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 251  
ID ADD50224 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 252  
ID ADD51235 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 253  
ID ACA66880 standard; cDNA; 2732 BP.

DE cDNA encoding human PRO polypeptide #40.  
PN US2003096635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 254  
ID ADC68632 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 10; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 255  
ID ADC48782 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 256  
ID ADE20953 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 257  
ID ADE05797 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 258  
ID ADD75026 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 259  
ID ADD75772 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 260  
ID ADD85004 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 261  
ID ADD86830 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 262  
ID ADE20707 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.

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PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 263
ID ADEB39004 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 264
ID ADE05551 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 265
ID ADD73536 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 266
ID ADD78376 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 267
ID ADE21199 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 268
ID ADD77314 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 269
ID ADE20461 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 270
ID ADD75526 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 271
ID ADD74042 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 272
ID ADD74288 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 273
ID ADD76018 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 274
ID ADE085510 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 275
ID ADE05059 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 276
ID ADD75272 standard; cDNA; 2732 BP.
DE Human PRO polynucleotide #40.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 277
ID ADD76816 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 278
ID ADE06584 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 279
ID ADD78052 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 11.0%; Score 62.6; DB 12; Length 2732;
RESULT 280
ID ADD77560 standard; cDNA; 2732 BP.
DE Novel human secreted and transmembrane protein PRO10282 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 281  
ID ADD77806 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 282  
ID ADD85264 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 283  
ID ADD73796 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 284  
ID ADD74534 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 285  
ID ADD77062 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 286  
ID ADD85756 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 287  
ID ADE05305 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 288  
ID ADD74780 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 289  
ID ADG05592 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003096959-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 290  
ID ADG27146 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 291  
ID ADG11209 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 292  
ID ADG11988 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 293  
ID ADF94545 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 294  
ID ADG06641 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 295  
ID ADH3985 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 296  
ID ADG34075 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 297  
ID ADI33545 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 298  
ID ADH69639 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;

Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 299  
ID AD129800 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 300  
ID ADM27197 standard; cDNA; 2732 BP.  
DE Novel human secreted and transmembrane protein PRO10282 cDNA.  
PN US200404179-A1.  
PD 04-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 301  
ID ADK6655 standard; cDNA; 2732 BP.  
DE Human PRO polynucleotide #40.  
PN US200404180-A1.  
PD 04-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2732;  
Best Local Similarity 88.3%; Pred. No. 0.084;  
RESULT 302  
ID ADO24087 standard; DNA; 2929 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6907.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 2929;  
Best Local Similarity 86.3%; Pred. No. 0.085;  
RESULT 303  
ID ADO22314 standard; DNA; 3058 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5134.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 11.0%; Score 62.6; DB 12; Length 3058;  
Best Local Similarity 83.5%; Pred. No. 0.085;  
RESULT 304  
ID ABS54600 standard; cDNA; 3082 BP.  
DE cDNA encoding human Ras-like protein.  
PN WO200262849-A2.  
PD 15-AUG-2002.  
PA (PEKE) PE CORP NY.  
Query Match 11.0%; Score 62.6; DB 6; Length 3082;  
Best Local Similarity 83.5%; Pred. No. 0.085;  
RESULT 305  
ID ABV54585 standard; cDNA; 257 BP.  
DE Human prostate expression marker cDNA 54576.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.9%; Score 62.4; DB 5; Length 257;  
Best Local Similarity 90.4%; Pred. No. 0.079;  
RESULT 306  
ID ABV58905 standard; cDNA; 337 BP.  
DE Human prostate expression marker cDNA 58896.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.9%; Score 62.4; DB 5; Length 337;  
Best Local Similarity 81.8%; Pred. No. 0.08;  
RESULT 307  
ID ACN87128 standard; DNA; 363 BP.  
DE Breast cancer related marker, seq id 8278.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.9%; Score 62.4; DB 11; Length 363;  
Best Local Similarity 69.2%; Pred. No. 0.081;

RESULT 308  
ID AAL25958 standard; cDNA; 422 BP.  
DE Human breast cancer expressed polynucleotide 18415.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.9%; Score 62.4; DB 4; Length 422;  
Best Local Similarity 86.2%; Pred. No. 0.081;  
RESULT 309  
ID ACN88851 standard; DNA; 422 BP.  
DE Breast cancer related marker, seq id 10001.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.9%; Score 62.4; DB 11; Length 422;  
Best Local Similarity 86.2%; Pred. No. 0.081;  
RESULT 310  
ID ACH4551 standard; cDNA; 445 BP.  
DE Human foetal brain cDNA #6276.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 10.9%; Score 62.4; DB 9; Length 445;  
Best Local Similarity 75.0%; Pred. No. 0.082;  
RESULT 311  
ID AAL19123 standard; cDNA; 466 BP.  
DE Human breast cancer expressed polynucleotide 11580.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.9%; Score 62.4; DB 4; Length 466;  
Best Local Similarity 86.2%; Pred. No. 0.082;  
RESULT 312  
ID ACN55464 standard; cDNA; 540 BP.  
DE Cotton androscium tissue EST Clone ID: LIB3828-024-Q6-N6-A3, SEQ:10245.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 10.9%; Score 62.4; DB 13; Length 540;  
Best Local Similarity 81.8%; Pred. No. 0.083;  
RESULT 313  
ID ACN45417 standard; cDNA; 565 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-G5, SEQ:198.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 10.9%; Score 62.4; DB 13; Length 565;  
Best Local Similarity 81.8%; Pred. No. 0.083;  
RESULT 314  
ID ABQ75355 standard; cDNA; 626 BP.  
DE Human lung specific nucleic acid sequence SEQ ID NO:94.  
PN WO200264788-A2.  
PD 22-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.9%; Score 62.4; DB 6; Length 626;  
Best Local Similarity 81.8%; Pred. No. 0.083;  
RESULT 315  
ID AAA26286 standard; cDNA; 2608 BP.  
DE Human secreted protein gene 6 SEQ ID NO:16.  
PN WO200011014-A1.  
PD 02-MAR-2000.  
PA (HOMA-) HUMAN GENOME SCI INC.  
Query Match 10.9%; Score 62.4; DB 3; Length 2608;

Best Local Similarity 86.2%; Pred. No. 0.091;  
RESULT 316  
ID AAF60867 standard; cDNA; 5714 BP.  
DE Human TAA R11 cDNA.  
PN DE19936563-A1.  
PD 08-FEB-2001.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Query Match 10.9%; Score 62.4; DB 4; Length 5714;  
Best Local Similarity 98.4%; Pred. No. 0.095;  
RESULT 317  
ID ABL3126 standard; DNA; 6338 BP.  
DE Human immune system associated gene SEQ ID NO: 1099.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIC-) EPIDENOMICS AG.  
Query Match 10.9%; Score 62.4; DB 6; Length 6338;  
Best Local Similarity 70.0%; Pred. No. 0.096;  
RESULT 318  
ID AAI87993 standard; cDNA; 416 BP.  
DE Human polynucleotide SEQ ID NO 8053.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.9%; Score 62.2; DB 4; Length 416;  
Best Local Similarity 84.3%; Pred. No. 0.088;  
RESULT 319  
ID ADI45027 standard; DNA; 448 BP.  
DE Human ovarian cancer DNA marker #18917.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.9%; Score 62.2; DB 5; Length 448;  
Best Local Similarity 61.3%; Pred. No. 0.088;  
RESULT 320  
ID ABV56397 standard; cDNA; 550 BP.  
DE Human prostate expression marker cDNA 56398.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.9%; Score 62.2; DB 5; Length 550;  
Best Local Similarity 67.2%; Pred. No. 0.09;  
RESULT 321  
ID AAF15652 standard; cDNA; 597 BP.  
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:87.  
PN WO200055174-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 10.9%; Score 62.2; DB 3; Length 597;  
Best Local Similarity 87.0%; Pred. No. 0.09;  
RESULT 322  
ID AAF16238 standard; cDNA; 1430 BP.  
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:673.  
PN WO200055174-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 10.9%; Score 62.2; DB 3; Length 1430;  
Best Local Similarity 76.0%; Pred. No. 0.095;  
RESULT 323  
ID ABA93758 standard; cDNA; 1537 BP.  
DE Human testis derived cDNA clone test3\_22124.  
PN WO200198454-A2.  
PD 27-DEC-2001.  
PA (GERH-) GERMAN HUMAN GENOME PROJECT.  
Query Match 10.9%; Score 62.2; DB 6; Length 1537;  
Best Local Similarity 89.3%; Pred. No. 0.095;  
RESULT 324  
ID AAF97884 standard; cDNA; 2329 BP.  
DE Human secreted protein cDNA, SEQ ID NO: 11.  
PN WO200121658-A1.  
PD 29-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.9%; Score 62.2; DB 4; Length 2329;  
Best Local Similarity 89.3%; Pred. No. 0.098;  
RESULT 325  
ID AAV40745 standard; cDNA; 2836 BP.  
DE C. felis esterase, nFE72836, coding sequence complementary strand.  
PN WO9821324-A1.  
PD 22-MAY-1998.  
PA (HESK-) HESKA CORP.  
Query Match 10.9%; Score 62.2; DB 2; Length 2836;  
Best Local Similarity 89.3%; Pred. No. 0.099;  
RESULT 326  
ID AAV40744 standard; cDNA; 2836 BP.  
DE C. felis esterase, nFE72836, coding sequence.  
PN WO9821324-A1.  
PD 22-MAY-1998.  
PA (HESK-) HESKA CORP.  
Query Match 10.9%; Score 62.2; DB 2; Length 2836;  
Best Local Similarity 89.3%; Pred. No. 0.099;  
RESULT 327  
ID AAD21170 standard; cDNA; 2836 BP.  
DE Ctenocephalides felis carboxylesterase full length cDNA, nFE72836.  
PN US6291222-B1.  
PD 18-SEP-2001.  
PA (HESK-) HESKA CORP.  
Query Match 10.9%; Score 62.2; DB 4; Length 2836;  
Best Local Similarity 89.3%; Pred. No. 0.099;  
RESULT 328  
ID ABL3416 standard; DNA; 6265 BP.  
DE Human immune system associated gene SEQ ID NO: 1389.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIC-) EPIDENOMICS AG.  
Query Match 10.9%; Score 62.2; DB 6; Length 6265;  
Best Local Similarity 76.8%; Pred. No. 0.1;  
RESULT 329  
ID ABV57838 standard; cDNA; 216 BP.  
DE Human prostate expression marker cDNA 57829.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.9%; Score 62; DB 5; Length 216;  
Best Local Similarity 72.7%; Pred. No. 0.092;  
RESULT 330  
ID ABV60981 standard; cDNA; 360 BP.  
DE Human prostate expression marker cDNA 60972.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.9%; Score 62; DB 5; Length 360;  
Best Local Similarity 70.3%; Pred. No. 0.095;  
RESULT 331  
ID ABX45485 standard; cDNA; 418 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #10650.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 10.9%; Score 62; DB 8; Length 418;  
Best Local Similarity 87.2%; Pred. No. 0.095;  
RESULT 332  
ID ACN58594 standard; cDNA; 486 BP.  
DE Cotton gynoecium tissue EST clone ID: L1B3829-010-06-M6-A7, SEQ:13375.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 10.9%; Score 62; DB 13; Length 486;  
Best Local Similarity 82.6%; Pred. No. 0.096;  
RESULT 333

ID AA27250 standard; cDNA; 985 BP.  
DE Human secreted protein cDNA encoding gene 18.  
PN MO9946289-A1.  
PD 15-SEP-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.9%; Score 62; DB 2; Length 985;  
Best Local Similarity 82.6%; Pred. No. 0.1;  
RESULT 334  
ID AAD29756 standard; DNA; 3459 BP.  
DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 2 DNA.  
PN WO200202630-A2.  
PD 10-JUN-2002.  
PA (SMITK) SMITHKLINE BEECHAM PLC.  
Query Match 10.9%; Score 62; DB 6; Length 3459;  
Best Local Similarity 70.3%; Pred. No. 0.11;  
RESULT 335  
ID AA18481 standard; cDNA; 388 BP.  
DE Human polynucleotide SEQ ID NO 4871.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.8%; Score 61.8; DB 4; Length 388;  
Best Local Similarity 74.3%; Pred. No. 0.1;  
RESULT 336  
ID ACH36139 standard; cDNA; 508 BP.  
DE Human endothelial cell cDNA #4272.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 10.8%; Score 61.8; DB 9; Length 508;  
Best Local Similarity 90.4%; Pred. No. 0.1;  
RESULT 337  
ID ABV58598 standard; cDNA; 608 BP.  
DE Human prostate expression marker cDNA 58589.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.8; DB 5; Length 608;  
Best Local Similarity 90.4%; Pred. No. 0.11;  
RESULT 338  
ID AD162858 standard; cDNA; 739 BP.  
DE Human apoptosis-associated cDNA SEQ ID 301.  
PN WO2003058021-A2.  
PD 17-JUL-2003.  
PA (XANT-) XANTOS BIOMEDICINE AG.  
Query Match 10.8%; Score 61.8; DB 10; Length 739;  
Best Local Similarity 53.5%; Pred. No. 0.11;  
RESULT 339  
ID AD162891 standard; cDNA; 739 BP.  
DE Human apoptosis-associated cDNA SEQ ID 334.  
PN WO2003058021-A2.  
PD 17-JUL-2003.  
PA (XANT-) XANTOS BIOMEDICINE AG.  
Query Match 10.8%; Score 61.8; DB 10; Length 739;  
Best Local Similarity 53.5%; Pred. No. 0.11;  
RESULT 340  
ID AD162874 standard; cDNA; 739 BP.  
DE Human apoptosis-associated cDNA SEQ ID 317.  
PN WO2003058021-A2.  
PD 17-JUL-2003.  
PA (XANT-) XANTOS BIOMEDICINE AG.  
Query Match 10.8%; Score 61.8; DB 10; Length 739;  
Best Local Similarity 53.5%; Pred. No. 0.11;  
RESULT 341  
ID AA194904 standard; cDNA; 754 BP.  
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 979.  
PN WO200166719-A1.  
PD 13-SEP-2001.  
PA (CHIB-) CHIBA PREFECTURE.

PA (HISM) HISAMITSU PHARM CO LTD.  
Query Match 10.8%; Score 61.8; DB 4; Length 754;  
Best Local Similarity 78.4%; Pred. No. 0.11;  
RESULT 342  
ID ABS57568 standard; cDNA; 1370 BP.  
DE Human SECP-24 cDNA from clone 7503458CD1 SEQ ID 24.  
PN WO200279441-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.8%; Score 61.8; DB 8; Length 1370;  
Best Local Similarity 77.3%; Pred. No. 0.11;  
RESULT 343  
ID AA11659 standard; cDNA; 1476 BP.  
DE Human secreted protein clone y690\_1 nucleotide sequence SEQ ID NO:83.  
PN WO200009552-A1.  
PD 24-FEB-2000.  
PA (GENT) GENENTICS INST INC.  
Query Match 10.8%; Score 61.8; DB 3; Length 1476;  
Best Local Similarity 85.2%; Pred. No. 0.11;  
RESULT 344  
ID AA265060 standard; cDNA; 1483 BP.  
DE Membrane-bound protein PRO1105 encoding cDNA.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GENT) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 3; Length 1483;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 345  
ID AAS46034 standard; cDNA; 1484 BP.  
DE Human DNA encoding PRO polypeptide sequence #110.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GENT) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 4; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 346  
ID AAF44206 standard; cDNA; 1484 BP.  
DE Human PRO1105 (UNQ548) nucleotide sequence SEQ ID NO:292.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GENT) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 5; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 347  
ID ACA89484 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 348  
ID ACA73494 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GENT) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 349  
ID ACA05809 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GENT) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 350  
ID ACA66643 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO protein #110.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GENT) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;

Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 351			
ID	ACH64353 standard; cDNA; 1484 BP.		
DE	Novel human secreted and transmembrane protein PRO1105 cDNA.		
PN	US2003003531-A1.		
PD	02-JAN-2003.		
PA	(GENTECH ) GENENTECH INC.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 352			
ID	ACF20218 standard; cDNA; 1484 BP.		
DE	Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.		
PN	US2003040063-A1.		
PD	27-FEB-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 353			
ID	ACF19604 standard; cDNA; 1484 BP.		
DE	Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.		
PN	US2003040064-A1.		
PD	27-FEB-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 354			
ID	ACD21892 standard; cDNA; 1484 BP.		
DE	Human secreted/transmembrane protein (PRO) cDNA #110.		
PN	US2003027267-A1.		
PD	06-FEB-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 355			
ID	ACF13057 standard; cDNA; 1484 BP.		
DE	Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.		
PN	US2003035160-A1.		
PD	20-FEB-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 356			
ID	ACD25160 standard; cDNA; 1484 BP.		
DE	Human secreted/transmembrane protein (PRO) cDNA #110.		
PN	US2003044925-A1.		
PD	06-MAR-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 357			
ID	ACF00209 standard; cDNA; 1484 BP.		
DE	Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.		
PN	US2003054474-A1.		
PD	20-MAR-2003.		
PA	(GENTECH ) GENENTECH INC.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 358			
ID	ACH72266 standard; cDNA; 1484 BP.		
DE	Novel human secreted and transmembrane protein PRO1105 cDNA.		
PN	US2003032114-A1.		
PD	13-FEB-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 359			
ID	ACD04790 standard; cDNA; 1484 BP.		
DE	Novel human secreted and transmembrane protein PRO1105 cDNA.		
PN	US2003032101-A1.		
PD	13-FEB-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 360			
ID	ACD18251 standard; cDNA; 1484 BP.		
DE	Human secreted/transmembrane protein (PRO) cDNA #110.		
PN	US2003036124-A1.		
PD	20-FEB-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	
RESULT 361			
ID	ACD18251 standard; cDNA; 1484 BP.		
DE	Human secreted/transmembrane protein (PRO) cDNA #110.		
PN	US2003036124-A1.		
PD	20-FEB-2003.		
Query Match	10.8%;	Score 61.8; DB 8;	Length 1484;
Best Local Similarity	67.4%;	Pred. No. 0.11;	

RESULT 361	ID ACD08258 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) CDNA #110.	
FN US2003040054-A1.	
PD 27-FEB-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 362	ID ACD8692 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.	
FN US2003036133-A1.	
PD 20-FEB-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 363	ID ACF70134 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.	
FN US2003036134-A1.	
PD 20-FEB-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 364	ID ACB12356 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.	
FN US2003022294-A1.	
PD 30-JAN-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 365	ID ACC74271 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219	
FN US2003027275-A1.	
PD 06-FEB-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 366	ID ACD15899 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.	
FN US2003027324-A1.	
PD 06-FEB-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 367	ID ACD25467 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.	
FN US2003036118-A1.	
PD 20-FEB-2003.	
PA (GETH ) GENENTECH INC.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 368	ID ACD17944 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.	
FN US2003036123-A1.	
PD 20-FEB-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 369	ID ACC88231 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219	
FN US2003036148-A1.	
PD 20-FEB-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 370	ID ACD21585 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.	
FN US2003040060-A1.	
PD 27-FEB-2003.	
Query Match	
Best Local Similarity	10.8%; Score 61.8; DB 8; Length 1484;
Pred. No. 0.11;	
RESULT 371	ID ACD18652 standard; cDNA; 1484 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 372  
ID ABX98262 standard; cDNA; 1484 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 219.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 373  
ID ACD14013 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 374  
ID ACD09793 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 375  
ID ACC88538 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 376  
ID ACD21278 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 377  
ID ABX75650 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1105.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 378  
ID ABX97853 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 379  
ID ACA97329 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 380  
ID ACA57792 standard; cDNA; 1484 BP.  
DE Human PRO1105 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 381  
ID ACD14320 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 382  
ID ACC91103 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 383  
ID ACC8845 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 384  
ID ACD07042 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 385  
ID ACA67493 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 386  
ID ACC81548 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 387  
ID ACC89152 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 388  
ID ACC86508 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 389  
ID ACC89766 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 390  
ID ACC92945 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 391  
ID ABX80812 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein cDNA, #120.  
PN US2003027162-A1.



PD 06-FEB-2003. 10.8%; Score 61.8; DB 8; Length 1484;  
Query Match  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 392  
ID ACA72573 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 393  
ID ACA89091 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 394  
ID ACA69827 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 395  
ID ACA96970 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 396  
ID ACA90966 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 397  
ID ACA70748 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 398  
ID ACA95258 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 399  
ID ACD44321 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO1105 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 400  
ID ACC86201 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 401  
ID ACC90073 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027271-A1.  
PD 06-FEB-2003.

Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 402  
ID ACD1681 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 403  
ID ACF1911 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 404  
ID ABX76855 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 405  
ID ACA73187 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003032300-A1.  
PD 30-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 406  
ID ACA68730 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 407  
ID ACA74574 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 408  
ID ACA70441 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 409  
ID ACD14627 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 410  
ID ACA68299 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 411  
ID ABX98764 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 412

ID ACC81241 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 413  
ID ACA95565 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 414  
ID ACDD4483 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 415  
ID ACC87924 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 416  
ID ACB12586 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 417  
ID ABX79492 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein cDNA, #120.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 418  
ID ACA96301 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 419  
ID ACA65075 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 420  
ID ACA73801 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 421  
ID ACA74213 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 422  
ID ACA96608 standard; cDNA; 1484 BP.

DE Human PRO polynucleotide #110.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 423  
ID ACD10714 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 424  
ID ACC91410 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 425  
ID ACA93513 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 426  
ID ACD02745 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 427  
ID ACC87310 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 428  
ID ACC85894 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 429  
ID ABX81195 standard; DNA; 1484 BP.  
DE Novel human secreted or transmembrane protein PRO511 DNA.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 430  
ID ACA65382 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 431  
ID ACA94199 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 8; Length 1484;  
67.4%; Pred. No. 0.11;  
RESULT 432  
ID ACA97943 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003036145-A1.

PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 433  
ID ACA91445 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 434  
ID ACA9659 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 435  
ID ACD16206 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 436  
ID ACD17367 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 437  
ID ACC92024 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 438  
ID ACA74881 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 439  
ID ACA91752 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 440  
ID ACA71396 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 441  
ID ACC90796 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 442  
ID ACA65806 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO protein #110.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;

RESULT 443  
ID ACA93011 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 444  
ID ACA94951 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 445  
ID ACD16513 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 446  
ID ACD1592 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 447  
ID ABX17095 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 448  
ID ABX16695 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein #110.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 449  
ID ACA67950 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
Query Match 10.8%; Score 61.8; DB 8; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 450  
ID ACA97636 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 451  
ID ACA99085 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 452  
ID ACC91717 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;

Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 453  
ID ACD1128 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 454  
ID ACD14978 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 455  
ID ACA88399 standard; cDNA; 1484 BP.  
DE Human secreted and transmembrane polypeptide PRO1105 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 456  
ID ACD81906 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO1105 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 457  
ID ACD11742 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 458  
ID ACC95871 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 459  
ID ACF16434 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003045455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 460  
ID ACF02552 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 461  
ID ACF02859 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 462  
ID ACF21446 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049769-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 463  
ID ACF10130 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 464  
ID ACF78023 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 465  
ID ACD46728 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 466  
ID ACD49491 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 467  
ID ACF28258 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 468  
ID ACD88948 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 469  
ID ACD84343 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 470  
ID ACD99117 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 471  
ID ADA77971 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003073180-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 472  
ID ACF4859 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 473  
ID ACD09179 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 474  
ID ACF11972 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 475  
ID ACF41206 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 476  
ID ACF1820 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 477  
ID ACF16127 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 478  
ID ACD31954 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 479  
ID ACF18762 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 480  
ID ACF09209 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 481  
ID ACF78330 standard; cDNA; 1484 BP.

DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 482  
ID ACF51929 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 483  
ID ACF25416 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 484  
ID ACF24209 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 485  
ID ACF63520 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 486  
ID ACF50394 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 487  
ID ACH07865 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 488  
ID ACF13671 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 489  
ID ACD41597 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 490  
ID ADA37803 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003008297-A1.

PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 491  
ID ACF32010 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 492  
ID ACF23288 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 493  
ID ACF39978 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 494  
ID ACD45500 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 495  
ID ACF53157 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 496  
ID ACF27337 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 497  
ID ACF45175 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 498  
ID ACF29793 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 499  
ID ACD89869 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068695-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 500  
ID ACD84650 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 501  
ID ACD98810 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 502  
ID ACF77102 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 503  
ID ACF76795 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 504  
ID ACF49780 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 505  
ID ACF50087 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 506  
ID ADA21489 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1105.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 507  
ID ACD09486 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 508  
ID ACD08565 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 509  
ID ACF12279 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036130-A1.

ID 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 510  
ID ACF94787 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 511  
ID ACD22506 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 512  
ID ACF15206 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 513  
ID ACF97301 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 514  
ID ACF92331 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 515  
ID ACF13978 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 516  
ID ACF14285 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 517  
ID ADA10276 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1105.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 518  
ID ACF09516 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 519

ID ACD45807 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 520  
ID ACD47956 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 521  
ID ACD67687 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 522  
ID ACF25495 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 523  
ID ACF29179 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 524  
ID ACD84957 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 525  
ID ACD84036 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 526  
ID ACD86027 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 527  
ID ACF30714 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 528  
ID ACF32317 standard; cDNA; 1484 BP.

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DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 529
ID ACHI1977 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 530
ID ACHI2284 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 531
ID ACDA0676 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 532
ID ADA17820 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO1105 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 533
ID ACF18148 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 534
ID ACF08595 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 535
ID ACF31396 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 536
ID ACF52236 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 537
ID ACDS0105 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 540
ID ACF24823 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 541
ID ACF46403 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 542
ID ACF27951 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 543
ID ACF89255 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 544
ID ACF63827 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 545
ID ACF60467 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 546
ID ACHI2591 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 61.8; DB 9; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
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Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 547  
ID ACHI0014 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 548  
ID ACDD3869 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 549  
ID ACD10407 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 550  
ID ACD12049 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 551  
ID ACF42434 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 552  
ID ADA27928 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 553  
ID ACF18455 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 554  
ID ACF02245 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 555  
ID ACF21753 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 556  
ID ACF10437 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073169-A1.

PD 17-APR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 557  
ID ACF33889 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 558  
ID ACF44851 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 559  
ID ACD90483 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 560  
ID ACD91096 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 561  
ID ACF30407 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 562  
ID ACD87106 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 563  
ID ACF60160 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 564  
ID ACF46710 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003067733-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 565  
ID ACF75567 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;

RESULT 566  
ID ADA79763 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 567  
ID ACF17227 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 568  
ID ACF22981 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 569  
ID ACF07981 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 570  
ID ACF08288 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 571  
ID ACF40592 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 572  
ID ACF53771 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 573  
ID ACD47035 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 574  
ID ACF47938 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 575  
ID ACF47324 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.

PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 576  
ID ACF46096 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 577  
ID ACD86185 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 578  
ID ACF52543 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 579  
ID ACF52850 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 580  
ID ACF64843 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 581  
ID ACF76488 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 582  
ID ACF61388 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 583  
ID ACF61695 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 584  
ID ACD30726 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;

Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 585  
ID ACD31647 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
RESULT 586  
ID ACD32568 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 587  
ID ACF17534 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 588  
ID ADA94508 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 589  
ID ACF07367 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 590  
ID ACF20525 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 591  
ID ACF21139 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 592  
ID ACF20832 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 593  
ID ACD47649 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 594  
ID ACF47631 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068736-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 595  
ID ACF53464 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 596  
ID ACD86799 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US200306867-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 597  
ID ACH05047 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 598  
ID ACF44544 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 599  
ID ADA81490 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 600  
ID ACD22199 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 601  
ID ACD24546 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 602  
ID ACD39749 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 603  
ID ACD40056 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;

RESULT 604  
ID ACF13364 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US200306446-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 605  
ID ACF03166 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US200304974-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 606  
ID ACF78637 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US200304978-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 607  
ID ACF11358 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US200307311-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 608  
ID ACF50701 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 609  
ID ACF34196 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 610  
ID ACD46421 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 611  
ID ACD48263 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 612  
ID ACF27644 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 613  
ID ACF24516 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PD 13-MAR-2003.

PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 614  
ID ACD85571 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 615  
ID ACD90176 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 616  
ID ACD83729 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 617  
ID ACF49166 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 618  
ID ACH07251 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 619  
ID ACH07558 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 620  
ID ACH08172 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 621  
ID ACH11363 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
Pred. No. 0.11;  
RESULT 622  
ID ACH11670 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003049767-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 623  
ID ACH10321 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 624  
ID ACF01324 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 625  
ID ACF40899 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 626  
ID ACD24239 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 627  
ID ACD1340 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 628  
ID ACF17841 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 629  
ID ADA38733 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 630  
ID ACF32624 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 631  
ID ACF40285 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 632  
ID ACF48245 standard; cDNA; 1484 BP.

DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 633  
ID ACF38194 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 634  
ID ACF25130 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 635  
ID ACF27030 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 636  
ID ACF29486 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 637  
ID ACD87720 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 638  
ID ACF76181 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 639  
ID ACF49473 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 640  
ID ACF43930 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 641  
ID ACH06275 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 642  
ID ACH05682 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 643  
ID ADA83288 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 644  
ID ACC92638 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 645  
ID ACC93252 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 646  
ID ACF19297 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 647  
ID ACD12988 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 648  
ID ACP06446 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 649  
ID ACC94480 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 650  
ID ACC97908 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 651  
ID ACC94173 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027270-A1.  
PD 06-FEB-2003.

Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 652  
ID ACF42127 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 653  
ID ACD31033 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 654  
ID ACD43062 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 655  
ID ACD43369 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 656  
ID ACF14899 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 657  
ID ADA92854 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 658  
ID ACF01631 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 659  
ID ACF31703 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 660  
ID ACD67380 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 661  
ID ACD48570 standard; cDNA; 1484 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 662  
ID ACD4877 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 663  
ID ACF51315 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 664  
ID ACF54078 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 665  
ID ACF25802 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 666  
ID ACF39115 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 667  
ID ACF28872 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 668  
ID ACD9789 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 669  
ID ACD8492 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 670  
ID ACH05354 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.

PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 671  
ID ACF65150 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 672  
ID ADB20331 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 673  
ID ACF43623 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 674  
ID ACH09093 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 675  
ID ACH09400 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 676  
ID ADA7583 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 677  
ID ACF09823 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 678  
ID ACF51008 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 679  
ID ACF23902 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068763-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 680  
 ID ACD88334 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US200306869-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 681  
 ID ACH09707 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003049776-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 682  
 ID ACH10628 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003049780-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 683  
 ID ACD11435 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003036126-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 684  
 ID ACC96485 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003044924-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 685  
 ID ACC98515 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003044927-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 686  
 ID ACF41820 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003040072-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 687  
 ID ACF16741 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003040073-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 688  
 ID ACD32261 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003054475-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 689  
 ID ACD30419 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.

PN US2003032124-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 690  
 ID ACD41290 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003064467-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 691  
 ID ACF07674 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003049759-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 692  
 ID ACF31089 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003064455-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 693  
 ID ACF77409 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003054465-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 694  
 ID ACF11051 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003073170-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 695  
 ID ACF32931 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003073176-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 696  
 ID ACF26109 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003068717-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 697  
 ID ACD83422 standard; cDNA; 1484 BP.  
 DE Human PRO polynucleotide #110.  
 PN US2003068728-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.8%; Score 61.8; DB 9; Length 1484;  
 RESULT 698  
 ID ACF23595 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) CDNA #110.  
 PN US2003068764-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.



Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 699  
ID ACF43009 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 700  
ID ACF4316 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 701  
ID ACH05968 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO polypeptide #110.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 702  
ID ACH08786 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 703  
ID ACC90380 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 704  
ID ACF10744 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 705  
ID ACC93559 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 706  
ID ACC96178 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 707  
ID ACD24853 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 708  
ID ACF01938 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.

PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 709  
ID ACF22060 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 710  
ID ACF22674 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 711  
ID ACF08902 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 712  
ID ACF33238 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 713  
ID ACF54692 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 714  
ID ACF48552 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 715  
ID ACD47342 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 716  
ID ACD49184 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 717  
ID ACF37887 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068686-A1.

PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 718  
 ID ACF30100 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003073178-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 719  
 ID ACD87413 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #110.  
 PN US2003068774-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 720  
 ID ACF62002 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003104538-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 721  
 ID ACH10935 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #110.  
 PN US2003049781-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 722  
 ID ACD10100 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #110.  
 PN US2003036158-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 723  
 ID ACD16825 standard; cDNA; 1484 BP.  
 DE cDNA encoding human PRO polypeptide #110.  
 PN US2003036151-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 724  
 ID ACH65467 standard; cDNA; 1484 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
 PN US2003044806-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 725  
 ID ACC99122 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003040067-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 726  
 ID ACF00516 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003054456-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 727  
 ID ACD40983 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #110.

PN US2003054482-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 728  
 ID ACF14592 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003054457-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 729  
 ID ACF22367 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003059883-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 730  
 ID ACF78944 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003049764-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 731  
 ID ACF11665 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003073177-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 732  
 ID ADA22415 standard; cDNA; 1484 BP.  
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO1105.  
 PN US2003040473-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 733  
 ID ACF51622 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003064442-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 734  
 ID ACF33545 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003064450-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 735  
 ID ACD49798 standard; cDNA; 1484 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #110.  
 PN US2003068731-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
 Best Local Similarity 67.4%; Pred. No. 0.11;  
 RESULT 736  
 ID ACF37580 standard; cDNA; 1484 BP.  
 DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
 PN US2003068683-A1.  
 PD 10-APR-2003.

Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 737  
ID ACF28565 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 738  
ID ACD88641 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 739  
ID ACF75260 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 740  
ID ACF61081 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 741  
ID ACF44237 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 742  
ID ACH08479 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 743  
ID ACD39457 standard; cDNA; 1484 BP.  
DE Human cDNA encoding PRO511.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 744  
ID ACC3866 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 745  
ID ACD20971 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 746  
ID ACF06753 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 747  
ID ACD20664 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 748  
ID ACD22813 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 749  
ID ACF41513 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 750  
ID ADA06581 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #90.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 751  
ID ADA39274 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 752  
ID ACF07060 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 753  
ID ACF77716 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 754  
ID ACD46114 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 755  
ID ACF47017 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 756

ID ACF5385 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 757  
ID ACF45789 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 758  
ID ACF45482 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 759  
ID ACF38501 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 760  
ID ACD89562 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 761  
ID ACD85264 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 762  
ID ACD8578 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 763  
ID ACF75874 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 764  
ID ACF60774 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 765  
ID ACH05661 standard; cDNA; 1484 BP.

DE cDNA encoding human PRO polypeptide #110.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 766  
ID ADA82654 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 767  
ID ADB96300 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 768  
ID ACF55920 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 9; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 769  
ID ACF55306 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 770  
ID ADB85962 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 771  
ID ACF56227 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 772  
ID ACF56534 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 773  
ID ACF55613 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 774  
ID ACF54999 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003068771-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 775  
ID ADC57772 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 776  
ID ADC55136 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 777  
ID ADC12003 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 778  
ID ADC56425 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 779  
ID ADC07480 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 780  
ID ADC11470 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 781  
ID ADC14592 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 782  
ID ADD08124 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 783  
ID ADC81949 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 784  
ID ADD07591 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;

Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 785  
ID ADC82482 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003059835-A1.  
PD 27-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 786  
ID ADD05692 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 787  
ID ADD08662 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 788  
ID ADD06911 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 789  
ID ADC83158 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 790  
ID ADD55265 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 791  
ID ADD56223 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 792  
ID ADD54661 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #90.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 793  
ID ADE25815 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 794  
ID ADD89050 standard; cDNA; 1484 BP.  
DE Encoding sequence TAT253.  
PN WO2003057160-A2.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.

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Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 795
ID ADE26282 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 796
ID ADF67219 standard; cDNA; 1484 BP.
DE Human PRO1105 nucleotide sequence SEQ ID NO:292.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 797
ID ADG02687 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 798
ID ADG01394 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 799
ID ADP95569 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 800
ID ADG12384 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 801
ID ADH09044 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 802
ID ADI35473 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 803
ID ADH99965 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 804
ID ABX78637 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #110.
PD 20-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 805
ID ACN75609 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 806
ID ACN71089 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 807
ID ACC87617 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 808
ID ACC87003 standard; cDNA; 1484 BP.
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 809
ID ACD04176 standard; cDNA; 1484 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #110.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 810
ID ABX77896 standard; cDNA; 1484 BP.
DE Human PRO polynucleotide #90.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 811
ID ABX80308 standard; cDNA; 1484 BP.
DE Novel human secreted or transmembrane protein PRO511 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 812
ID ACN69214 standard; cDNA; 1484 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1105.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 813
ID ACN69507 standard; cDNA; 1484 BP.
DE cDNA encoding human PRO polypeptide #110.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
  10.8%; Score 61.8; DB 10; Length 1484;
Best Local Similarity 67.4%; Pred. No. 0.11;
RESULT 814
ID ACN90352 standard; cDNA; 1484 BP.
DE Novel human secreted and transmembrane protein PRO1105 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
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Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 815  
ID ACC89459 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 816  
ID ABX90285 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein cDNA, #120.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 817  
ID ACA98250 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 818  
ID ACA93892 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 819  
ID ACD15285 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 820  
ID ACD08872 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 821  
ID ACC96792 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 822  
ID ACF15513 standard; cDNA; 1484 BP.  
DE Human secreted polypeptide PRO1105-encoding cDNA, SEQ ID NO:219.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 823  
ID ABX64131 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO1105 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 824  
ID ACA72880 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 825  
ID ACD03052 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 826  
ID ACD01867 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 827  
ID ACA92059 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 10.8%; Score 61.8; DB 10; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 828  
ID ADL32825 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 11; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 829  
ID ADM30359 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 11; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 830  
ID ADE74356 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 831  
ID ADE74968 standard; cDNA; 1484 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #110.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 832  
ID ADF35418 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO1105 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 833  
ID ADG11668 standard; cDNA; 1484 BP.  
DE cDNA encoding human PRO1105 polypeptide.  
PN US2003228653-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 834  
ID ADF96181 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003215909-A1.  
PD 20-NOV-2003.

Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 835  
ID ADG04452 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 836  
ID ADG00612 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 837  
ID ADG82868 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 838  
ID ADH26149 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 839  
ID ADH19538 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003282656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 840  
ID ADH33118 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 841  
ID ADH21031 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003283358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 842  
ID ADH20071 standard; cDNA; 1484 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1105.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 843  
ID ADJ54857 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;

RESULT 844  
ID ADJ64628 standard; cDNA; 1484 BP.  
DE Human PRO polynucleotide #110.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 845  
ID ADM31524 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 846  
ID ADM36571 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 847  
ID ADM40376 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 848  
ID ADN37994 standard; cDNA; 1484 BP.  
DE Novel human secreted and transmembrane protein PRO1105 cDNA.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 61.8; DB 12; Length 1484;  
Best Local Similarity 67.4%; Pred. No. 0.11;  
RESULT 849  
ID AAV41257 standard; cDNA; 2082 BP.  
DE Mouse neuronal PAS domain protein NPAS1 cDNA.  
PN WO9831804-A1.  
PD 23-JUL-1998.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 10.8%; Score 61.8; DB 2; Length 2082;  
Best Local Similarity 77.3%; Pred. No. 0.11;  
RESULT 850  
ID ACC69465 standard; cDNA; 2350 BP.  
DE Human malignant neoplasm related protein encoding cDNA SEQ ID NO:1.  
PN WO2003025135-A2.  
PD 27-MAR-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.8%; Score 61.8; DB 8; Length 2350;  
Best Local Similarity 77.3%; Pred. No. 0.11;  
RESULT 851  
ID ADK61480 standard; DNA; 246 BP.  
DE Ovarian cancer-related DNA #635 with altered ovarian cancer expression.  
PN WO2003068054-A2.  
PD 21-AUG-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 10.8%; Score 61.6; DB 10; Length 246;  
Best Local Similarity 76.0%; Pred. No. 0.11;  
RESULT 852  
ID ADK61470 standard; DNA; 320 BP.  
DE Ovarian cancer-related DNA #625 with altered ovarian cancer expression.  
PN WO2003068054-A2.  
PD 21-AUG-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 10.8%; Score 61.6; DB 10; Length 320;  
Best Local Similarity 76.0%; Pred. No. 0.11;



Best Local Similarity 73.1%; Pred. No. 0.11;  
RESULT 853  
ID ABV56614 standard; cDNA; 442 BP.  
DE Human prostate expression marker cDNA 56605.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 442;  
Best Local Similarity 70.1%; Pred. No. 0.11;  
RESULT 854  
ID ABV48154 standard; cDNA; 458 BP.  
DE Human prostate expression marker cDNA 48145.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 458;  
Best Local Similarity 76.0%; Pred. No. 0.11;  
RESULT 855  
ID AAS41678 standard; cDNA; 524 BP.  
DE cDNA encoding novel human enzyme polypeptide #894.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.8%; Score 61.6; DB 4; Length 524;  
Best Local Similarity 79.3%; Pred. No. 0.11;  
RESULT 856  
ID ABV54778 standard; cDNA; 541 BP.  
DE Human prostate expression marker cDNA 54769.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 541;  
Best Local Similarity 88.2%; Pred. No. 0.11;  
RESULT 857  
ID AAS29155 standard; cDNA; 713 BP.  
DE cDNA encoding for human DNA-binding protein #126.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 713;  
Best Local Similarity 79.3%; Pred. No. 0.12;  
RESULT 858  
ID ABS68295 standard; cDNA; 713 BP.  
DE cDNA encoding human DNA-binding protein #126.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BAR/) BARASH S C.  
Query Match 10.8%; Score 61.6; DB 6; Length 713;  
Best Local Similarity 79.3%; Pred. No. 0.12;  
RESULT 859  
ID ADC25289 standard; cDNA; 713 BP.  
DE Human cDNA from extracellular matrix gene 126.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.8%; Score 61.6; DB 10; Length 713;  
Best Local Similarity 79.3%; Pred. No. 0.12;  
RESULT 860  
ID AAS41417 standard; cDNA; 785 BP.  
DE cDNA encoding novel human enzyme polypeptide #633.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.8%; Score 61.6; DB 4; Length 785;  
Best Local Similarity 79.3%; Pred. No. 0.12;  
RESULT 861  
ID ADQ23347 standard; DNA; 1084 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8167.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 10.8%; Score 61.6; DB 12; Length 1084;  
Best Local Similarity 88.2%; Pred. No. 0.12;  
RESULT 862  
ID ADB58406 standard; DNA; 1591 BP.  
DE Toxicity-related gene, SEQ ID 3432.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.8%; Score 61.6; DB 10; Length 1591;  
Best Local Similarity 83.3%; Pred. No. 0.12;  
RESULT 863  
ID ADB52986 standard; DNA; 1591 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3528.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.8%; Score 61.6; DB 10; Length 1591;  
Best Local Similarity 83.3%; Pred. No. 0.12;  
RESULT 864  
ID ABR42053 standard; DNA; 1591 BP.  
DE Toxicity modelling related rat gene SEQ ID NO 1755.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.8%; Score 61.6; DB 10; Length 1591;  
Best Local Similarity 83.3%; Pred. No. 0.12;  
RESULT 865  
ID ACN39160 standard; cDNA; 2126 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA35414, SEQ ID NO:3133.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.6; DB 13; Length 2126;  
Best Local Similarity 65.0%; Pred. No. 0.12;  
RESULT 866  
ID ADP23018 standard; cDNA; 2126 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:112.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 10.8%; Score 61.6; DB 13; Length 2126;  
Best Local Similarity 65.0%; Pred. No. 0.12;  
RESULT 867  
ID ABV23975 standard; cDNA; 2843 BP.  
DE Human prostate expression marker cDNA 23966.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 868  
ID ABV24137 standard; cDNA; 2843 BP.  
DE Human prostate expression marker cDNA 24128.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 869  
ID ABV20348 standard; cDNA; 2843 BP.  
DE Human prostate expression marker cDNA 20339.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 870  
ID ABV20569 standard; cDNA; 2843 BP.  
DE Human prostate expression marker cDNA 20560.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;

Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 871  
ID ABV29860 standard; cDNA; 2843 BP.  
DE Human prostate expression marker CDNA 29851.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 872  
ID ABV29747 standard; cDNA; 2843 BP.  
DE Human prostate expression marker CDNA 29738.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 873  
ID ABV23868 standard; cDNA; 2843 BP.  
DE Human prostate expression marker CDNA 23859.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 874  
ID ABV26408 standard; cDNA; 2843 BP.  
DE Human prostate expression marker CDNA 26399.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 875  
ID ABV28716 standard; cDNA; 2843 BP.  
DE Human prostate expression marker CDNA 28707.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 876  
ID ABV22885 standard; cDNA; 2843 BP.  
DE Human prostate expression marker CDNA 22876.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 877  
ID ABV26181 standard; cDNA; 2843 BP.  
DE Human prostate expression marker CDNA 26172.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.6; DB 5; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 878  
ID ACN92620 standard; DNA; 2843 BP.  
DE Breast cancer related marker, seq id 13770.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.8%; Score 61.6; DB 11; Length 2843;  
Best Local Similarity 88.2%; Pred. No. 0.13;  
RESULT 879  
ID ABL92106 standard; cDNA; 4168 BP.  
DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 235.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 10.8%; Score 61.6; DB 6; Length 4168;  
Best Local Similarity 83.3%; Pred. No. 0.13;

RESULT 880  
ID ABX72031 standard; DNA; 4168 BP.  
DE DNA encoding human tumour endothelial marker TEM 21.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 10.8%; Score 61.6; DB 10; Length 4168;  
Best Local Similarity 83.3%; Pred. No. 0.13;  
RESULT 881  
ID ABV56502 standard; cDNA; 239 BP.  
DE Human prostate expression marker CDNA 56493.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.4; DB 5; Length 239;  
Best Local Similarity 91.5%; Pred. No. 0.12;  
RESULT 882  
ID ABL66854 standard; DNA; 257 BP.  
DE Lung cancer related gene sequence SEQ ID NO:5191.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AYAL-) AYALON PHARM.  
Query Match 10.8%; Score 61.4; DB 6; Length 257;  
Best Local Similarity 98.4%; Pred. No. 0.12;  
RESULT 883  
ID ABN96764 standard; DNA; 257 BP.  
DE Gene #3262 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.8%; Score 61.4; DB 6; Length 257;  
Best Local Similarity 98.4%; Pred. No. 0.12;  
RESULT 884  
ID ACN47867 standard; cDNA; 311 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-016-Q1-N6-B4, SEQ:2648.  
PN US200412340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIRG/) ZIRGLER T E.  
Query Match 10.8%; Score 61.4; DB 13; Length 311;  
Best Local Similarity 81.6%; Pred. No. 0.12;  
RESULT 885  
ID AAI84413 standard; cDNA; 332 BP.  
DE Human polynucleotide SEQ ID NO 4473.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.8%; Score 61.4; DB 4; Length 332;  
Best Local Similarity 73.2%; Pred. No. 0.12;  
RESULT 886  
ID AAI84912 standard; cDNA; 364 BP.  
DE Human polynucleotide SEQ ID NO 4972.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.8%; Score 61.4; DB 4; Length 364;  
Best Local Similarity 69.7%; Pred. No. 0.12;  
RESULT 887  
ID ABX44260 standard; cDNA; 377 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #9425.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 10.8%; Score 61.4; DB 8; Length 377;  
Best Local Similarity 77.9%; Pred. No. 0.12;  
RESULT 888  
ID ABV56784 standard; cDNA; 505 BP.  
DE Human prostate expression marker CDNA 56775.

PN W0200160860-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.8%; Score 61.4; DB 5; Length 505;  
Best Local Similarity 91.5%; Pred. No. 0.12;  
RESULT 899  
ID AAI95102 standard; cDNA; 794 BP.  
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1177.  
PN W0200166719-A1.  
PD 13-SEP-2001.  
PA (CHIB-) CHIBA PREFECTURE.  
PA (HISM-) HISAMITSU PHARM CO LTD.  
Query Match 10.8%; Score 61.4; DB 4; Length 794;  
Best Local Similarity 66.4%; Pred. No. 0.13;  
RESULT 890  
ID ABA93750 standard; cDNA; 1316 BP.  
DE Human cell structure and motility cDNA clone test\_16b5.  
PN W0200198454-A2.  
PD 27-DEC-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 10.8%; Score 61.4; DB 6; Length 1316;  
Best Local Similarity 91.5%; Pred. No. 0.13;  
RESULT 891  
ID AAX16675 standard; DNA; 1554 BP.  
DE Xenopus WA545 protein encoding DNA.  
PN W09902678-A1.  
PD 21-JAN-1999.  
PA (GEMV-) GENETICS INST INC.  
PA (WHEB-) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 10.8%; Score 61.4; DB 2; Length 1554;  
Best Local Similarity 91.5%; Pred. No. 0.13;  
RESULT 892  
ID ABK35953 standard; cDNA; 1554 BP.  
DE cDNA sequence #344 encoding novel human secreted protein.  
PN W0200177289-A2.  
PD 18-OCT-2001.  
PA (GEMV-) GENETICS INST INC.  
Query Match 10.8%; Score 61.4; DB 6; Length 1554;  
Best Local Similarity 91.5%; Pred. No. 0.13;  
RESULT 893  
ID ADJ74992 standard; DNA; 1554 BP.  
DE Marker gene SEQ ID NO:244.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 10.8%; Score 61.4; DB 12; Length 1554;  
Best Local Similarity 65.9%; Pred. No. 0.13;  
RESULT 894  
ID AAX60810 standard; DNA; 1656 BP.  
DE Human secreted protein encoding DNA (clone yb8-1).  
PN W09926961-A1.  
PD 03-JUN-1999.  
PA (GEMV-) GENETICS INST INC.  
Query Match 10.8%; Score 61.4; DB 2; Length 1656;  
Best Local Similarity 91.5%; Pred. No. 0.13;  
RESULT 895  
ID AAS59216 standard; cDNA; 1656 BP.  
DE Human cDNA encoding a secreted protein yb8\_1.  
PN W0200175068-A2.  
PD 11-OCT-2001.  
PA (GEMV-) GENETICS INST INC.  
Query Match 10.8%; Score 61.4; DB 4; Length 1656;  
Best Local Similarity 91.5%; Pred. No. 0.13;  
RESULT 896  
ID ABA90885 standard; cDNA; 1656 BP.  
DE Human polynucleotide SEQ ID NO 19.  
PN US2001039335-A1.  
PD 08-NOV-2001.  
PA (JACO-) JACOBS K.  
PA (MCCO-) MCCOY J M.  
PA (LAVA-) LAVALLE E R.  
PA (COLL-) COLLINS-RACIE L A.  
PA (EVAN-) EVANS C.

PA (MERB-) MERBERG D.  
PA (TREA-) TREACY M.  
PA (AGOS-) AGOSTINO M J.  
PA (STRI-) STEININGER R J.  
PA (SPAU-) SPAULDING V.  
PA (WONG-) WONG G G.  
PA (CLAR-) CLARK H.  
PA (FECH-) FECHTEL K.  
Query Match 10.8%; Score 61.4; DB 6; Length 1656;  
Best Local Similarity 91.5%; Pred. No. 0.13;  
RESULT 897  
ID AAC98993 standard; cDNA; 1756 BP.  
DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:221.  
PN W0200055320-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.8%; Score 61.4; DB 3; Length 1756;  
Best Local Similarity 86.7%; Pred. No. 0.13;  
RESULT 898  
ID AAX20412 standard; DNA; 1761 BP.  
DE Human secreted protein gene 1.  
PN W09906423-A1.  
PD 11-FEB-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.8%; Score 61.4; DB 2; Length 1761;  
Best Local Similarity 86.7%; Pred. No. 0.13;  
RESULT 899  
ID ADD90196 standard; cDNA; 1761 BP.  
DE Novel human secreted protein cDNA seq id 11.  
PN US2003199683-A1.  
PD 23-OCT-2003.  
PA (RUBE-) RUBEN S M.  
PA (FENG-) FENG P.  
PA (LAFU-) LAFLEUR D W.  
PA (MOOR-) MOORE P A.  
PA (SHIY-) SHI Y.  
PA (KYAM-) KYAM H.  
PA (LIYY-) LI Y.  
PA (ZENG-) ZENG Z.  
PA (CART-) CARTER K C.  
PA (ENDR-) ENDRESS G A.  
PA (WEIR-) WEI Y.  
PA (FANP-) FAN P.  
PA (ROSE-) ROSEN C A.  
Query Match 10.8%; Score 61.4; DB 10; Length 1761;  
Best Local Similarity 86.7%; Pred. No. 0.13;  
RESULT 900  
ID ADG90015 standard; cDNA; 1761 BP.  
DE Human cDNA from secreted protein gene 1.  
PN US200316541-A1.  
PD 04-SEP-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.8%; Score 61.4; DB 10; Length 1761;  
Best Local Similarity 86.7%; Pred. No. 0.13;  
RESULT 901  
ID AAZ33323 standard; cDNA; 2364 BP.  
DE Human secreted protein clone pm749\_8 nucleotide sequence SEQ ID NO:15.  
PN W09957132-A1.  
PD 11-NOV-1999.  
PA (GEMV-) GENETICS INST INC.  
Query Match 10.8%; Score 61.4; DB 3; Length 2364;  
Best Local Similarity 91.5%; Pred. No. 0.13;  
RESULT 902  
ID ABL34984 standard; cDNA; 2538 BP.  
DE Rat cDNA isolated from skin cells SEQ ID NO: 511.  
PN W0200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 10.8%; Score 61.4; DB 6; Length 2538;  
Best Local Similarity 91.5%; Pred. No. 0.13;  
RESULT 903  
ID AAF28356 standard; cDNA; 2850 BP.  
DE Human BSR Gene X cDNA.

PN WO200100825-A2.  
PD 04-JAN-2001.  
PA (CHIR ) CHIRON CORP.  
Query Match  
Best Local Similarity 10.8%; Score 61.4; DB 4; Length 2850;  
RESULT 904  
ID AAS14756 standard; cDNA; 2968 BP.  
DE Human protease cDNA.  
PN US6294368-B1.  
PD 25-SEP-2001.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 10.8%; Score 61.4; DB 5; Length 2968;  
RESULT 905  
ID ABL41523 standard; cDNA; 2968 BP.  
DE Human metalloprotease encoding sequence.  
PN US6344352-B1.  
PD 05-FEB-2002.  
PA (PEKE ) PE CORP.  
Query Match  
Best Local Similarity 10.8%; Score 61.4; DB 6; Length 2968;  
RESULT 906  
ID ADG47800 standard; cDNA; 2968 BP.  
DE Human protease cDNA.  
PN US2002137183-A1.  
PD 26-SEP-2002.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 10.8%; Score 61.4; DB 12; Length 2968;  
RESULT 907  
ID ABZ23375 standard; cDNA; 445 BP.  
DE Reverse complement of oestrogen receptor alpha cofactor CF17 cDNA.  
PN WO200270689-A2.  
PD 12-SEP-2002.  
PA (LION-) LION BIOSCIENCE AG.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 6; Length 445;  
RESULT 908  
ID ABZ23374 standard; cDNA; 445 BP.  
DE Nucleotide sequence of oestrogen receptor alpha cofactor CF17.  
PN WO200270689-A2.  
PD 12-SEP-2002.  
PA (LION-) LION BIOSCIENCE AG.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 6; Length 445;  
RESULT 909  
ID ACN87190 standard; DNA; 592 BP.  
DE Breast cancer related marker, seq id 8340.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 11; Length 592;  
RESULT 910  
ID AAV58509 standard; cDNA; 789 BP.  
DE 3' fragment of prostate tumour specific gene J1-21.  
PN WO9837418-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 2; Length 789;  
RESULT 911  
ID AAV61275 standard; cDNA; 789 BP.  
DE 3' cDNA sequence of prostate tumour clone J1-21.  
PN WO9837093-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 2; Length 789;  
RESULT 912  
ID AAA06272 standard; cDNA; 789 BP.  
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:32.  
PN WO20000419-A2.

PD 27-JAN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 3; Length 789;  
RESULT 913  
ID ABS71177 standard; cDNA; 789 BP.  
DE Human prostate tumour protein partial DNA sequence #32.  
PN US2002090372-A1.  
PD 11-JUL-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 3; Length 789;  
RESULT 914  
ID AAH93388 standard; cDNA; 789 BP.  
DE Human prostate-specific 3' cDNA sequence J1-21.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 789;  
RESULT 915  
ID AAS63480 standard; cDNA; 789 BP.  
DE Human prostate cDNA sequence #32.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 789;  
RESULT 916  
ID AAH02453 standard; cDNA; 789 BP.  
DE Prostate tumour antigen determined 3' cDNA sequence for J1-21.  
PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 789;  
RESULT 917  
ID AAH84702 standard; cDNA; 789 BP.  
DE Human prostate-specific 3' cDNA sequence J1-21.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 789;  
RESULT 918  
ID ACA59289 standard; cDNA; 789 BP.  
DE Prostate cancer therapy associated cDNA #32.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HART/) HARTOCKER S L.  
PA (UTAN/) UTANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNETILL P D.  
PA (HOUN/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOYT T M.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 5; Length 789;

Best Local Similarity 81.2%; Pred. No. 0.14;  
RESULT 919  
ID AAS10031 standard; cDNA; 789 BP.  
DE Human prostate tumour cDNA J1-21.  
PN US6262245-A1.  
PD 17-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 10.7%; Score 61.2; DB 5; Length 789;  
Best Local Similarity 81.2%; Pred. No. 0.14;  
RESULT 920  
ID ABL94852 standard; cDNA; 789 BP.  
DE Human J1-21 3' cDNA sequence SEQ ID NO 32.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIANG/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISK/) LI S X.  
PA (WANG/) WANG A.  
PA (SKET/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
Query Match 10.7%; Score 61.2; DB 6; Length 789;  
Best Local Similarity 81.2%; Pred. No. 0.14;  
RESULT 921  
ID ABS58561 standard; cDNA; 789 BP.  
DE Prostate tumour cDNA #32.  
PN US2002081580-A1.  
PD 27-JUN-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
Query Match 10.7%; Score 61.2; DB 6; Length 789;  
Best Local Similarity 81.2%; Pred. No. 0.14;  
RESULT 922  
ID ACC95016 standard; cDNA; 789 BP.  
DE Prostate tumour specific cDNA sequence SEQ ID 32.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 10.7%; Score 61.2; DB 8; Length 789;  
Best Local Similarity 81.2%; Pred. No. 0.14;  
RESULT 923  
ID ADB13482 standard; cDNA; 789 BP.  
DE Human prostate specific cDNA J1-21.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 10.7%; Score 61.2; DB 10; Length 789;  
Best Local Similarity 81.2%; Pred. No. 0.14;  
RESULT 924  
ID ADG26898 standard; cDNA; 789 BP.  
DE Human prostate-specific cDNA #33.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 10.7%; Score 61.2; DB 10; Length 789;  
Best Local Similarity 81.2%; Pred. No. 0.14;  
RESULT 925  
ID AAA78426 standard; cDNA; 1028 BP.  
DE Human secreted protein gene 46 SEQ ID NO:56.  
PN WO200035937-A1.  
PD 22-JUN-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61.2; DB 3; Length 1028;

Best Local Similarity 60.4%; Pred. No. 0.14;  
RESULT 926  
ID AAS29631 standard; cDNA; 1437 BP.  
DE Human endocrine polypeptide encoding cDNA SEQ ID NO 131.  
PN WO200155364-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61.2; DB 5; Length 1437;  
Best Local Similarity 66.9%; Pred. No. 0.14;  
RESULT 927  
ID AAS02065 standard; cDNA; 1477 BP.  
DE Human MANGO 511 cDNA sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 61.2; DB 4; Length 1477;  
Best Local Similarity 73.6%; Pred. No. 0.14;  
RESULT 928  
ID AAS02102 standard; cDNA; 1477 BP.  
DE Human MANGO 511, variant #1 cDNA sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 61.2; DB 4; Length 1477;  
Best Local Similarity 73.6%; Pred. No. 0.14;  
RESULT 929  
ID AAS02104 standard; cDNA; 1477 BP.  
DE Human MANGO 511, variant #3 cDNA sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 61.2; DB 4; Length 1477;  
Best Local Similarity 73.6%; Pred. No. 0.14;  
RESULT 930  
ID AAS02105 standard; cDNA; 1477 BP.  
DE Human MANGO 511, variant #4 cDNA sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 61.2; DB 4; Length 1477;  
Best Local Similarity 73.6%; Pred. No. 0.14;  
RESULT 931  
ID AAS02103 standard; cDNA; 1477 BP.  
DE Human MANGO 511, variant #2 cDNA sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 61.2; DB 4; Length 1477;  
Best Local Similarity 73.6%; Pred. No. 0.14;  
RESULT 932  
ID ABQ54407 standard; cDNA; 1898 BP.  
DE Human ovarian antigen H86767 cDNA, SEQ ID NO:287.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61.2; DB 6; Length 1898;  
Best Local Similarity 89.2%; Pred. No. 0.14;  
RESULT 933  
ID AAZ41321 standard; cDNA; 2042 BP.  
DE Human normal ovarian tissue derived cDNA 100.  
PN DE19816395-A1.  
PD 07-OCT-1999.  
PA (METR-) METRAGEN GBS GENOMFORSCHUNG MBH.  
Query Match 10.7%; Score 61.2; DB 2; Length 2042;  
Best Local Similarity 89.2%; Pred. No. 0.14;  
RESULT 934  
ID AAS31306 standard; cDNA; 2272 BP.  
DE Human cDNA encoding a novel extracellular matrix protein, Seq ID NO 120.  
PN WO200155368-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61.2; DB 4; Length 2272;  
Best Local Similarity 71.1%; Pred. No. 0.15;

RESULT 935  
ID ABO66630 standard; cDNA; 2272 BP.  
DE Human polynucleotide SEQ ID NO 120.  
PN US2002042386-A1.  
PD 11-APR-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 6; Length 2272;  
RESULT 936  
ID ADCl0652 standard; cDNA; 2272 BP.  
DE Human cDNA from extracellular matrix gene 110.  
PN US2003058975-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 10; Length 2272;  
RESULT 937  
ID ACN88739 standard; DNA; 2310 BP.  
DE Breast cancer related marker, seq id 9889.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 11; Length 2310;  
RESULT 938  
ID AAD05588 standard; cDNA; 2762 BP.  
DE Human secreted protein-encoding gene 10 cDNA clone HTJML75, SEQ ID NO:20.  
PN WO200134627-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 4; Length 2762;  
RESULT 939  
ID ADA40188 standard; cDNA; 2762 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 8; Length 2762;  
RESULT 940  
ID ADC73727 standard; DNA; 2762 BP.  
DE Human secreted protein-related DNA - SEQ ID 360.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 10; Length 2762;  
RESULT 941  
ID ADA56348 standard; DNA; 2762 BP.  
DE Gene encoding human secreted protein #527.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 10; Length 2762;  
RESULT 942  
ID ADU48200 standard; DNA; 3505 BP.  
DE Maize oil-associated gene #18.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAYA/) RAYANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match  
Best Local Similarity 10.7%; Score 61.2; DB 12; Length 3505;  
RESULT 943  
ID ABV59005 standard; cDNA; 196 BP.  
DE Human prostate expression marker cDNA 58996.  
PN

PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 5; Length 196;  
RESULT 944  
ID ABZ08427 standard; cDNA; 290 BP.  
DE Human leukocyte derived cDNA SEQ ID NO 8418.  
PN WO200257414-A2.  
PD 25-JUL-2002.  
PA (BIOC-) BIOCARDIA INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 6; Length 290;  
RESULT 945  
ID ABV60857 standard; cDNA; 352 BP.  
DE Human prostate expression marker cDNA 60848.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 5; Length 352;  
RESULT 946  
ID AA185189 standard; cDNA; 417 BP.  
DE Human polynucleotide SEQ ID NO 3249.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 4; Length 417;  
RESULT 947  
ID AA188584 standard; cDNA; 427 BP.  
DE Human polynucleotide SEQ ID NO 8644.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 4; Length 427;  
RESULT 948  
ID ADL43473 standard; DNA; 438 BP.  
DE Human ovarian cancer DNA marker #17363.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 5; Length 438;  
RESULT 949  
ID ACH28067 standard; cDNA; 488 BP.  
DE Human adult ovary cDNA #6447.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 9; Length 488;  
RESULT 950  
ID ACH22923 standard; cDNA; 489 BP.  
DE Human adult ovary cDNA #1303.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 9; Length 489;  
RESULT 951  
ID AAS29116 standard; cDNA; 583 BP.  
DE cDNA encoding for human DNA-binding protein #87.  
PN WO200155162-A1.

PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61; DB 5; Length 583;  
Best Local Similarity 70.1%; Pred. No. 0.14;  
RESULT 952  
ID ABS68256 standard; cDNA; 583 BP.  
DE cDNA encoding human DNA-binding protein #87.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 10.7%; Score 61; DB 6; Length 583;  
Best Local Similarity 70.1%; Pred. No. 0.14;  
RESULT 953  
ID ADC25250 standard; cDNA; 583 BP.  
DE Human cDNA from extracellular matrix gene 87.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61; DB 10; Length 583;  
Best Local Similarity 70.1%; Pred. No. 0.14;  
RESULT 954  
ID AAV58363 standard; cDNA; 772 BP.  
DE Coding sequence for secreted protein of clone EQ219\_1.  
PN WO9837094-A2.  
PD 27-AUG-1998.  
PA (GEM/) GENETICS INST INC.  
Query Match 10.7%; Score 61; DB 2; Length 772;  
Best Local Similarity 82.4%; Pred. No. 0.15;  
RESULT 955  
ID AAT70132 standard; cDNA to mRNA; 1023 BP.  
DE Max-interacting protein coding sequence (clone 20).  
PN US5624818-A.  
PD 29-APR-1997.  
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
Query Match 10.7%; Score 61; DB 2; Length 1023;  
Best Local Similarity 64.5%; Pred. No. 0.15;  
RESULT 956  
ID AAF21764 standard; DNA; 1066 BP.  
DE Human breast and ovarian cancer associated antigen gene SEQ ID 151.  
PN WO200055173-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61; DB 3; Length 1066;  
Best Local Similarity 60.2%; Pred. No. 0.15;  
RESULT 957  
ID AAQ05879 standard; DNA; 1394 BP.  
DE Placenta-specific protein-9 gene.  
PN EP386733-A.  
PD 12-SEP-1990.  
PA (BEHW) BEHRINGER AG.  
Query Match 10.7%; Score 61; DB 2; Length 1394;  
Best Local Similarity 87.0%; Pred. No. 0.15;  
RESULT 958  
ID AAF97914 standard; cDNA; 1651 BP.  
DE Human secreted protein cDNA, SEQ ID NO: 41.  
PN WO200121658-A1.  
PD 29-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61; DB 4; Length 1651;  
Best Local Similarity 64.9%; Pred. No. 0.15;  
RESULT 959  
ID ADQ24380 standard; DNA; 1781 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7200.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.7%; Score 61; DB 12; Length 1781;  
Best Local Similarity 78.5%; Pred. No. 0.15;  
RESULT 960  
ID AAC90463 standard; cDNA; 2517 BP.  
DE Human uncoupling protein cDNA #12.

PN WO200061614-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 61; DB 3; Length 2517;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 961  
ID AAS75804 standard; cDNA; 2891 BP.  
DE DNA encoding novel human diagnostic protein #11608.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.7%; Score 61; DB 5; Length 2891;  
Best Local Similarity 78.5%; Pred. No. 0.16;  
RESULT 962  
ID AAZ65058 standard; cDNA; 3333 BP.  
DE Membrane-bound protein PRO1106 encoding cDNA.  
PN WO963088-A2.  
PD 09-DEC-1999.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 3; Length 3333;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 963  
ID AAF92086 standard; cDNA; 3334 BP.  
DE Human PRO1106 cDNA.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 4; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 964  
ID AAF44204 standard; cDNA; 3334 BP.  
DE Human PRO1106 (UNQ549) nucleotide sequence SEQ ID NO:288.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 5; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 965  
ID ABS74406 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 6; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 966  
ID ACA64351 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 967  
ID ACA91192 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 968  
ID ACD81569 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 969  
ID ACA60391 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003018183-A1.

PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 970  
ID AC658838 standard; cDNA; 3334 BP.  
DE cDNA encoding human secreted polypeptide PRO1106.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 971  
ID AC6464014 standard; cDNA; 3334 BP.  
DE cDNA encoding human PRO polypeptide #29.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 972  
ID AC691278 standard; cDNA; 3334 BP.  
DE cDNA encoding human PRO polypeptide #29.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 973  
ID ABX80810 standard; cDNA; 3334 BP.  
DE Human secreted/transmembrane protein cDNA, #118.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 974  
ID AC644319 standard; cDNA; 3334 BP.  
DE cDNA encoding human PRO1106 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 975  
ID AC645177 standard; cDNA; 3334 BP.  
DE Human secreted/transmembrane polypeptide PRO1106 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 976  
ID AC693725 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 977  
ID AC667299 standard; cDNA; 3334 BP.  
DE cDNA encoding human secreted polypeptide PRO1106.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 978  
ID AC666272 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003027996-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 979  
ID ABX79490 standard; cDNA; 3334 BP.  
DE Human secreted/transmembrane protein cDNA, #118.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 980  
ID AC693511 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 981  
ID ABX81193 standard; cDNA; 3334 BP.  
DE Novel human secreted or transmembrane protein PRO1291 DNA.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 982  
ID ACD02326 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 983  
ID AC689317 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 984  
ID AC68954 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 985  
ID AC693009 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 986  
ID AC698476 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 987  
ID ABX17093 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 8; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 988  
ID AC67948 standard; cDNA; 3334 BP.



DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 989  
ID ACA63401 standard; cDNA; 3334 BP.  
DE cDNA encoding human PRO polypeptide #29.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 990  
ID ACA88397 standard; cDNA; 3334 BP.  
DE Human secreted and transmembrane polypeptide PRO1106 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 991  
ID ACD81904 standard; cDNA; 3334 BP.  
DE cDNA encoding human PRO1106 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 992  
ID ADB17114 standard; cDNA; 3334 BP.  
DE Human cDNA clone (SeqId 57) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 993  
ID ADA37799 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 994  
ID ADA21485 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1106.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 995  
ID ACH03604 standard; cDNA; 3334 BP.  
DE Human secreted/transmembrane polypeptide PRO 11106 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 996  
ID ADA10272 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1106.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 997  
ID ADA19919 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US200306394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 998  
ID ADB17302 standard; cDNA; 3334 BP.  
DE Human cDNA clone (SeqId 57) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 999  
ID ADA17816 standard; cDNA; 3334 BP.  
DE cDNA encoding human PRO1106 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1000  
ID ADA27924 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1001  
ID ADA20091 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1002  
ID ACD82118 standard; cDNA; 3334 BP.  
DE Human secreted/transmembrane polypeptide PRO 11106 cDNA.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1003  
ID ADA94504 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1004  
ID ADA38729 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1005  
ID ADA92850 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1006  
ID ADA00388 standard; cDNA; 3334 BP.  
DE Human secreted/transmembrane polypeptide PRO 1106 cDNA.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1007  
ID ACH65465 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003044806-A1.

PD 06-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1008  
ID ADA22411 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1106.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1009  
ID ACD39455 standard; cDNA; 3334 BP.  
DE Human cDNA encoding FRO1291.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1010  
ID ADA06577 standard; cDNA; 3334 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #88.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1011  
ID ADA39270 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1012  
ID ADH85630 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1013  
ID ADB96296 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1014  
ID ADB68309 standard; cDNA; 3334 BP.  
DE Human PRO1106 cDNA.  
PN US2003065161-A1.  
PD 03-APR-2003.  
Query Match 10.7%; Score 61; DB 9; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1015  
ID ADB68116 standard; cDNA; 3334 BP.  
DE Human PRO1106 cDNA.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1016  
ID ADB90933 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1017  
ID ADC57768 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.

PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1018  
ID ADC55132 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1019  
ID ADC11999 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1020  
ID ADC07013 standard; cDNA; 3334 BP.  
DE Human PRO1106 cDNA.  
PN US2003050602-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1021  
ID ADC56423 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1022  
ID ADC17192 standard; cDNA; 3334 BP.  
DE cDNA sequence encoding a PRO polypeptide (SeqID 57).  
PN US2003065143-A1.  
PD 03-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1023  
ID ADC07476 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1024  
ID ADC11466 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1025  
ID ADC14990 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003073208-A1.  
PD 17-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1026  
ID ADC52385 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1027  
ID ADC14588 standard; cDNA; 3334 BP.

DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1028  
ID ADD08120 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1029  
ID ADC81945 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1030  
ID ADD07587 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1031  
ID ADC82478 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1032  
ID ADD08658 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1033  
ID ADD06907 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1034  
ID ADC83154 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1035  
ID ADD55261 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1036  
ID ADD30661 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003105299-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1037  
ID ADD56219 standard; cDNA; 3334 BP.

DE Human PRO polynucleotide #88.  
PN US2003079594-A1.  
PD 24-APR-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1038  
ID ADD54657 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1039  
ID ADE26811 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1040  
ID ADE26278 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1041  
ID ADF67215 standard; cDNA; 3334 BP.  
DE Human PRO1106 nucleotide sequence SEQ ID NO:288.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1042  
ID ADG01062 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1043  
ID ADG08615 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1044  
ID ADF95236 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1045  
ID ADH24089 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1046  
ID ADH34115 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.



RESULT 1065  
ID ADH52040 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1066  
ID ADH49895 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1067  
ID ADI25405 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1068  
ID ADH90198 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1069  
ID ADI25375 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1070  
ID ADH97749 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1071  
ID ADI35469 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1072  
ID ADI03597 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1073  
ID ADI11954 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1074  
ID ADH90028 standard; cDNA; 3334 BP.

DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1075  
ID ADH99961 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1076  
ID ADH98429 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1077  
ID ADI11104 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1078  
ID ADI11614 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1079  
ID ADH98259 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1080  
ID ADH98599 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1081  
ID ADH98089 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1082  
ID ABX77894 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #88.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 61; DB 10; Length 3334;  
RESULT 1083  
ID ABX80306 standard; cDNA; 3334 BP.  
DE Novel human secreted or transmembrane protein PRO1391 DNA.  
PN US2002132252-A1.  
PD 19-SEP-2002.

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PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1084  
ID ACB69212 standard; cDNA; 3334 BP.  
DE Human cdna encoding secreted/transmembrane protein PROI106.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1085  
ID ABX90283 standard; cDNA; 3334 BP.  
DE Human secreted/transmembrane protein CDNA, #118.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1086  
ID ABX64129 standard; cDNA; 3334 BP.  
DE CDNA encoding human PROI106 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1087  
ID ADIO5077 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PROI106 CDNA.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1088  
ID ADIO3427 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PROI106 CDNA.  
PN US2003181554-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1089  
ID ADIO4822 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PROI106 CDNA.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1090  
ID ADH78276 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003181658-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1091  
ID ADI19620 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PROI106 CDNA.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1092  
ID ADH90368 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PROI106 CDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1093  
ID ADH90368 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PROI106 CDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match      10.7%; Score 61; DB 10; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1094
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Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1093		
ID AD103087 standard; cDNA; 3334 BP.		
DE Novel human secreted and transmembrane protein PRO1106 cDNA.		
FN US2003181653-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1099		
ID ADH77936 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181666-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1095		
ID ADH97919 standard; cDNA; 3334 BP.		
DE Novel human secreted and transmembrane protein PRO1106 cDNA.		
FN US2003181674-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1096		
ID AD101304 standard; cDNA; 3334 BP.		
DE Novel human secreted and transmembrane protein PRO1106 cDNA.		
FN US2003190669-A1.		
PD 09-OCT-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1097		
ID AD101999 standard; cDNA; 3334 BP.		
DE Novel human secreted and transmembrane protein PRO1106 cDNA.		
FN US2003181652-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1098		
ID AD103257 standard; cDNA; 3334 BP.		
DE Novel human secreted and transmembrane protein PRO1106 cDNA.		
FN US2003181655-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1099		
ID AD111444 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181681-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1100		
ID AD102346 standard; cDNA; 3334 BP.		
DE Novel human secreted and transmembrane protein PRO1106 cDNA.		
FN US2003181650-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1101		
ID AD111784 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181685-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1102		
ID AD111784 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181685-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1103		
ID AD111784 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181685-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1104		
ID AD111784 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181685-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1105		
ID AD111784 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181685-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1106		
ID AD111784 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181685-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1107		
ID AD111784 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181685-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1108		
ID AD111784 standard; cDNA; 3334 BP.		
DE Human PRO polynucleotide #29.		
FN US2003181685-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	10.7%;	Score 61; DB 10; Length 3334
Best Local Similarity	87.0%;	Pred. No. 0.16;
RESULT 1109		
ID AD111		

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RESULT 1102
ID AD104651 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1103
ID ADH79493 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1104
ID AD119450 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1105
ID AD105251 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1106
ID ADH79663 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1107
ID AD101489 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1108
ID AD101659 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1109
ID ADH79833 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1110
ID ADH79833 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1111
ID AD104651 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1112
ID AD102787 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1113
ID ADH78106 standard; cDNA; 3334 BP.
DE Human PRO polynucleotide #29.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1114
ID AD125745 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1115
ID AD125915 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1116
ID ADK65427 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1117
ID ADH98769 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1118
ID ADH80010 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 10; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1119
ID ADL93741 standard; cDNA; 3334 BP.
DE Novel human secreted and transmembrane protein PRO1106 CDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 61; DB 11; Length 3334;
Best Local Similarity 87.0%; Pred. No. 0.16;
RESULT 1120
ID ADC52195 standard; cDNA; 3334 BP.
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DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003130483-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1121  
ID ADF35414 standard; cDNA; 3334 BP.  
DE cDNA encoding human PRO1106 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1122  
ID ADG11664 standard; cDNA; 3334 BP.  
DE cDNA encoding human PRO1106 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1123  
ID ADH06627 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1124  
ID ADH06457 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1125  
ID ADG68878 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1126  
ID ADH27768 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1127  
ID ADH25109 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1128  
ID ADH33741 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1129  
ID ADH02384 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003180839-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1130  
ID ADH07991 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1131  
ID ADG69388 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1132  
ID ADH33209 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1133  
ID ADG83949 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1134  
ID ADH19534 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1135  
ID ADG85493 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1136  
ID ADH06287 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1137  
ID ADH30117 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1138  
ID ADH24429 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180910-A1.  
PD 25-SEP-2003.



PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1139  
ID ADG69558 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1140  
ID ADH07821 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1141  
ID ADG85833 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1142  
ID ADH3379 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1143  
ID ADH33571 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1144  
ID ADH33911 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1145  
ID ADH01121 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1146  
ID ADG69728 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1147  
ID ADH21027 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 10.7%; Score 61; DB 12; Length 3334;

Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1148  
ID ADH02214 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1149  
ID ADG69218 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1150  
ID ADG86003 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1151  
ID ADH24939 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1152  
ID ADH35556 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1153  
ID ADH20067 standard; cDNA; 3334 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1106.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1154  
ID ADH02554 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1155  
ID ADG69048 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1156  
ID ADH07651 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;

RESULT 1157  
ID ADG86173 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1158  
ID ADH24769 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1159  
ID ADH25817 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1160  
ID ADH38383 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1161  
ID ADH52209 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1162  
ID ADH52209 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1163  
ID ADH49576 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1164  
ID ADH90538 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1165  
ID ADI11274 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1166  
ID ADH79082 standard; cDNA; 3334 BP.

ID ADH98939 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1167  
ID ADI02169 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1168  
ID ADH90708 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1169  
ID ADJ98583 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1170  
ID ADJ98753 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1171  
ID ADH78912 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1172  
ID ADJ99146 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1173  
ID ADJ99316 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1174  
ID ADJ98934 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1175  
ID ADH79082 standard; cDNA; 3334 BP.

DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1176  
ID ADK00942 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1177  
ID ADK14463 standard; cDNA; 3334 BP.  
DE Novel human secreted and transmembrane protein PRO1106 cDNA.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1178  
ID ADM80912 standard; cDNA; 3334 BP.  
DE Human PRO polynucleotide #29.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 61; DB 12; Length 3334;  
Best Local Similarity 87.0%; Pred. No. 0.16;  
RESULT 1179  
ID AAI58310 standard; cDNA; 4419 BP.  
DE Human polynucleotide SEQ ID NO 513.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.7%; Score 61; DB 4; Length 4419;  
Best Local Similarity 58.6%; Pred. No. 0.16;  
RESULT 1180  
ID ADQ98517 standard; cDNA; 4419 BP.  
DE DNA encoding human GPCR-like protein seqid 187.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.7%; Score 61; DB 5; Length 4419;  
Best Local Similarity 58.6%; Pred. No. 0.16;  
RESULT 1181  
ID ADB48277 standard; cDNA; 4419 BP.  
DE Novel human cDNA SEQ ID NO 187.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 10.7%; Score 61; DB 9; Length 4419;  
Best Local Similarity 58.6%; Pred. No. 0.16;  
RESULT 1182  
ID ABV58256 standard; cDNA; 304 BP.  
DE Human prostate expression marker cDNA 58247.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.7%; Score 60.8; DB 5; Length 304;  
Best Local Similarity 89.0%; Pred. No. 0.15;  
RESULT 1183  
ID ACN88196 standard; DNA; 375 BP.  
DE Breast cancer related marker, seq id 9346.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 60.8; DB 11; Length 375;

Best Local Similarity 71.3%; Pred. No. 0.15;  
RESULT 1184  
ID ADF50926 standard; cDNA; 400 BP.  
DE Human cysteine rich intestinal protein 1 cDNA (seqid 25).  
PN WO2003060164-A1.  
PD 24-JUL-2003.  
PA (ARCT-) ARCTURUS ENG INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 10.7%; Score 60.8; DB 10; Length 400;  
Best Local Similarity 80.7%; Pred. No. 0.15;  
RESULT 1185  
ID AAI86835 standard; cDNA; 435 BP.  
DE Human polynucleotide SEQ ID NO 6895.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.7%; Score 60.8; DB 4; Length 435;  
Best Local Similarity 90.3%; Pred. No. 0.15;  
RESULT 1186  
ID ACN49982 standard; cDNA; 441 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-033-Q6-N6-F1, SEQ:4763.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 10.7%; Score 60.8; DB 13; Length 441;  
Best Local Similarity 69.2%; Pred. No. 0.15;  
RESULT 1187  
ID ABV58572 standard; cDNA; 455 BP.  
DE Human prostate expression marker cDNA 58563.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.7%; Score 60.8; DB 5; Length 455;  
Best Local Similarity 87.8%; Pred. No. 0.15;  
RESULT 1188  
ID ACN51998 standard; cDNA; 464 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-E3, SEQ:6779.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 10.7%; Score 60.8; DB 13; Length 464;  
Best Local Similarity 80.7%; Pred. No. 0.15;  
RESULT 1189  
ID ACH39052 standard; cDNA; 465 BP.  
DE Human foetal brain cDNA #419.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 10.7%; Score 60.8; DB 9; Length 465;  
Best Local Similarity 70.2%; Pred. No. 0.15;  
RESULT 1190  
ID ACN56061 standard; cDNA; 474 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-031-Q6-N6-F7, SEQ:10842.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 10.7%; Score 60.8; DB 13; Length 474;  
Best Local Similarity 80.7%; Pred. No. 0.15;  
RESULT 1191  
ID ACH44386 standard; cDNA; 493 BP.

DE Human foetal brain cDNA #5111.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 9; Length 493;  
 RESULT 1192  
 ID ABV5433 standard; cDNA; 499 BP.  
 DE Human prostate expression marker cDNA 54324.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 5; Length 499;  
 RESULT 1193  
 ID ACN61287 standard; cDNA; 512 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-035-Q1-N6-E12, SEQ:16068.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIRG/) ZIEGLER T E.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 13; Length 512;  
 RESULT 1194  
 ID AAS60634 standard; cDNA; 520 BP.  
 DE Human cancer agent-resistance marker #389.  
 PN WO200179556-A2.  
 PD 25-OCT-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 4; Length 520;  
 RESULT 1195  
 ID ABV58049 standard; cDNA; 564 BP.  
 DE Human prostate expression marker cDNA 58040.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 5; Length 564;  
 RESULT 1196  
 ID ACN87651 standard; DNA; 635 BP.  
 DE Breast cancer related marker, seq id 8801.  
 PN US2003099974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 11; Length 635;  
 RESULT 1197  
 ID ADN37279 standard; cDNA; 663 BP.  
 DE Wheat chaumatin-like protein encoding cDNA SEQ ID NO:23.  
 PN WO2004035790-A1.  
 PD 29-APR-2004.  
 PA (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.  
 PA (GRAI-) GRAINS RES & DEV CORP.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 12; Length 663;  
 RESULT 1198  
 ID ADN37275 standard; cDNA; 663 BP.  
 DE Wheat chaumatin-like protein encoding cDNA SEQ ID NO:19.  
 PN WO2004035790-A1.  
 PD 29-APR-2004.  
 PA (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.  
 PA (GRAI-) GRAINS RES & DEV CORP.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 12; Length 663;  
 RESULT 1199  
 ID ABQ54901 standard; cDNA; 783 BP.

DE Human ovarian antigen HLYAR61 cDNA, SEQ ID NO:781.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 6; Length 783;  
 RESULT 1200  
 ID ACC00704 standard; cDNA; 1249 BP.  
 DE Zea mays oil trait related cDNA sequence SEQ ID NO:157.  
 PN WO2003002751-A2.  
 PD 09-JAN-2003.  
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 8; Length 1249;  
 RESULT 1201  
 ID ADQ23409 standard; DNA; 1302 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6229.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 12; Length 1302;  
 RESULT 1202  
 ID AAD17173 standard; cDNA; 1779 BP.  
 DE Human ion channel-31d6 (ion31d6) cDNA.  
 PN WO200168849-A2.  
 PD 20-SEP-2001.  
 PA (PHAA-) PHARMACIA & UPJOHN CO.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 4; Length 1779;  
 RESULT 1203  
 ID ACD01559 standard; cDNA; 1779 BP.  
 DE cDNA clone Ion31c4 encoding human ion channel.  
 PN WO2003023014-A2.  
 PD 20-MAR-2003.  
 PA (PHAA-) PHARMACIA & UPJOHN CO.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 8; Length 1779;  
 RESULT 1204  
 ID ADE29300 standard; cDNA; 1779 BP.  
 DE Novel human ion channel ion-31d6 cDNA.  
 PN US2003190714-A1.  
 PD 09-OCT-2003.  
 PA (ROBE-) ROBERTS S L.  
 PA (BENU-) BENJAMIN C W.  
 PA (KARN-) KARNOVSKY A M.  
 PA (RUBL-) RUBLE C L.  
 PA (LINS-) LINSKE-O'CONNELL L I.  
 PA (WANG-) WANG.  
 PA (LIUD-) LIU D.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 10; Length 1779;  
 RESULT 1205  
 ID ABS57347 standard; cDNA; 1851 BP.  
 DE cDNA encoding human cancer cell growth suppressing protein P6068.  
 PN CN1351080-A.  
 PD 29-MAY-2002.  
 PA (SHAN-) SHANGHAI INST ONCOLOGY.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 6; Length 1851;  
 RESULT 1206  
 ID AAC81052 standard; cDNA; 1859 BP.  
 DE Human secreted protein cDNA sequence #25.  
 PN WO200063330-A2.  
 PD 26-OCT-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 60.8; DB 3; Length 1859;  
 RESULT 1207  
 ID ACD01569 standard; DNA; 1865 BP.  
 DE DNA clone SHT-3C encoding human ion channel.  
 PN WO2003023014-A2.

PD 20-MAR-2003.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Query Match 10.7%; Score 60.8; DB 8; Length 1865;  
Best Local Similarity 71.4%; Pred. No. 0.17;  
RESULT 1208  
ID ABK14606 standard; DNA; 2131 BP.  
DE DNA encoding novel human ion channel, 5HT3C.  
PD WO200202639-A2.  
PD 10-JUN-2002.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Query Match 10.7%; Score 60.8; DB 6; Length 2131;  
Best Local Similarity 71.4%; Pred. No. 0.17;  
RESULT 1209  
ID ADE54669 standard; DNA; 2287 BP.  
DE Human gene NM\_003026, SEQ ID NO 474.  
PD WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.7%; Score 60.8; DB 10; Length 2287;  
Best Local Similarity 90.3%; Pred. No. 0.17;  
RESULT 1210  
ID AAC76596 standard; cDNA; 2429 BP.  
DE Human ORFX ORF2151 polynucleotide sequence SEQ ID NO:4301.  
PD WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.7%; Score 60.8; DB 3; Length 2429;  
Best Local Similarity 90.3%; Pred. No. 0.17;  
RESULT 1211  
ID AAD05229 standard; cDNA; 3143 BP.  
DE Human secreted protein-encoding gene 10 cDNA clone HHEP23, SEQ ID NO:20.  
PD WO200134629-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.7%; Score 60.8; DB 4; Length 3143;  
Best Local Similarity 63.9%; Pred. No. 0.17;  
RESULT 1212  
ID AA161619 standard; cDNA; 3508 BP.  
DE Human secreted protein clone 10311\_8 nucleotide sequence SEQ ID NO:3.  
PD WO200009552-A1.  
PD 24-FEB-2000.  
PA (GEMY ) GENETICS INST INC.  
Query Match 10.7%; Score 60.8; DB 3; Length 3508;  
Best Local Similarity 85.0%; Pred. No. 0.17;  
RESULT 1213  
ID ACN47721 standard; cDNA; 180 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-014-Q1-K6-B9, SEQ:2502.  
PD US200413340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 10.6%; Score 60.6; DB 13; Length 180;  
Best Local Similarity 79.1%; Pred. No. 0.16;  
RESULT 1214  
ID ABV58603 standard; cDNA; 267 BP.  
DE Human prostate expression marker cDNA 58594.  
PD WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.6%; Score 60.6; DB 5; Length 267;  
Best Local Similarity 69.8%; Pred. No. 0.16;  
RESULT 1215  
ID ACN54560 standard; cDNA; 432 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-K6-D3, SEQ:9341.  
PD US200413340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.

Query Match 10.6%; Score 60.6; DB 13; Length 432;  
Best Local Similarity 75.0%; Pred. No. 0.17;  
RESULT 1216  
ID ADC38691 standard; cDNA; 438 BP.  
DE Human cDNA encoding a secreted protein #25.  
PD US2002193567-A1.  
PD 19-DEC-2002.  
PA (GEMY ) GENETICS INST INC.  
Query Match 10.6%; Score 60.6; DB 10; Length 438;  
Best Local Similarity 88.0%; Pred. No. 0.17;  
RESULT 1217  
ID ACH22246 standard; cDNA; 460 BP.  
DE Human adult ovary cDNA #626.  
PD US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 10.6%; Score 60.6; DB 9; Length 460;  
Best Local Similarity 88.0%; Pred. No. 0.17;  
RESULT 1218  
ID AA185012 standard; cDNA; 497 BP.  
DE Human polynucleotide SEQ ID NO 5072.  
PD WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.6%; Score 60.6; DB 4; Length 497;  
Best Local Similarity 78.4%; Pred. No. 0.17;  
RESULT 1219  
ID ACN54072 standard; cDNA; 640 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.  
PD US200413340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 10.6%; Score 60.6; DB 13; Length 640;  
Best Local Similarity 88.0%; Pred. No. 0.17;  
RESULT 1220  
ID AAN40162 standard; cDNA; 766 BP.  
DE Sequence of preproparathyroid cDNA.  
PD WO8401173-A.  
PD 29-MAR-1984.  
PA (IMMU-) IMMUNO NUCLEAR CORP.  
Query Match 10.6%; Score 60.6; DB 1; Length 766;  
Best Local Similarity 88.0%; Pred. No. 0.17;  
RESULT 1221  
ID AAC74426 standard; cDNA; 860 BP.  
DE Human secreted protein gene 31 SEQ ID NO:41.  
PD WO200058496-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.6%; Score 60.6; DB 3; Length 860;  
Best Local Similarity 88.0%; Pred. No. 0.17;  
RESULT 1222  
ID AAT72173 standard; cDNA to mRNA; 882 BP.  
DE Alzheimer's disease DNA sequence from plaamid pGCS1180.  
PD WO9721807-A1.  
PD 19-JUN-1997.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 10.6%; Score 60.6; DB 2; Length 882;  
Best Local Similarity 88.0%; Pred. No. 0.17;  
RESULT 1223  
ID AAC89723 standard; cDNA; 1091 BP.  
DE Maize Zmgen1-1 glucanase cDNA.  
PD WO200073470-A2.  
PD 07-DEC-2000.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 10.6%; Score 60.6; DB 4; Length 1091;  
Best Local Similarity 88.0%; Pred. No. 0.18;

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RESULT 1224
ID ABX95035 standard; cDNA; 1091 BP.
PD cDNA encoding maize coleoptile endo-1,3,1,4-beta-glucanase.
PN US6501008-B1.
PA (REGC ) UNIV CALIFORNIA.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1091;
  RESULT 1225
  ID AAA39072 standard; cDNA; 1157 BP.
  DE Human secreted protein gene 21 SEQ ID NO:31.
  PN WO200017222-A1.
  PD 30-MAR-2000.
  PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 3; Length 1157;
  RESULT 1226
  ID ACMA0941 standard; cDNA; 1194 BP.
  DE Tumor-associated antigenic target (TAT) cDNA DNA326971, SEQ ID NO:6056.
  PN 15-APR-2004.
  PD 15-APR-2004.
  PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 13; Length 1194;
  RESULT 1227
  ID ACCT4280 standard; cDNA; 1233 BP.
  DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
  PN US2003027275-A1.
  PD 06-FEB-2003.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1233;
  RESULT 1228
  ID AA546043 standard; cDNA; 1234 BP.
  DE Human DNA encoding PRO polypeptide sequence #119.
  PN WO200168848-A2.
  PD 20-SEP-2001.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 4; Length 1234;
  RESULT 1229
  ID AAF92089 standard; cDNA; 1234 BP.
  DE Human PRO3566 cDNA.
  PN WO200116318-A2.
  PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 4; Length 1234;
  RESULT 1230
  ID ABS74409 standard; cDNA; 1234 BP.
  DE Human cDNA encoding secreted/transmembrane protein PRO3566.
  PN US2002119130-A1.
  PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 6; Length 1234;
  RESULT 1231
  ID ACA89493 standard; cDNA; 1234 BP.
  DE cDNA encoding human PRO polypeptide #119.
  PN US2003036141-A1.
  PD 20-FEB-2003.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1232
  ID ACA73503 standard; cDNA; 1234 BP.
  DE Human secreted/transmembrane protein (PRO) cDNA #119.
  PN US2003036146-A1.
  PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1233
  ID ACA05818 standard; cDNA; 1234 BP.
  DE Human secreted/transmembrane protein (PRO) cDNA #119.
  RESULT 1234
  ID US2003036162-A1.
  PD 20-FEB-2003.
  PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1235
  ID ACB66652 standard; cDNA; 1234 BP.
  DE cDNA encoding human PRO protein #119.
  PN US2003036137-A1.
  PD 20-FEB-2003.
  PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1236
  ID ACA91195 standard; cDNA; 1234 BP.
  DE Novel human secreted and transmembrane protein PRO3566 cDNA.
  PN US2003018173-A1.
  PD 23-JUN-2003.
  PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1237
  ID ACD81572 standard; cDNA; 1234 BP.
  DE Human cDNA encoding secreted/transmembrane protein PRO3566.
  PN US2003009013-A1.
  PD 09-JUN-2003.
  PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1238
  ID ACF19613 standard; cDNA; 1234 BP.
  DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
  PN US2003040063-A1.
  PD 27-FEB-2003.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1239
  ID ACD21901 standard; cDNA; 1234 BP.
  DE Human secreted/transmembrane protein (PRO) cDNA #119.
  PN US2003027267-A1.
  PD 06-FEB-2003.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1240
  ID ACF13066 standard; cDNA; 1234 BP.
  DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
  PN US2003036160-A1.
  PD 20-FEB-2003.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1241
  ID ACD25169 standard; cDNA; 1234 BP.
  DE Human secreted/transmembrane protein (PRO) cDNA #119.
  PN US2003044925-A1.
  PD 06-MAR-2003.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1242
  ID ACF00218 standard; cDNA; 1234 BP.
  DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
  PN US2003034474-A1.
  PD 20-MAR-2003.
  PA (GETH ) GENENTECH INC.
Query Match
  Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;
  RESULT 1243
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ID ACA60394 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1244  
ID ACA72275 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1245  
ID ACD04799 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1246  
ID ACD18260 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1247  
ID ACD08267 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1248  
ID ACA88701 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1249  
ID ACA70143 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1250  
ID ACD12365 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1251  
ID ACD15908 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1252  
ID ACD23476 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1253  
ID ACD17953 standard; cDNA; 1234 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1254  
ID ACC88240 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1255  
ID ACD21594 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1256  
ID ACD18661 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1257  
ID ACA58841 standard; cDNA; 1234 BP.  
DE cDNA encoding human secreted polypeptide PRO3566.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1258  
ID ABX98271 standard; cDNA; 1234 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 237.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1259  
ID ACD14022 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1260  
ID ACD09802 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1261  
ID ACC88547 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1262  
ID ACD21287 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1263  
ID ABX75659 standard; cDNA; 1234 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3566.

PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1264  
ID ACA64017 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #32.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1265  
ID ABX97862 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1266  
ID ACA97338 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1267  
ID ACA57801 standard; cDNA; 1234 BP.  
DE Human PRO3566 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1268  
ID ACD14329 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1269  
ID ACC91112 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1270  
ID ACC88854 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1271  
ID ACD07051 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1272  
ID ACA67502 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1273  
ID ACC81557 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.

PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1274  
ID ACA91281 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #32.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1275  
ID ACC89161 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1276  
ID ACC86517 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1277  
ID ACC89775 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1278  
ID ACC92954 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1279  
ID ACA72582 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1280  
ID ACA89100 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1281  
ID ACA69836 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1282  
ID ACA96979 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 8; Length 1234;  
Pred. No. 0.18;  
RESULT 1283  
ID ACA90975 standard; cDNA; 1234 BP.  
DE Human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032108-A1.



PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1284  
ID ACA70757 standard; cDNA, 1234 BP.  
DE Human secreted/transmembrane protein (PRO) CDNA #119.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1285  
ID ACA95267 standard; cDNA, 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1286  
ID ACC96210 standard; cDNA, 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003032763-A1.  
PD 06-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1287  
ID ACD45180 standard; cDNA, 1234 BP.  
DE Human secreted/transmembrane polypeptide PRO3566 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1288  
ID ACC93082 standard; cDNA, 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1289  
ID ACD12690 standard; cDNA, 1234 BP.  
DE Human secreted/transmembrane protein (PRO) CDNA #119.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1290  
ID ACF19920 standard; cDNA, 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1291  
ID ABX76864 standard; cDNA, 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1292  
ID ACA73196 standard; cDNA, 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003023300-A1.  
PD 30-JAN-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1293  
ID ACA68739 standard; cDNA, 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.

Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1294  
ID ACA74583 standard; cDNA, 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1295  
ID ACA70450 standard; cDNA, 1234 BP.  
DE Human secreted/transmembrane protein (PRO) CDNA #119.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1296  
ID ACD14636 standard; cDNA, 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1297  
ID ACA93728 standard; cDNA, 1234 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO3566.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1298  
ID ACA68308 standard; cDNA, 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1299  
ID ABX98773 standard; cDNA, 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1300  
ID ACA67302 standard; cDNA, 1234 BP.  
DE cDNA encoding human secreted polypeptide PRO3566.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1301  
ID ACC81250 standard; cDNA, 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US200302120-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1302  
ID ACA95574 standard; cDNA, 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1303  
ID ACD04492 standard; cDNA, 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;

Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1304  
ID ACC87933 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1305  
ID ACF12595 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1306  
ID ACH66275 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1307  
ID ACA96310 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1308  
ID ACA65084 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1309  
ID ACA73810 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1310  
ID ACA74222 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1311  
ID ACA96617 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1312  
ID ACD10723 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1313  
ID ACC91419 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1314  
ID ACC92033 standard; cDNA; 1234 BP.

RESULT 1314  
ID ACD02754 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1315  
ID ACC87319 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1316  
ID ACC85903 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1317  
ID ACA65391 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1318  
ID ACA94208 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1319  
ID ACA97952 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1320  
ID ACA91454 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1321  
ID ACA90668 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1322  
ID ACD16215 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1323  
ID ACD17376 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1324  
ID ACC92033 standard; cDNA; 1234 BP.

DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1325  
ID ACDD2329 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1326  
ID ACA74890 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1327  
ID ACA31761 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1328  
ID ACA89320 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1329  
ID ACA71405 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1330  
ID ACC90805 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1331  
ID ACA65815 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO protein #119.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1332  
ID ACA8957 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1333  
ID ACA94960 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1334  
ID ACD16522 standard; cDNA; 1234 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1335  
ID ACD15601 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1336  
ID ACA98479 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #32.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1337  
ID ABX16704 standard; cDNA; 1234 BP.  
DE Human cDNA encoding secreted/transmembrane protein #119.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 8; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1338  
ID ACA63404 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #32.  
PN US2003032042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1339  
ID ACA97645 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1340  
ID ACA99094 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1341  
ID ACC91726 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1342  
ID ACD1137 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1343  
ID ACD14987 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;

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RESULT 1344
ID ACD11751 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1345
ID ACC95880 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1346
ID ACF16443 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054455-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1347
ID ACF02561 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049741-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1348
ID ACF02868 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049743-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1349
ID ACF21455 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049769-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1350
ID ACF10139 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068743-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1351
ID ACF78032 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054479-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1352
ID ACD46737 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068685-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1353
ID ACD49500 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1354
ID ACD8957 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068752-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1355
ID ACD8957 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068752-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1356
ID ACD84352 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068701-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1357
ID ACD99126 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003068755-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1358
ID ADA77989 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003073180-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1359
ID ACF48968 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1360
ID ACD09188 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US200306131-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1361
ID ACF11981 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1362
ID ACF41215 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054459-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1363
ID ACF41215 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054459-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
RESULT 1364
ID ACF41215 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054459-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;
Pred. No. 0.18;
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Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1363  
ID ACF15829 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1364  
ID ACF16136 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1365  
ID ACD31963 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1366  
ID ACF18771 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1367  
ID ACF09218 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1368  
ID ACF78339 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1369  
ID ACF51938 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1370  
ID ACF26425 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1371  
ID ACF24218 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1372  
ID ACF63529 standard; cDNA; 1234 BP.

DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1373  
ID ACF50403 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1374  
ID ACH07874 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1375  
ID ACF13680 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1376  
ID ACD41606 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1377  
ID ACF32019 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1378  
ID ACF23297 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1379  
ID ACF39887 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1380  
ID ACD45509 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
RESULT 1381  
ID ACF53166 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.

PN US2003068721-A1.  
PA 10-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF27346 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068699-A1.  
PA 10-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF45184 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068707-A1.  
PA 10-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF29802 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073175-A1.  
PA 17-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACD9878 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068695-A1.  
PA 10-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACD84659 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003068703-A1.  
PA 10-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACD84659 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003068703-A1.  
PA 10-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACD98819 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003068732-A1.  
PA 10-APR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF7711 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003082717-A1.  
PA 01-MAY-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF76804 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104548-A1.  
PA 05-JUN-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF49789 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104542-A1.  
PA 05-JUN-2003.

Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF50096 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104543-A1.  
PA 05-JUN-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACD09495 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036127-A1.  
PA 20-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACD08574 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040061-A1.  
PA 27-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACH03607 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane polypeptide PRO 3566 cDNA.  
PN US2003018172-A1.  
PA 23-JAN-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF12288 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036130-A1.  
PA 20-FEB-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACC94796 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054468-A1.  
PA 20-MAR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACD22515 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054470-A1.  
PA 20-MAR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACF15215 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003044917-A1.  
PA 06-MAR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACC97310 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003044929-A1.  
PA 06-MAR-2003.  
Query Match  
Best Local Similarity 10.6%; Score 60.6; DB 9; Length 1234;  
Pred. No. 0.18;  
ID ACC92340 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003059880-A1.  
PA 27-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1401  
ID ACF13987 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1402  
ID ACF14294 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1403  
ID ACF09525 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1404  
ID ACD45816 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1405  
ID ACD47965 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1406  
ID ACD67696 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1407  
ID ACF25504 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1408  
ID ACF29188 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1409  
ID ACD64966 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1410  
ID ACD84045 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1411  
ID ACD88036 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1412  
ID ACF30723 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1413  
ID ACF32326 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1414  
ID ACH11986 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1415  
ID ACH12293 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1416  
ID ADA19925 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1417  
ID ACD40685 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1418  
ID ADB17308 standard; cDNA; 1234 BP.  
DE Human cDNA clone (SeqID 63) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;

RESULT 1419  
ID ACF18157 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1420  
ID ACF08604 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US200304978-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1421  
ID ACF31405 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1422  
ID ACF52245 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1423  
ID ACD50114 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US200306873-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1424  
ID ACF38817 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1425  
ID ACF26732 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1426  
ID ACF24832 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1427  
ID ACF46412 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1428  
ID ACF27960 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1429  
ID ACD89264 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1430  
ID ACF63836 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1431  
ID ACF60476 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1432  
ID ACHI2600 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1433  
ID ACHI0023 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1434  
ID ACD03878 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1435  
ID ACD10416 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1436  
ID ACD12058 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1437  
ID ACF42443 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.



Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1438  
ID ACF18464 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1439  
ID ACF02254 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1440  
ID ACF21762 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1441  
ID ACF10446 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1442  
ID ACF33898 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1443  
ID ACF44860 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1444  
ID ACD90492 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1445  
ID ACD91105 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1446  
ID ACF30416 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;

RESULT 1447  
ID ACD87115 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1448  
ID ACF60169 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1449  
ID ACF46719 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1450  
ID ACF75576 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1451  
ID ADA79781 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1452  
ID ACF17236 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1453  
ID ACF22990 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1454  
ID ACF07990 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1455  
ID ACF08297 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1456  
ID ACF40601 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064448-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1457  
ID ACF53780 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1458  
ID ACD47044 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1459  
ID ACF47947 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1460  
ID ACF47333 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1461  
ID ACF46105 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1462  
ID ACD86194 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1463  
ID ACF52552 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1464  
ID ACF52859 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1465  
ID ACF64852 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;

RESULT 1466  
ID ACF76497 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1467  
ID ACF61397 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1468  
ID ACF61704 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1469  
ID ACD30735 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1470  
ID ACD31656 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1471  
ID ACD32577 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1472  
ID ADA20097 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1473  
ID ACD82121 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane polypeptide PRO 3566 cDNA.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1474  
ID ACF17543 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1475  
ID ACF07376 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.

PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1476  
ID ACF20534 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1477  
ID ACF20841 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1478  
ID ACF21148 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1479  
ID ACD47658 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1480  
ID ACF47640 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1481  
ID ACF53473 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US200306879-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1482  
ID ACD86808 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1483  
ID ACH05056 standard; cDNA; 1234 BP.  
DE CDNA encoding human PRO polypeptide #119.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1484  
ID ACF44553 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1485  
ID ADA81508 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1486  
ID ACD22208 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1487  
ID ACD24555 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1488  
ID ACD39758 standard; cDNA; 1234 BP.  
DE CDNA encoding human PRO polypeptide #119.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1489  
ID ACD40065 standard; cDNA; 1234 BP.  
DE CDNA encoding human PRO polypeptide #119.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1490  
ID ACF13373 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1491  
ID ACF03175 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1492  
ID ACF78646 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1493  
ID ACF11367 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1494  
ID ACF50710 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SRQ ID NO:237.

PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1495  
ID ACF34205 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1496  
ID ACD46430 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1497  
ID ACD48272 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1498  
ID ACF27653 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1499  
ID ACF24525 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;  
RESULT 1500  
ID ACD85580 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 60.6; DB 9; Length 1234;  
Best Local Similarity 79.1%; Pred. No. 0.18;